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(54) Title: **PROTEIN COMPLEXES OF CELLULAR NETWORKS UNDERLYING THE DEVELOPMENT OF CANCER AND OTHER DISEASES**

(57) Abstract: The present invention relates to protein complexes involved in cellular processes which have been shown to be critical for the development of various forms of cancer, component proteins of the said complexes, fragments and derivatives of the component proteins, and antibodies specific to the complexes. The present invention also relates to methods for use of the complexes and their interacting proteins in, inter alia, screening, diagnosis, and therapy, as well as to methods of preparing the complexes.



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PROTEIN COMPLEXES OF CELLULAR NETWORKS UNDERLYING THE DEVELOPMENT OF CANCER AND OTHER DISEASES

1. FIELD OF THE INVENTION

The present invention relates to protein complexes involved in cellular processes which have been shown to be critical for the development of various forms of cancer, component proteins of the said complexes, fragments and derivatives of the component proteins, and antibodies specific to the complexes. The present invention also relates to methods for use of the complexes and their interacting proteins in, inter alia, screening, diagnosis, and therapy, as well as to methods of preparing the complexes.

2. BACKGROUND OF THE INVENTION

Despite enormous efforts, cancer still remains as one of the major types of diseases affecting humans. Although significant progress has been made in the development of therapies, the situation in the cancer field in general, an urgent need for new therapies, i.e. new medicaments exists. To progress, a better understanding of the molecular mechanisms is necessary, serving as a basis for a directed identification of suitable drug targets. To further address the biological context of proteins which have been identified to be key players in the development of several cancers, protein interactors were searched for. By applying a novel approach, it was shown that the proteins, rather than interacting with individual proteins, form aggregations which could also be described as "protein complexes". The proteins which have been analysed as being key players in processes underlying the development of cancer are further described below.

Pot1

In all eukaryotic species the ends of chromosomes have specialized non-coding DNA sequences that, together with associated proteins, are known as telomeres. Telomeres act as protective caps, preventing both degradation of the ends of chromosomes and their recognition as double-strand breaks, which otherwise would result in aberrant recombination. Telomeric DNA consists of simple tandem repeats of guanine-rich sequences (hexanucleotide repeats d(TTAGGG) in vertebrates). The extreme 3' end is

single stranded and typically 100-200 bases long. It is extensively associated with a variety of proteins. One of them is the Pot1 protein (protection of telomeres) which was described in fission yeast and humans.

However, despite various lines of evidence were presented so far, the full biological context of Pot1 and thus, the role of the proteins associated with Pot1 in the cell and particularly in pathogenic conditions have remained largely elusive.

Her2

Growth factors and their transmembrane receptor tyrosine kinases play important roles in cell proliferation, survival, migration and differentiation. One group of growth factors, comprising epidermal growth factor (EGF)-like proteins and neuregulins, stimulates cells to divide by activating members of the EGF receptor (EGFR) family, which consists of the EGFR itself and the receptors known as HER2-4. Her receptors exist as monomers but dimerize on ligand binding. No Her2-specific ligand has been identified but Her2 is the preferred heterodimerization partner for other Her receptors. Amplification of the Her2 gene or overexpression of the Her2 protein is associated with malignancy and a poor prognosis in breast cancer.

Thus, despite various lines of evidence were presented so far, the full biological context of Her2 and thus, the role of the proteins associated with Her2 in the cell and particularly in pathogenic conditions have remained largely elusive.

Ringo1

Cyclin-dependent kinases (Cdks) are essential regulators of the eukaryotic cell division cycle. Cdks are subject to many modes and levels of regulation in response to both intracellular and extracellular signals. They are activated through their association with regulatory subunits called cyclins that are synthesized and degraded in a cell cycle-dependent manner. CDK-cyclin complexes are in turn regulated by the cyclin-dependent kinase inhibitors (CKIs), which generally inhibit cell cycle progression. Recently it has been shown that Cdk1 (Cdc2) and Cdk2 can also be activated by a protein called Ringo. Ringo has no similarity to cyclins at the amino acid sequence level. Cdk-Ringo complexes may be active under conditions in which cyclin-bound Cdks are inhibited and therefore play different regulatory roles.

Thus, despite various lines of evidence were presented so far, the full biological context of Ringo and thus, the role of the proteins associated with Ringo in the cell and particularly in pathogenic conditions have remained largely elusive.

Gab1

The GAB1 complex plays an important role in various cytokines, growth factors, and antigen receptors signaling. Several signaling molecules, such as MET (HGFR), EGFR, SHP2, PI 3-kinase, GRB2, SHIP2, SHC, SOS, PLC gamma, and CRK, have been found associated directly or indirectly with GAB1. GAB1 is expressed in all tissues examined except liver, lung, and kidney. The larger splice variant was cloned and used in this experiment as a entry point of retrieval. We have seen, that complex formation is mediated via tyrosine phosphorylation of GAB1 (data available in a separate document). Upon induction of tyrosine phosphorylation with vanadate as well as HGF, we have identified most of the known interactor, validating our findings, as well as several novel components that include, detailed below that may influence GAB1 activity and play important roles in proliferation and metastatic signaling. We have also identified several novel interactors in the absence of tyrosine phosphorylation that could be sequestered by GAB1 to keep them inactive.

However, despite various lines of evidence were presented so far, the full biological context of Gab1 and thus, the role of the proteins associated with Gab1 in the cell and particularly in pathogenic conditions have remained largely elusive.

Bcl2

Bcl-2 family proteins are key regulators of programmed cell death. The Bcl-2 family includes both anti- and pro-apoptotic proteins with opposing biological functions in either inhibiting or promoting cell death. High expression of anti-apoptotic members such as Bcl-2 and Bcl-XL commonly found in human cancers contributes to neoplastic cell expansion and interferes with the therapeutic action of many chemotherapeutic drugs. The functional blockade of Bcl-2 or Bcl-XL could either restore the apoptotic process in tumor cells or sensitize these tumors for chemo- and radiotherapies.

Thus, despite various lines of evidence were presented so far, the full biological context of Bcl-2 and thus, the role of the proteins associated with Bcl-2 in the cell and particularly in pathogenic conditions have remained largely elusive.

3. SUMMARY OF THE INVENTION

An object of the present invention was to identify protein complexes formed around protein which have been shown to be critical for the development of various forms of cancer, component proteins of the said complexes, fragments and derivatives of the component proteins, and antibodies specific to the complexes. The present invention also relates to methods for use of these proteins and their interacting proteins in, inter alia, screening, diagnosis, and therapy, as well as to methods of preparing the complexes.

By applying the process according to the invention said complexes were identified. The components are listed in table 1.

Said object is further achieved by the characterization of component proteins. These proteins are listed in table 2.

Thus, the invention relates to the following embodiments:

1. A protein complex selected from complex (I) and comprising
 - (a) at least one first protein, which first protein is selected from the group of proteins in table 1, fourth column of a given complex, or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said protein, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions; and
 - (b) at least one second protein, which second protein is selected from the group of proteins in table 1, fifth column of said given complex, or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said second protein, said variant being encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions;
- and a complex (II) comprising at least two of said second proteins,

wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

2. A protein complex comprising a first protein selected from the proteins listed in table 1, fourth column of a given complex or a homologue or variant thereof, or a functionally active fragment or functionally active derivative of said first protein, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said first protein under low stringency conditions, and at least one second protein selected from the group of proteins in table 1, fifth column of a given complex, or a variant or homologue thereof, or a functionally active fragment or a functionally active derivative of said second protein, the variant of said second protein being encoded by a nucleic acid that hybridizes to the nucleic acid of said second protein under low-stringency conditions, and wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.
3. A protein complex comprising all proteins selected from the proteins in table 1, third column of a given complex or at least one protein being a homologue thereof, or a variant thereof or functionally active fragment or functionally active derivative of said protein, said variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said protein under low stringency conditions;
wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM

Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

4. A protein complex that comprises all proteins as listed in table 1, third column for a given complex or at least one protein being a homologue or a variant thereof, or a functionally active fragment or a functionally active derivative thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of any of said proteins under low stringency conditions, except at least one protein of the proteins listed in table 5, third column, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C, with the proviso that the complex comprises at least one protein selected from table 1, fifth column of a given complex.
5. The complex of any of No. 1 - 4 comprising at least one functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein.
6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.
7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.
8. The complex of any of No. 1 - 7 that is involved in at least one biochemical activity as stated in table 3.

9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps:
expressing a protein of the complex, preferably a tagged protein, in a target cell, or a tissue or an organ, isolating the protein complex which is attached to the protein, preferably the tagged protein, and optionally disassociating the protein complex and isolating the individual complex members.
10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.
11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.
12. Component of a protein complex obtainable by a process according to any of No. 9 - 11.
13. Protein selected from the group of proteins in table 1, sixth column of a given complex or a homologue or a variant of thereof, or a functionally active fragment or a functionally active derivative of said protein, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.
14. Nucleic acid encoding a protein according to No. 13.
15. Construct, preferably a vector construct, comprising
 - (a) a nucleic acid according to No. 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or

- (b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative thereof, or a homologue or a variant thereof, at least one of said proteins being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, being selected from the second group of proteins according to No. 1 (b) or
 - (c) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative thereof, or a homologue or a variant thereof, said proteins being selected from the proteins of complex (II) according to No. 1.
16. Host cell, containing a vector comprising at least one nucleic acid of No. 14 and /or a construct of No. 15 or containing several vectors each comprising at least one nucleic acid encoding at least one protein selected from the first group of proteins according to No. 1 (a) and at least one nucleic acid encoding at least one protein selected from the second group of proteins according to No. 1 (b).
17. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and an antibody or a fragment of said antibody containing the binding domain thereof which binds to any of the proteins of the group of proteins according to No. 13.
18. A kit comprising in one or more containers:
- (a) the complex of any of No. 1 – 8 and/or the proteins of No. 13 and/or
 - (b) an antibody according to No. 17 and/or
 - (c) a nucleic acid encoding a protein of the complex of any of No. 1 – 8 and/or a protein of No. 13 and/or
 - (d) cells expressing the complex of any of No. 1 – 8 and/or a protein of No. 13 and, optionally,
 - (e) further components such as reagents, buffers and working instructions.
19. The kit according to No. 18 for processing a substrate of a complex of any one of No. 1 - 8.

20. The kit according to No. 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as those as stated in column 2, table 4 of a given complex.
21. Array, preferably a microarray, in which at least a complex according to any of No. 1 - 8 and/or at least one protein according to No. 13 and/or at least one antibody according to No. 17 is attached to a solid carrier.
22. A process for modifying a substrate of a complex of any one of No. 1 - 8 comprising the step of bringing into contact a complex of any of No. 1 - 8 with said substrate, such that said substrate is modified.
23. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or a protein according to No. 13.
24. A pharmaceutical composition according to No. 23 for the treatment of diseases and disorders, preferentially for diseases or disorders such as those as stated in column 2, table 4 of a given complex.
25. A method for screening for a molecule that binds to a complex of any one of No. 1 - 8 and/or a protein of No. 13, comprising the following steps:
 - (a) exposing said complex or protein, or a cell or organism containing said complex or said protein, to one or more candidate molecules; and
 - (b) determining whether said candidate molecule is bound to the complex or protein.
26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of a complex of any one of No. 1 - 8 comprising the steps of:
 - (a) exposing said complex, or a cell or organism containing said complex to one or more candidate molecules; and
 - (b) determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene regulated by the complex and/or the abundance and/or activity of a protein or protein complex dependent upon the function of the complex and/or product of a gene

dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene regulated by the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity, or composition of said complex.

27. The method of No. 26, wherein the amount of said complex is determined.
28. The method of No. 26, wherein the activity of said complex is determined.
29. The method of No. 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.
30. The method of No. 26, wherein the amount of the individual protein components of said complex is determined.
31. The method of No. 30, wherein said determining step comprises determining whether any of the proteins listed in table 1, third column of said complex, or a functionally active fragment or a functionally active derivative thereof, or a variant or a homologue thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said protein under low-stringency conditions, is present in the complex.
32. The method of any of No. 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder, preferentially of a disease or disorder selected from the diseases or disorders such as those as stated in column 2, table 4 of a given complex.

33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder, preferentially of a disease or disorder such as those as stated in column 2, table 4 of a given complex.
34. A method for the production of a pharmaceutical composition comprising carrying out the method of No. 26 - 31 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.
35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, component disposition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene regulated by the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in a corresponding sample from a subject not having the disease or disorder or predisposition indicated the presence in the subject of the disease or disorder or predisposition in the subject.
36. The method of No. 35, wherein the amount of said complex is determined.
37. The method of No. 35, wherein the activity of said complex is determined.
38. The method of No. 37, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the

absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

39. The method of No. 35, wherein the amount of the individual protein components of said complex is determined.
40. The method of No. 39, wherein said determining step comprises determining whether any of the proteins according to No. 13 is present in the complex.
41. The complex of any one of No. 1 - 8, or a protein of No. 13 or an antibody or fragment thereof of No. 17, for use in a method of diagnosing a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as those as stated in column 2, table 4 of a given complex.
42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity of, component composition of or intracellular localization of, the complex of any one of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, activity of, or protein composition of, said complex.
43. The method according to No. 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.
44. The method according to No. 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.
45. Complex of No. 1 - 8 and/or a protein as listed in table 1, fifth column of said complex as a target for an active agent of a pharmaceutical, preferably a drug target, in the treatment or prevention of a disease or disorder, preferentially of a disease or disorder such as a neurodegenerative disease such as those as stated in column 2, table 4 of a given complex.

3.1 DEFINITIONS

The term "activity" as used herein, refers to the function of a molecule in its broadest sense. It generally includes, but is not limited to, biological, biochemical, physical or chemical functions of the molecule. It includes for example the enzymatic activity, the ability to interact with other molecules and ability to activate, facilitate, stabilize, inhibit, suppress or destabilize the function of other molecules, stability, ability to localize to certain subcellular locations. Where applicable, said term also relates to the function of a protein complex in its broadest sense.

The term "agonist" as used herein, means a molecule which modulates the formation of a protein complex or which, when bound to a complex or protein of the invention or a molecule in the protein complex, increases the amount of, or prolongs the duration of, the activity of the complex. The stimulation may be direct or indirect, including effects on the expression of a gene encoding a member of the protein complex, or by a competitive or non-competitive mechanism. Agonists may include proteins, nucleic acids, carbohydrates or any other organic or anorganic molecule or metals. Agonists also include a functional peptide or peptide fragment derived from a protein member of the complexes of the invention or a protein member itself of the complexes of the invention. Preferred activators are those which, when added to the complex and/or the protein of the invention under physiological conditions and/or in vitro assays, including diagnostic or prognostic assays, result in a change of the level of any of the activities of the protein complex and/or the proteins of the invention as exemplary illustrated above by at least 10%, at least 25%, at least 50%, at least 100%, at least, 200%, at least 500% or at least 1000% at a concentration of the activator $1\mu\text{g ml}^{-1}$, $10\mu\text{g ml}^{-1}$, $100\mu\text{g ml}^{-1}$, $500\mu\text{g ml}^{-1}$, 1mg ml^{-1} , 10mg ml^{-1} or 100mg ml^{-1} . Any combination of the above mentioned degrees of percentages and concentration may be used to define an agonist of the invention, with greater effect at lower concentrations being preferred.

The term "amount" as used herein and as applicable to the embodiment described relates to the amount of the particular protein or protein complex described, including the value of null, i.e. where no protein or protein complex described in that particular embodiment is present under the or any of the conditions which might be specified in that particular embodiment.

The term "animal" as used herein includes, but is not limited to mammals, preferably mammals such as cows, pigs, horses, mice, rats, cats, dogs, sheep, goats

18. A kit comprising in one or more containers:
 - (a) the complex of any of No. 1 – 8 and/or the proteins of No. 13 and/or
 - (b) an antibody according to No. 17 and/or
 - (c) a nucleic acid encoding a protein of the complex of any of No. 1 – 8 and/or a protein of No. 13 and/or
 - (d) cells expressing the complex of any of No. 1 – 8 and/or a protein of No. 13 and, optionally,
 - (e) further components such as reagents, buffers and working instructions.
19. The kit according to No. 18 for processing a substrate of a complex of any one of No. 1 - 8.
20. The kit according to No. 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as those as stated in column 2, table 4 of a given complex.
21. Array, preferably a microarray, in which at least a complex according to any of No. 1 - 8 and/or at least one protein according to No. 13 and/or at least one antibody according to No. 17 is attached to a solid carrier.
22. A process for modifying a substrate of a complex of any one of No. 1 - 8 comprising the step of bringing into contact a complex of any of No. 1 - 8 with said substrate, such that said substrate is modified.
23. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or a protein according to No. 13.
24. A pharmaceutical composition according to No. 23 for the treatment of diseases and disorders, preferentially for diseases or disorders such as those as stated in column 2, table 4 of a given complex.
25. A method for screening for a molecule that binds to a complex of any one of No. 1 - 8 and/or a protein of No. 13, comprising the following steps:

- (a) exposing said complex or protein, or a cell or organism containing said complex or said protein, to one or more candidate molecules; and
- (b) determining whether said candidate molecule is bound to the complex or protein.

26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of a complex of any one of No. 1 - 8 comprising the steps of:

- (a) exposing said complex, or a cell or organism containing said complex to one or more candidate molecules; and
- (b) determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene regulated by the complex and/or the abundance and/or activity of a protein or protein complex dependent upon the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene regulated by the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity, or composition of said complex.

27. The method of No. 26, wherein the amount of said complex is determined.

28. The method of No. 26, wherein the activity of said complex is determined.

29. The method of No. 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

30. The method of No. 26, wherein the amount of the individual protein components of said complex is determined.
31. The method of No. 30, wherein said determining step comprises determining whether any of the proteins listed in table 1, third column of said complex, or a functionally active fragment or a functionally active derivative thereof, or a variant or a homologue thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said protein under low-stringency conditions, is present in the complex.
32. The method of any of No. 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder, preferentially of a disease or disorder selected from the diseases or disorders such as those as stated in column 2, table 4 of a given complex.
33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder, preferentially of a disease or disorder such as those as stated in column 2, table 4 of a given complex.
34. A method for the production of a pharmaceutical composition comprising carrying out the method of No. 26 - 31 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.
35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, component disposition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene regulated by the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said

amount, activity, or protein components of, said complex in a corresponding sample from a subject not having the disease or disorder or predisposition indicated the presence in the subject of the disease or disorder or predisposition in the subject.

36. The method of No. 35, wherein the amount of said complex is determined.
37. The method of No. 35, wherein the activity of said complex is determined.
38. The method of No. 37, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.
39. The method of No. 35, wherein the amount of the individual protein components of said complex is determined.
40. The method of No. 39, wherein said determining step comprises determining whether any of the proteins according to No. 13 is present in the complex.
41. The complex of any one of No. 1 - 8, or a protein of No. 13 or an antibody or fragment thereof of No. 17, for use in a method of diagnosing a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as those as stated in column 2, table 4 of a given complex.
42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity of, component composition of or intracellular localization of, the complex of any one of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, activity of, or protein composition of, said complex.

43. The method according to No. 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.
44. The method according to No. 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.
45. Complex of No. 1 - 8 and/or a protein as listed in table 1, fifth column of said complex as a target for an active agent of a pharmaceutical, preferably a drug target, in the treatment or prevention of a disease or disorder, preferentially of a disease or disorder such as a neurodegenerative disease such as those as stated in column 2, table 4 of a given complex.

Animal models are also provided herein.

Preferably, the protein components of the complexes described herein are all mammalian proteins. The complexes can also consist only of the respective homologues from other mammals such as mouse, rat, pig, cow, dog, monkey, sheep or horse or other species such as *D. melanogaster*, *C. elegans* or chicken. In another preferred embodiment, the complexes are a mixture of proteins from two or more species.

TABLES:

Table 1: Composition of Complexes

First column ('Name of complex'): Lists the name of the protein complexes as used herein.

Second column ('Entry point'): Lists the bait proteins that have been chosen for the purification of the given complex.

Third column ('All interactors'): Lists all novel interactors which have been identified as members of the complex and all interactors which have been known to be associated with the bait so far.

Fourth column ('Known interactors'): Lists all interactors which have been known to be associated with the bait so far.

Fifth column ('Novel interactors of the complex'): Lists all novel interactors of the complex which have been identified in the experiments provided herein.

Sixth column: Separately lists the members of the newly identified complex which have not been annotated previously.

Table 2: Individual Proteins of the Complexes

First column ('Protein'): Lists in alphabetical order all proteins which have been identified as interactors of the complexes presented herein.

Second column ('SEQ ID'): Lists the SEQ ID (Sequence Identifications) of the proteins herein as used herein.

Third column ('IPI-Numbers'): Lists the IPI-Numbers of the proteins herein. The IPI-Numbers refer to the International Protein Index created by the European Bioinformatics Institute (EMBL-EBI), Hinxton, UK.

Fourth column ('Molecular Weight'): Lists the Molecular Weight of the proteins in Dalton.

Table 3: Biochemical Activities of the Complexes of the invention.

First column ('Name of complex'): Lists the name of the protein complexes as used herein.

Second column ('Biochemical Activity'): Lists biochemical activities of the complexes. Assays in order to test these activities are also provided herein (infra).

Table 4: Medical Applications of the Complexes of the invention

First column ('Name of complex'): Lists the name of the protein complexes as used herein

Second column ('Medical application'): lists disorder, diseases, disease areas etc. which are treatable and/or preventable and/or diagnosable etc. by therapeutics and methods interacting with/acting via the complex.

4.1 PROTEIN COMPLEXES/PROTEINS OF THE INVENTION

The protein complexes of the present invention and their component proteins are described in the Tables 1 - 4. The protein complexes and component proteins can be obtained by methods well known in the art for protein purification and recombinant protein expression. For example, the protein complexes of the present invention can be isolated using the TAP method described in Section 5, infra, and in WO 00/09716 and Rigaut et al., 1999, Nature Biotechnol. 17:1030-1032, which are each incorporated by

reference in their entirety. Additionally, the protein complexes can be isolated by immunoprecipitation of the component proteins and combining the immunoprecipitated proteins. The protein complexes can also be produced by recombinantly expressing the component proteins and combining the expressed proteins.

The nucleic and amino acid sequences of the component proteins of the protein complexes of the present invention are provided herein (SEQ ID NO 1 - 198), and can be obtained by any method known in the art, e.g., by PCR amplification using synthetic primers hybridizable to the 3' and 5' ends of each sequence, and/or by cloning from a cDNA or genomic library using an oligonucleotide specific for each nucleotide sequence.

Homologues (e.g., nucleic acids encoding component proteins from other species) or other related sequences (e.g., variants, paralogs) which are members of a native cellular protein complex can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular nucleic acid sequence as a probe, using methods well known in the art for nucleic acid hybridization and cloning.

Exemplary moderately stringent hybridization conditions are as follows: prehybridization of filters containing DNA is carried out for 8 hours to overnight at 65°C in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 µg/ml denatured salmon sperm DNA. Filters are hybridized for 48 hours at 65°C in prehybridization mixture containing 100 µg/ml denatured salmon sperm DNA and 5-20 X 10⁶ cpm of ³²P-labeled probe. Washing of filters is done at 37°C for 1 hour in a solution containing 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA. This is followed by a wash in 0.1X SSC at 50 °C for 45 min before autoradiography. Alternatively, exemplary conditions of high stringency are as follows: e.g., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1xSSC/0.1% SDS at 68°C (Ausubel et al., eds., 1989, Current Protocols in Molecular Biology, Vol. 1, Green Publishing Associates, Inc., and John Wiley & sons, Inc., New York, at p. 2.10.3). Other conditions of high stringency which may be used are well known in the art. Exemplary low stringency hybridization conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 µg/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

For recombinant expression of one or more of the proteins, the nucleic acid containing all or a portion of the nucleotide sequence encoding the protein can be inserted into an appropriate expression vector, i.e., a vector that contains the necessary elements for the transcription and translation of the inserted protein coding sequence. The necessary transcriptional and translational signals can also be supplied by the native promoter of the component protein gene, and/or flanking regions.

A variety of host-vector systems may be utilized to express the protein coding sequence. These include but are not limited to mammalian cell systems infected with virus (e.g., vaccinia virus, adenovirus, etc.); insect cell systems infected with virus (e.g., baculovirus); microorganisms such as yeast containing yeast vectors; or bacteria transformed with bacteriophage, DNA, plasmid DNA, or cosmid DNA. The expression elements of vectors vary in their strengths and specificities. Depending on the host-vector system utilized, any one of a number of suitable transcription and translation elements may be used.

In a preferred embodiment, a complex of the present invention is obtained by expressing the entire coding sequences of the component proteins in the same cell, either under the control of the same promoter or separate promoters. In yet another embodiment, a derivative, fragment or homologue of a component protein is recombinantly expressed. Preferably the derivative, fragment or homologue of the protein forms a complex with the other components of the complex, and more preferably forms a complex that binds to an anti-complex antibody. Such an antibody is further described infra.

Any method available in the art can be used for the insertion of DNA fragments into a vector to construct expression vectors containing a chimeric gene consisting of appropriate transcriptional/translational control signals and protein coding sequences. These methods may include in vitro recombinant DNA and synthetic techniques and in vivo recombinant techniques (genetic recombination). Expression of nucleic acid sequences encoding a component protein, or a derivative, fragment or homologue thereof, may be regulated by a second nucleic acid sequence so that the gene or fragment thereof is expressed in a host transformed with the recombinant DNA molecule(s). For example, expression of the proteins may be controlled by any promoter/enhancer known in the art. In a specific embodiment, the promoter is not native to the gene for the component protein. Promoters that may be used can be

selected from among the many known in the art, and are chosen so as to be operative in the selected host cell.

In a specific embodiment, a vector is used that comprises a promoter operably linked to nucleic acid sequences encoding a component protein, or a fragment, derivative or homologue thereof, one or more origins of replication, and optionally, one or more selectable markers (e.g., an antibiotic resistance gene).

In another specific embodiment, an expression vector containing the coding sequence, or a portion thereof, of a component protein, either together or separately, is made by subcloning the gene sequences into the EcoRI restriction site of each of the three pGEX vectors (glutathione S-transferase expression vectors; Smith and Johnson, 1988, Gene 7:31-40). This allows for the expression of products in the correct reading frame.

Expression vectors containing the sequences of interest can be identified by three general approaches: (a) nucleic acid hybridization, (b) presence or absence of "marker" gene function, and (c) expression of the inserted sequences. In the first approach, coding sequences can be detected by nucleic acid hybridization to probes comprising sequences homologous and complementary to the inserted sequences. In the second approach, the recombinant vector/host system can be identified and selected based upon the presence or absence of certain "marker" functions (e.g., resistance to antibiotics, occlusion body formation in baculovirus, etc.) caused by insertion of the sequences of interest in the vector. For example, if a component protein gene, or portion thereof, is inserted within the marker gene sequence of the vector, recombinants containing the encoded protein or portion will be identified by the absence of the marker gene function (e.g., loss of β -galactosidase activity). In the third approach, recombinant expression vectors can be identified by assaying for the component protein expressed by the recombinant vector. Such assays can be based, for example, on the physical or functional properties of the interacting species in in vitro assay systems, e.g., formation of a complex comprising the protein or binding to an anti-complex antibody.

Once recombinant component protein molecules are identified and the complexes or individual proteins isolated, several methods known in the art can be used to propagate them. Using a suitable host system and growth conditions, recombinant expression vectors can be propagated and amplified in quantity. As previously described, the expression vectors or derivatives which can be used include, but are not limited to, human or animal viruses such as vaccinia virus or adenovirus; insect viruses

such as baculovirus, yeast vectors; bacteriophage vectors such as lambda phage; and plasmid and cosmid vectors.

In addition, a host cell strain may be chosen that modulates the expression of the inserted sequences, or modifies or processes the expressed proteins in the specific fashion desired. Expression from certain promoters can be elevated in the presence of certain inducers; thus expression of the genetically-engineered component proteins may be controlled. Furthermore, different host cells have characteristic and specific mechanisms for the translational and post-translational processing and modification (e.g., glycosylation, phosphorylation, etc.) of proteins. Appropriate cell lines or host systems can be chosen to ensure that the desired modification and processing of the foreign protein is achieved. For example, expression in a bacterial system can be used to produce an unglycosylated core protein, while expression in mammalian cells ensures "native" glycosylation of a heterologous protein. Furthermore, different vector/host expression systems may effect processing reactions to different extents.

In other specific embodiments, a component protein or a fragment, homologue or derivative thereof, may be expressed as fusion or chimeric protein product comprising the protein, fragment, homologue, or derivative joined via a peptide bond to a heterologous protein sequence of a different protein. Such chimeric products can be made by ligating the appropriate nucleic acid sequences encoding the desired amino acids to each other by methods known in the art, in the proper coding frame, and expressing the chimeric products in a suitable host by methods commonly known in the art. Alternatively, such a chimeric product can be made by protein synthetic techniques, e.g., by use of a peptide synthesizer. Chimeric genes comprising a portion of a component protein fused to any heterologous protein-encoding sequences may be constructed.

In particular, protein component derivatives can be made by altering their sequences by substitutions, additions or deletions that provide for functionally equivalent molecules. Due to the degeneracy of nucleotide coding sequences, other DNA sequences that encode substantially the same amino acid sequence as a component gene or cDNA can be used in the practice of the present invention. These include but are not limited to nucleotide sequences comprising all or portions of the component protein gene that are altered by the substitution of different codons that encode a functionally equivalent amino acid residue within the sequence, thus producing a silent change. Likewise, the derivatives of the invention include, but are not limited to, those

containing, as a primary amino acid sequence, all or part of the amino acid sequence of a component protein, including altered sequences in which functionally equivalent amino acid residues are substituted for residues within the sequence resulting in a silent change. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of a similar polarity that acts as a functional equivalent, resulting in a silent alteration. Substitutes for an amino acid within the sequence may be selected from other members of the class to which the amino acid belongs. For example, the nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine. The polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine. The positively charged (basic) amino acids include arginine, lysine and histidine. The negatively charged (acidic) amino acids include aspartic acid and glutamic acid.

In a specific embodiment, up to 1%, 2%, 5%, 10%, 15% or 20% of the total number of amino acids in the wild type protein are substituted or deleted; or 1, 2, 3, 4, 5, or 6 or up to 10 or up to 20 amino acids are inserted, substituted or deleted relative to the wild type protein.

In a specific embodiment of the invention, the nucleic acids encoding a protein component and protein components consisting of or comprising a fragment of or consisting of at least 6 (continuous) amino acids of the protein are provided. In other embodiments, the fragment consists of at least 10, 20, 30, 40, or 50 amino acids of the component protein. In specific embodiments, such fragments are not larger than 35, 100 or 200 amino acids. Derivatives or analogs of component proteins include, but are not limited, to molecules comprising regions that are substantially homologous to the component proteins, in various embodiments, by at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% identity over an amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to a sequence encoding the component protein under stringent, moderately stringent, or nonstringent conditions.

In a specific embodiment, proteins are provided herein, which share an identical region of 20, 30, 40, 50 or 60 contiguous amino acids of the proteins listed in table 2.

The protein component derivatives and analogs of the invention can be produced by various methods known in the art. The manipulations which result in their production

can occur at the gene or protein level. For example, the cloned gene sequences can be modified by any of numerous strategies known in the art (Sambrook et al., 1989, *Molecular Cloning, A Laboratory Manual*, 2d Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York). The sequences can be cleaved at appropriate sites with restriction endonuclease(s), followed by further enzymatic modification if desired, isolated, and ligated in vitro. In the production of the gene encoding a derivative, homologue or analog of a component protein, care should be taken to ensure that the modified gene retains the original translational reading frame, uninterrupted by translational stop signals, in the gene region where the desired activity is encoded.

Additionally, the encoding nucleic acid sequence can be mutated in vitro or in vivo, to create and/or destroy translation, initiation, and/or termination sequences, or to create variations in coding regions and/or form new restriction endonuclease sites or destroy pre-existing ones, to facilitate further in vitro modification. Any technique for mutagenesis known in the art can be used, including but not limited to, chemical mutagenesis and in vitro site-directed mutagenesis (Hutchinson et al., 1978, *J. Biol. Chem.* 253:6551-6558), amplification with PCR primers containing a mutation, etc.

Once a recombinant cell expressing a component protein, or fragment or derivative thereof, is identified, the individual gene product or complex can be isolated and analyzed. This is achieved by assays based on the physical and/or functional properties of the protein or complex, including, but not limited to, radioactive labeling of the product followed by analysis by gel electrophoresis, immunoassay, cross-linking to marker-labeled product, etc.

The component proteins and complexes may be isolated and purified by standard methods known in the art (either from natural sources or recombinant host cells expressing the complexes or proteins), including but not restricted to column chromatography (e.g., ion exchange, affinity, gel exclusion, reversed-phase high pressure, fast protein liquid, etc.), differential centrifugation, differential solubility, or by any other standard technique used for the purification of proteins. Functional properties may be evaluated using any suitable assay known in the art.

Alternatively, once a component protein or its derivative, is identified, the amino acid sequence of the protein can be deduced from the nucleic acid sequence of the chimeric gene from which it was encoded. As a result, the protein or its derivative can be synthesized by standard chemical methods known in the art (e.g., Hunkapiller et al., 1984, *Nature* 310:105-111).

reading frame prediction and plotting, and determination of sequence homologies, etc., can be accomplished using computer software programs available in the art.

Other methods of structural analysis including but not limited to X-ray crystallography (Engstrom, 1974, Biochem. Exp. Biol. 11:7-13), mass spectroscopy and gas chromatography (Methods in Protein Science, J. Wiley and Sons, New York, 1997), and computer modeling (Fletterick and Zoller, eds., 1986, Computer Graphics and Molecular Modeling, In: Current Communications in Molecular Biology, Cold Spring Harbor Laboratory, Cold Spring Harbor Press, New York) can also be employed.

4.2 ANTIBODIES TO PROTEIN COMPLEXES/PROTEINS OF THE INVENTION

According to the present invention, a protein complex of the present invention comprising a first protein, or a functionally active fragment or functionally active derivative thereof, selected from the group consisting of proteins listed in fourth column of table 1; and a second protein, or a functionally active fragment or functionally active derivative thereof, selected from the group consisting of proteins listed in fifth column of table 1, or a functionally active fragment or functionally active derivative thereof, can be used as an immunogen to generate antibodies which immunospecifically bind such immunogen. According to the present invention, also a protein complex of the present invention can be used as an immunogen to generate antibodies which immunospecifically bind to such immunogen comprising all proteins listed in fifth column of table 1.

Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, Fab fragments, and an Fab expression library. In a specific embodiment, antibodies to a complex comprising human protein components are produced. In another embodiment, a complex formed from a fragment of said first protein and a fragment of said second protein, which fragments contain the protein domain that interacts with the other member of the complex, are used as an immunogen for antibody production. In a preferred embodiment, the antibody specific for the complex in that the antibody does not bind the individual protein components of the complex.

Polyclonal antibodies can be prepared as described above by immunizing a suitable subject with a polypeptide of the invention as an immunogen. Preferred

Manipulations of component protein sequences may be made at the protein level. Included within the scope of the invention is a complex in which the component proteins or derivatives and analogs that are differentially modified during or after translation, e.g., by glycosylation, acetylation, phosphorylation, amidation, derivatization, by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous chemical modifications may be carried out by known techniques, including but not limited to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, NaBH_4 , acetylation, formylation, oxidation, reduction, metabolic synthesis in the presence of tunicamycin, etc.

In specific embodiments, the amino acid sequences are modified to include a fluorescent label. In another specific embodiment, the protein sequences are modified to have a heterofunctional reagent; such heterofunctional reagents can be used to crosslink the members of the complex.

In addition, complexes of analogs and derivatives of component proteins can be chemically synthesized. For example, a peptide corresponding to a portion of a component protein, which comprises the desired domain or mediates the desired activity in vitro (e.g., complex formation) can be synthesized by use of a peptide synthesizer. Furthermore, if desired, non-classical amino acids or chemical amino acid analogs can be introduced as a substitution or addition into the protein sequence.

In cases where natural products are suspected of being mutant or are isolated from new species, the amino acid sequence of a component protein isolated from the natural source, as well as those expressed in vitro, or from synthesized expression vectors in vivo or in vitro, can be determined from analysis of the DNA sequence, or alternatively, by direct sequencing of the isolated protein. Such analysis can be performed by manual sequencing or through use of an automated amino acid sequenator.

The complexes can also be analyzed by hydrophilicity analysis (Hopp and Woods, 1981, Proc. Natl. Acad. Sci. USA 78:3824-3828). A hydrophilicity profile can be used to identify the hydrophobic and hydrophilic regions of the proteins, and help predict their orientation in designing substrates for experimental manipulation, such as in binding experiments, antibody synthesis, etc. Secondary structural analysis can also be done to identify regions of the component proteins, or their derivatives, that assume specific structures (Chou and Fasman, 1974, Biochemistry 13:222-23). Manipulation, translation, secondary structure prediction, hydrophilicity and hydrophobicity profile predictions, open

EBV-hybridoma technique (Cole et al., 1985, Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc., pp. 77-96) or trioma techniques. The technology for producing hybridomas is well known (see generally Current Protocols in Immunology 1994, Coligan et al. (eds.) John Wiley & Sons, Inc., New York, NY). Hybridoma cells producing a monoclonal antibody of the invention are detected by screening the hybridoma culture supernatants for antibodies that bind the polypeptide of interest, e.g., using a standard ELISA assay.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody directed against a polypeptide of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (e.g., an antibody phage display library) with the polypeptide of interest. Kits for generating and screening phage display libraries are commercially available (e.g., the Pharmacia Recombinant Phage Antibody System, Catalog No. 27-9400-01; and the Stratagene SurfZAP Phage Display Kit, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs et al., 1991, Bio/Technology 9:1370-1372; Hay et al., 1992, Hum. Antibod. Hybridomas 3:81-85; Huse et al., 1989, Science 246:1275-1281; Griffiths et al., 1993, EMBO J. 12:725-734.

Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. A chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region. (See, e.g., Cabilly et al., U.S. Patent No. 4,816,567; and Boss et al., U.S. Patent No. 4,816,397, which are incorporated herein by reference in their entirety.) Humanized antibodies are antibody molecules from non-human species having one or more complementarily determining regions (CDRs) from the non-human species and a framework region from a human immunoglobulin molecule. (See, e.g., Queen, U.S. Patent No. 5,585,089, which is incorporated herein by reference in its entirety.) Such chimeric and humanized monoclonal antibodies can be

polyclonal antibody compositions are ones that have been selected for antibodies directed against a polypeptide or polypeptides of the invention. Particularly preferred polyclonal antibody preparations are ones that contain only antibodies directed against a polypeptide or polypeptides of the invention. Particularly preferred immunogen compositions are those that contain no other human proteins such as, for example, immunogen compositions made using a non-human host cell for recombinant expression of a polypeptide of the invention. In such a manner, the only human epitope or epitopes recognized by the resulting antibody compositions raised against this immunogen will be present as part of a polypeptide or polypeptides of the invention.

The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized polypeptide. If desired, the antibody molecules can be isolated from the mammal (e.g., from the blood) and further purified by well-known techniques, such as protein A chromatography to obtain the IgG fraction. Alternatively, antibodies specific for a protein or polypeptide of the invention can be selected for (e.g., partially purified) or purified by, e.g., affinity chromatography. For example, a recombinantly expressed and purified (or partially purified) protein of the invention is produced as described herein, and covalently or non-covalently coupled to a solid support such as, for example, a chromatography column. The column can then be used to affinity purify antibodies specific for the proteins of the invention from a sample containing antibodies directed against a large number of different epitopes, thereby generating a substantially purified antibody composition, i.e., one that is substantially free of contaminating antibodies. By a substantially purified antibody composition is meant, in this context, that the antibody sample contains at most only 30% (by dry weight) of contaminating antibodies directed against epitopes other than those on the desired protein or polypeptide of the invention, and preferably at most 20%, yet more preferably at most 10%, and most preferably at most 5% (by dry weight) of the sample is contaminating antibodies. A purified antibody composition means that at least 99% of the antibodies in the composition are directed against the desired protein or polypeptide of the invention.

At an appropriate time after immunization, e.g., when the specific antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein, 1975, *Nature* 256:495-497, the human B cell hybridoma technique (Kozbor et al., 1983, *Immunol. Today* 4:72), the

produced by recombinant DNA techniques known in the art, for example using methods described in PCT Publication No. WO 87/02671; European Patent Application 184,187; European Patent Application 171,496; European Patent Application 173,494; PCT Publication No. WO 86/01533; U.S. Patent No. 4,816,567; European Patent Application 125,023; Better et al., 1988, Science 240:1041-1043; Liu et al., 1987, Proc. Natl. Acad. Sci. USA 84:3439-3443; Liu et al., 1987, J. Immunol. 139:3521-3526; Sun et al., 1987, Proc. Natl. Acad. Sci. USA 84:214-218; Nishimura et al., 1987, Canc. Res. 47:999-1005; Wood et al., 1985, Nature 314:446-449; and Shaw et al., 1988, J. Natl. Cancer Inst. 80:1553-1559; Morrison, 1985, Science 229:1202-1207; Oi et al., 1986, Bio/Techniques 4:214; U.S. Patent 5,225,539; Jones et al., 1986, Nature 321:552-525; Verhoeyan et al., 1988, Science 239:1534; and Beidler et al., 1988, J. Immunol. 141:4053-4060.

Completely human antibodies are particularly desirable for therapeutic treatment of human patients. Such antibodies can be produced, for example, using transgenic mice which are incapable of expressing endogenous immunoglobulin heavy and light chains genes, but which can express human heavy and light chain genes. The transgenic mice are immunized in the normal fashion with a selected antigen, e.g., all or a portion of a polypeptide of the invention. Monoclonal antibodies directed against the antigen can be obtained using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar, 1995, Int. Rev. Immunol. 13:65-93). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, e.g., U.S. Patent 5,625,126; U.S. Patent 5,633,425; U.S. Patent 5,569,825; U.S. Patent 5,661,016; and U.S. Patent 5,545,806. In addition, companies such as Abgenix, Inc. (Freemont, CA), can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, e.g., a murine antibody, is used to guide the selection of a completely human antibody recognizing the same epitope. (Jespers et al., 1994, Bio/technology 12:899-903).

Antibody fragments that contain the idiotypes of the complex can be generated by techniques known in the art. For example, such fragments include, but are not limited to, the F(ab')₂ fragment which can be produced by pepsin digestion of the antibody molecule; the Fab' fragment that can be generated by reducing the disulfide bridges of the F(ab')₂ fragment; the Fab fragment that can be generated by treating the antibody molecular with papain and a reducing agent; and Fv fragments.

In the production of antibodies, screening for the desired antibody can be accomplished by techniques known in the art, e.g., ELISA (enzyme-linked immunosorbent assay). To select antibodies specific to a particular domain of the complex, or a derivative thereof, one may assay generated hybridomas for a product that binds to the fragment of the complex, or a derivative thereof, that contains such a domain. For selection of an antibody that specifically binds a complex of the present, or a derivative, or homologue thereof, but which does not specifically bind to the individual proteins of the complex, or a derivative, or homologue thereof, one can select on the basis of positive binding to the complex and a lack of binding to the individual protein components.

Antibodies specific to a domain of the complex, or a derivative, or homologue thereof, are also provided.

The foregoing antibodies can be used in methods known in the art relating to the localization and/or quantification of the complexes of the invention, e.g., for imaging these proteins, measuring levels thereof in appropriate physiological samples (by immunoassay), in diagnostic methods, etc. This hold true also for a derivative, or homologue thereof of a complex.

In another embodiment of the invention (see *infra*), an antibody to a complex or a fragment of such antibodies containing the antibody binding domain, is a therapeutic.

4.3 DIAGNOSTIC, PROGNOSTIC, AND SCREENING USES OF THE PROTEIN COMPLEXES/PROTEINS OF THE INVENTION

The particular protein complexes and proteins of the present invention may be markers of normal physiological processes, and thus have diagnostic utility. Further, definition of particular groups of patients with elevations or deficiencies of a protein complex of the present invention, or wherein the protein complex has a change in protein

component composition, can lead to new nosological classifications of diseases, furthering diagnostic ability.

Examples for diseases or disorders are those as listed in table 4

Detecting levels of protein complexes, or individual component proteins that form the complexes, or detecting levels of the mRNAs encoding the components of the complex, may be used in diagnosis, prognosis, and/or staging to follow the course of a disease state, to follow a therapeutic response, etc.

A protein complex of the present invention and the individual components of the complex and a derivative, analog or subsequence thereof, encoding nucleic acids (and sequences complementary thereto), and anti-complex antibodies and antibodies directed against individual components that can form the complex, are useful in diagnostics. The foregoing molecules can be used in assays, such as immunoassays, to detect, prognose, diagnose, or monitor various conditions, diseases, and disorders characterized by aberrant levels of a complex or aberrant component composition of a complex, or monitor the treatment of such various conditions, diseases, and disorders.

In particular, such an immunoassay is carried out by a method comprising contacting a sample derived from a patient with an anti-complex antibody under conditions such that immunospecific binding can occur, and detecting or measuring the amount of any immunospecific binding by the antibody. In a specific aspect, such binding of antibody, in tissue sections, can be used to detect aberrant complex localization, or aberrant (e.g., high, low or absent) levels of a protein complex or complexes. In a specific embodiment, an antibody to the complex can be used to assay a patient tissue or serum sample for the presence of the complex, where an aberrant level of the complex is an indication of a diseased condition. By "aberrant levels" is meant increased or decreased levels relative to that present, or a standard level representing that present, in an analogous sample from a portion or fluid of the body, or from a subject not having the disorder.

The immunoassays which can be used include but are not limited to competitive and non-competitive assay systems using techniques such as Western blots, radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoprecipitation assays, precipitin reactions, gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays, complement-fixation assays, immunoradiometric assays, fluorescent immunoassays, protein A immunoassays, to name but a few known in the art.

Nucleic acids encoding the components of the protein complex and related nucleic acid sequences and subsequences, including complementary sequences, can be used in hybridization assays. The nucleic acid sequences, or subsequences thereof, comprising about at least 8 nucleotides, can be used as hybridization probes. Hybridization assays can be used to detect, prognose, diagnose, or monitor conditions, disorders, or disease states associated with aberrant levels of the mRNAs encoding the components of a complex as described, *supra*. In particular, such a hybridization assay is carried out by a method comprising contacting a sample containing nucleic acid with a nucleic acid probe capable of hybridizing to component protein coding DNA or RNA, under conditions such that hybridization can occur, and detecting or measuring any resulting hybridization.

In specific embodiments, diseases and disorders involving or characterized by aberrant levels of a protein complex or aberrant complex composition can be diagnosed, or its suspected presence can be screened for, or a predisposition to develop such disorders can be detected, by determining the component protein composition of the complex, or detecting aberrant levels of a member of the complex or un-complexed component proteins or encoding nucleic acids, or functional activity including, but not restricted to, binding to an interacting partner, or by detecting mutations in component protein RNA, DNA or protein (e.g., mutations such as translocations, truncations, changes in nucleotide or amino acid sequence relative to wild-type that cause increased or decreased expression or activity of a complex, and/or component protein).

Such diseases and disorders include, but are not limited to neurodegenerative disease such as listed in table 4.

By way of example, levels of a protein complex and the individual components of a complex can be detected by immunoassay, levels of component protein RNA or DNA can be detected by hybridization assays (e.g., Northern blots, dot blots, RNase protection assays), and binding of component proteins to each other (e.g., complex formation) can be measured by binding assays commonly known in the art. Translocations and point mutations in component protein genes can be detected by Southern blotting, RFLP analysis, PCR using primers that preferably generate a fragment spanning at least most of the gene by sequencing of genomic DNA or cDNA obtained from the patient, etc.

Assays well known in the art (e.g., assays described above such as immunoassays, nucleic acid hybridization assays, activity assays, etc.) can be used to

determine whether one or more particular protein complexes are present at either increased or decreased levels, or are absent, in samples from patients suffering from a particular disease or disorder, or having a predisposition to develop such a disease or disorder, as compared to the levels in samples from subjects not having such a disease or disorder, or having a predisposition to develop such a disease or disorder. Additionally, these assays can be used to determine whether the ratio of the complex to the un-complexed components of the complex, is increased or decreased in samples from patients suffering from a particular disease or disorder, or having a predisposition to develop such a disease or disorder, as compared to the ratio in samples from subjects not having such a disease or disorder.

In the event that levels of one or more particular protein complexes (i.e., complexes formed from component protein derivatives, homologs, fragments, or analogs) are determined to be increased in patients suffering from a particular disease or disorder, or having a predisposition to develop such a disease or disorder, then the particular disease or disorder, or predisposition for a disease or disorder, can be diagnosed, have prognosis defined for, be screened for, or be monitored by detecting increased levels of the one or more protein complexes, increased levels of the mRNA that encodes one or more members of the one or more particular protein complexes, or by detecting increased complex functional activity.

Accordingly, in a specific embodiment of the present invention, diseases and disorders involving increased levels of one or more protein complexes can be diagnosed, or their suspected presence can be screened for, or a predisposition to develop such disorders can be detected, by detecting increased levels of the one or more protein complexes, the mRNA encoding both members of the complex, or complex functional activity, or by detecting mutations in the component proteins that stabilize or enhance complex formation, e.g., mutations such as translocations in nucleic acids, truncations in the gene or protein, changes in nucleotide or amino acid sequence relative to wild-type, that stabilize or enhance complex formation.

In the event that levels of one or more particular protein complexes are determined to be decreased in patients suffering from a particular disease or disorder, or having a predisposition to develop such a disease or disorder, then the particular disease or disorder or predisposition for a disease or disorder can be diagnosed, have its prognosis determined, be screened for, or be monitored by detecting decreased levels of the one or more protein complexes, the mRNA that encodes one or more members of

the particular one or more protein complexes, or by detecting decreased protein complex functional activity.

Accordingly, in a specific embodiment of the invention, diseases and disorders involving decreased levels of one or more protein complexes can be diagnosed, or their suspected presence can be screened for, or a predisposition to develop such disorders can be detected, by detecting decreased levels of the one or more protein complexes, the mRNA encoding one or more members of the one or more complexes, or complex functional activity, or by detecting mutations in the component proteins that decrease complex formation, e.g., mutations such as translocations in nucleic acids, truncations in the gene or protein, changes in nucleotide or amino acid sequence relative to wild-type, that decrease complex formation.

Accordingly, in a specific embodiment of the invention, diseases and disorders involving aberrant compositions of the complexes can be diagnosed, or their suspected presence can be screened for, or a predisposition to develop such disorders can be detected, by detecting the component proteins of one or more complexes, or the mRNA encoding the members of the one or more complexes.

The use of detection techniques, especially those involving antibodies against a protein complex, provides a method of detecting specific cells that express the complex or component proteins. Using such assays, specific cell types can be defined in which one or more particular protein complexes are expressed, and the presence of the complex or component proteins can be correlated with cell viability, state, health, etc.

Also embodied are methods to detect a protein complex of the present invention in cell culture models that express particular protein complexes or derivatives thereof, for the purpose of characterizing or preparing the complexes for harvest. This embodiment includes cell sorting of prokaryotes such as but not restricted to bacteria (Davey and Kell, 1996, *Microbiol. Rev.* 60:641-696), primary cultures and tissue specimens from eukaryotes, including mammalian species such as human (Steele et al., 1996, *Clin. Obstet. Gynecol* 39:801-813), and continuous cell cultures (Orfao and Ruiz-Arguelles, 1996, *Clin. Biochem.* 29:5-9). Such isolations can be used as methods of diagnosis, described, *supra*.

In a further specific embodiment, a modulation of the formation process of a complex can be determined.

Such a modulation can either be a change in the typical time course of its formation or a change in the typical steps leading to the formation of the complete complex.

Such changes can for example be detected by analysing and comparing the process of complex formation in untreated wild type cells of a particular type and/or cells showing or having the predisposition to develop a certain disease phenotype and/or cells which have been treated with particular conditions and/or particular agents in a particular situation.

Methods to study such changes in time course are well known in the art and include for example Western-blot analysis of the proteins in the complex isolated at different steps of its formation.

Furthermore an aberrant intracellular localization of the protein complex and/or an aberrant transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or a gene dependent on the complex can serve as a marker for a disease and thus have diagnostic utility for any disease which is caused by an aberrant activity, function, composition or formation of the complex of the invention.

Methods to study the intracellular localization are well known in the art and include, but are not limited to immunofluorescence analysis using antibodies specific for components of the protein. Preferentially, double-stainings including staining of other cellular structures are being used to facilitate the detection of the intracellular localization. Methods to analyse the transcription levels of a gene dependent on the complex are also well known in the art and include Northern blot analysis, quantitative PCR etc. The abundance of proteins dependent on the protein can be analyzed as described supra. Methods to study changes in the activity of proteins dependent on complex depend on the protein. The choice of such methods will be apparent to any person skilled in the art.

4.4 THERAPEUTIC USES OF PROTEIN COMPLEXES/PROTEINS OF THE INVENTION

The present invention is directed to a method for treatment or prevention of various diseases and disorders by administration of a therapeutic compound (termed herein "therapeutic"). Such "therapeutics" include, but are not limited to, a protein

complex of the present invention, the individual component proteins, and analogs and derivatives (including fragments) of the foregoing (e.g., as described hereinabove); antibodies thereto (as described hereinabove); nucleic acids encoding the component protein, and analogs or derivatives, thereof (e.g., as described hereinabove); component protein antisense nucleic acids, and agents that modulate complex formation and/or activity (i.e., agonists and antagonists).

The protein complexes as identified herein can be implicated in processes which are implicated in or associated with pathological conditions.

Diseases and disorders which can be treated and/or prevented and/or diagnosed by therapeutics interacting with any of the complexes provided herein are for example those listed in table 4.

These disorders are treated or prevented by administration of a therapeutic that modulates (i.e. inhibits or promotes) protein complex activity or formation or modulates its function or composition. Diseases or disorders associated with aberrant levels of complex activity or formation, or aberrant levels or activity of the component proteins, or aberrant complex composition or a change in the function, may be treated by administration of a therapeutic that modulates complex formation or activity or by the administration of a protein complex.

Therapeutics may also be administered to modulate complex formation or activity or level thereof in a microbial organism such as yeast, fungi such as candida albicans causing an infectious disease in animals or humans.

Diseases and disorders characterized by increased (relative to a subject not suffering from the disease or disorder) complex levels or activity can be treated with therapeutics that antagonize (i.e., reduce or inhibit) complex formation or activity. Therapeutics that can be used include, but are not limited to, the component proteins or an analog, derivative or fragment of the component protein; anti-complex antibodies (e.g., antibodies specific for the protein complex, or a fragment or derivative of the antibody containing the binding region thereof; nucleic acids encoding the component proteins; antisense nucleic acids complementary to nucleic acids encoding the component proteins; and nucleic acids encoding the component protein that are dysfunctional due to, e.g., a heterologous insertion within the protein coding sequence, that are used to "knockout" endogenous protein function by homologous recombination, see, e.g., Capecchi, 1989, Science 244:1288-1292. In one embodiment, a therapeutic is

1, 2 or more antisense nucleic acids which are complementary to 1, 2, or more nucleic acids, respectfully, that encode component proteins of a complex.

In a specific embodiment of the present invention, a nucleic acid containing a portion of a component protein gene in which gene sequences flank (are both 5' and 3' to) a different gene sequence, is used as a component protein antagonist, or to promote component protein inactivation by homologous recombination (see also, Koller and Smithies, 1989, Proc. Natl. Acad. Sci. USA 86:8932-8935; Zijlstra et al., 1989, Nature 342: 435-438). Additionally, mutants or derivatives of a component protein that has greater affinity for another component protein or the complex than wild type may be administered to compete with wild type protein for binding, thereby reducing the levels of complexes containing the wild type protein. Other therapeutics that inhibit complex function can be identified by use of known convenient in vitro assays, e.g., based on their ability to inhibit complex formation, or as described in Section 4.5, *infra*.

In specific embodiments, therapeutics that antagonize complex formation or activity are administered therapeutically, including prophylactically, (1) in diseases or disorders involving an increased (relative to normal or desired) level of a complex, for example, in patients where complexes are overactive or overexpressed; or (2) in diseases or disorders where an in vitro (or in vivo) assay (see *infra*) indicates the utility of antagonist administration. Increased levels of a complex can be readily detected, e.g., by quantifying protein and/or RNA, by obtaining a patient tissue sample (e.g., from biopsy tissue) and assaying it in vitro for RNA or protein levels, or structure and/or activity of the expressed complex (or the encoding mRNA). Many methods standard in the art can be thus employed including, but not limited to, immunoassays to detect complexes and/or visualize complexes (e.g., Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate polyacrylamide gel electrophoresis [SDS-PAGE], immunocytochemistry, etc.), and/or hybridization assays to detect concurrent expression of component protein mRNA (e.g., Northern assays, dot blot analysis, in situ hybridization, etc.).

A more specific embodiment of the present invention is directed to a method of reducing complex expression (i.e., expression of the protein components of the complex and/or formation of the complex) by targeting mRNAs that express the protein moieties. RNA therapeutics currently fall within three classes, antisense species, ribozymes, or RNA aptamers (Good et al., 1997, Gene Therapy 4:45-54).

Antisense oligonucleotides have been the most widely used. By way of example, but not limitation, antisense oligonucleotide methodology to reduce complex formation is presented below, *infra*. Ribozyme therapy involves the administration, induced expression, etc. of small RNA molecules with enzymatic ability to cleave, bind, or otherwise inactivate specific RNAs, to reduce or eliminate expression of particular proteins (Grassi and Marini, 1996, *Annals of Medicine* 28:499-510; Gibson, 1996, *Cancer and Metastasis Reviews* 15:287-299). RNA aptamers are specific RNA ligand proteins, such as for Tat and Rev RNA (Good et al., 1997, *Gene Therapy* 4:45-54) that can specifically inhibit their translation. Aptamers specific for component proteins can be identified by many methods well known in the art, for example, by affecting the formation of a complex in the protein-protein interaction assay described, *infra*.

In another embodiment, the activity or levels of a component protein are reduced by administration of another component protein, or the encoding nucleic acid, or an antibody that immunospecifically binds to the component protein, or a fragment or a derivative of the antibody containing the binding domain thereof.

In another aspect of the invention, diseases or disorders associated with increased levels of an component protein of the complex may be treated or prevented by administration of a therapeutic that increases complex formation if the complex formation acts to reduce or inactivate the component protein through complex formation. Such diseases or disorders can be treated or prevented by administration of one component member of the complex, administration of antibodies or other molecules that stabilize the complex, etc.

Diseases and disorders associated with underexpression of a complex, or a component protein, are treated or prevented by administration of a therapeutic that promotes (i.e., increases or supplies) complex levels and/or function, or individual component protein function. Examples of such a therapeutic include but are not limited to a complex or a derivative, analog or fragment of the complex that are functionally active (e.g., able to form a complex), un-complexed component proteins and derivatives, analogs, and fragments of un-complexed component proteins, and nucleic acids encoding the members of a complex or functionally active derivatives or fragments of the members of the complex, e.g., for use in gene therapy. In a specific embodiment, a therapeutic includes derivatives, homologs or fragments of a component protein that increase and/or stabilize complex formation. Examples of other agonists can be identified using *in vitro* assays or animal models, examples of which are described, *infra*.

In yet other specific embodiments of the present invention, therapeutics that promote complex function are administered therapeutically, including prophylactically, (1) in diseases or disorders involving an absence or decreased (relative to normal or desired) level of a complex, for example, in patients where a complex, or the individual components necessary to form the complex, is lacking, genetically defective, biologically inactive or underactive, or under-expressed; or (2) in diseases or disorders wherein an in vitro or in vivo assay (see, *infra*) indicates the utility of complex agonist administration. The absence or decreased level of a complex, component protein or function can be readily detected, e.g., by obtaining a patient tissue sample (e.g., from biopsy tissue) and assaying it in vitro for RNA or protein levels, structure and/or activity of the expressed complex and/or the concurrent expression of mRNA encoding the two components of the complex. Many methods standard in the art can be thus employed, including but not limited to immunoassays to detect and/or visualize a complex, or the individual components of a complex (e.g., Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate polyacrylamide gel electrophoresis [SDS-PAGE], immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs encoding the individual protein components of a complex by detecting and/or visualizing component mRNA concurrently or separately using, e.g., Northern assays, dot blot analysis, in situ hybridization, etc.

In specific embodiments, the activity or levels of a component protein are increased by administration of another component protein of the same complex, or a derivative, homolog or analog thereof, a nucleic acid encoding the other component, or an agent that stabilizes or enhances the other component, or a fragment or derivative of such an agent.

Generally, administration of products of species origin or species reactivity (in the case of antibodies) that is the same species as that of the patient is preferred. Thus, in a preferred embodiment, a human complex, or derivative, homolog or analog thereof; nucleic acids encoding the members of the human complex or a derivative, homolog or analog thereof; an antibody to a human complex, or a derivative thereof; or other human agents that affect component proteins or the complex, are therapeutically or prophylactically administered to a human patient.

Preferably, suitable in vitro or in vivo assays are utilized to determine the effect of a specific therapeutic and whether its administration is indicated for treatment of the affected tissue or individual.

In various specific embodiments, in vitro assays can be carried out with representative cells of cell types involved in a patient's disorder, to determine if a therapeutic has a desired effect upon such cell types.

Compounds for use in therapy can be tested in suitable animal model systems prior to testing in humans, including, but not limited to, rats, mice, chicken, cows, monkeys, rabbits, etc. For in vivo testing, prior to administration to humans, any animal model system known in the art may be used. Additional descriptions and sources of therapeutics that can be used according to the invention are found in Sections 4.1 to 4.3 and 4.7 herein.

4.4.1 GENE THERAPY

In a specific embodiment of the present invention, nucleic acids comprising a sequence encoding the component proteins, or a functional derivative thereof, are administered to modulate complex activity or formation by way of gene therapy. Gene therapy refers to therapy performed by the administration of a nucleic acid to a subject. In this embodiment of the present invention, the nucleic acid expresses its encoded protein(s) that mediates a therapeutic effect by modulating complex activity or formation. Any of the methods for gene therapy available in the art can be used according to the present invention. Exemplary methods are described below.

For general reviews of the methods of gene therapy, see Goldspiel et al., 1993, Clinical Pharmacy 12:488-505; Wu and Wu, 1991, Biotherapy 3:87-95; Tolstoshev, 1993, Ann. Rev. Pharmacol. Toxicol. 32:573-596; Mulligan, 1993, Science 260:926-932; Morgan and Anderson, 1993, Ann. Rev. Biochem. 62:191-217; and May, 1993, TIBTECH 11:155-215. Methods commonly known in the art of recombinant DNA technology which can be used are described in Ausubel et al., eds., 1993, Current Protocols in Molecular Biology, John Wiley & Sons, NY; and Kriegler, 1990, Gene Transfer and Expression, A Laboratory Manual, Stockton Press, NY.

In a preferred aspect, the therapeutic comprises a nucleic acid that is part of an expression vector that expresses one or more of the component proteins, or fragments or chimeric proteins thereof, in a suitable host. In particular, such a nucleic acid has a promoter operably linked to the protein coding region(s) (or, less preferably separate promoters linked to the separate coding regions separately), said promoter being

inducible or constitutive, and optionally, tissue-specific. In another particular embodiment, a nucleic acid molecule is used in which the coding sequences, and any other desired sequences, are flanked by regions that promote homologous recombination at a desired site in the genome, thus providing for intra-chromosomal expression of the component protein nucleic acids (Koller and Smithies, 1989, Proc. Natl. Acad. Sci. USA 86:8932-8935; Zijlstra et al., 1989, Nature 342:435-438).

Delivery of the nucleic acid into a patient may be either direct, in which case the patient is directly exposed to the nucleic acid or nucleic acid-carrying vector, or indirect, in which case, cells are first transformed with the nucleic acid in vitro, then transplanted into the patient. These two approaches are known, respectively, as in vivo or ex vivo gene therapy.

In a specific embodiment, the nucleic acid is directly administered in vivo, where it is expressed to produce the encoded product. This can be accomplished by any of numerous methods known in the art, e.g., by constructing it as part of an appropriate nucleic acid expression vector and administering it so that it becomes intracellular, e.g., by infection using a defective or attenuated retroviral or other viral vector (U.S. Patent No. 4,980,286), or by direct injection of naked DNA, or by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or coating with lipids or cell-surface receptors, or through use of transfecting agents, by encapsulation in liposomes, microparticles, or microcapsules, or by administering it in linkage to a peptide that is known to enter the nucleus, or by administering it in linkage to a ligand subject to receptor-mediated endocytosis that can be used to target cell types specifically expressing the receptors (e.g., Wu and Wu, 1987, J. Biol. Chem. 262:4429-4432), etc. In another embodiment, a nucleic acid-ligand complex can be formed in which the ligand comprises a fusogenic viral peptide that disrupts endosomes, allowing the nucleic acid to avoid lysosomal degradation. In yet another embodiment, the nucleic acid can be targeted in vivo for cell specific uptake and expression, by targeting a specific receptor (see, e.g., International Patent Publications WO 92/06180; WO 92/22635; WO 92/20316; WO 93/14188; and WO 93/20221. Alternatively, the nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination (Koller and Smithies, 1989, Proc. Natl. Acad. Sci. USA 86:8932-8935; Zijlstra et al., 1989, Nature 342:435-438).

In a specific embodiment, a viral vector that contains the component protein encoding nucleic acids is used. For example, a retroviral vector can be used (Miller et

al., 1993, *Meth. Enzymol.* 217:581-599). These retroviral vectors have been modified to delete retroviral sequences that are not necessary for packaging of the viral genome and integration into host cell DNA. The encoding nucleic acids to be used in gene therapy is/are cloned into the vector, which facilitates delivery of the gene into a patient. More detail about retroviral vectors can be found in Boesen et al., 1994, *Biotherapy* 6:291-302, which describes the use of a retroviral vector to deliver the *mdr1* gene to hematopoietic stem cells in order to make the stem cells more resistant to chemotherapy. Other references illustrating the use of retroviral vectors in gene therapy are Clowes et al., 1994, *J. Clin. Invest.* 93:644-651; Kiem et al., 1994, *Blood* 83:1467-1473; Salmons and Gunzberg, 1993, *Human Gene Therapy* 4:129-141; and Grossman and Wilson, 1993, *Curr. Opin. in Genetics and Devel.* 3:110-114.

Adenoviruses are other viral vectors that can be used in gene therapy. Adenoviruses are especially attractive vehicles for delivering genes to respiratory epithelia. Adenoviruses naturally infect respiratory epithelia where they cause a mild disease. Other targets for adenovirus-based delivery systems are the liver, the central nervous system, endothelial cells and muscle. Adenoviruses have the advantage of being capable of infecting non-dividing cells. Kozarsky and Wilson, 1993, *Curr. Opin. Genet. Devel.* 3:499-503, discuss adenovirus-based gene therapy. The use of adenovirus vectors to transfer genes to the respiratory epithelia of rhesus monkeys has been demonstrated by Bout et al., 1994, *Human Gene Therapy* 5:3-10. Other instances of the use of adenoviruses in gene therapy can be found in Rosenfeld et al., 1991, *Science* 252:431-434; Rosenfeld et al., 1992, *Cell* 68:143-155; and Mastrangeli et al., 1993, *J. Clin. Invest.* 91:225-234.

Adeno-associated virus (AAV) has also been proposed for use in gene therapy (Walsh et al., 1993, *Proc. Soc. Exp. Biol. Med.* 204:289-300).

Another approach to gene therapy involves transferring a gene into cells in tissue culture by methods such as electroporation, lipofection, calcium phosphate-mediated transfection, or viral infection. Usually, the method of transfer includes the transfer of a selectable marker to the cells. The cells are then placed under selection to isolate those cells that have taken up and are expressing the transferred gene from those that have not. Those cells are then delivered to a patient.

In this embodiment, the nucleic acid is introduced into a cell prior to administration in vivo of the resulting recombinant cell. Such introduction can be carried out by any method known in the art including, but not limited to, transfection by electroporation,

microinjection, infection with a viral or bacteriophage vector containing the nucleic acid sequences, cell fusion, chromosome-mediated gene transfer, microcell-mediated gene transfer, spheroplast fusion, etc. Numerous techniques are known in the art for the introduction of foreign genes into cells (see, e.g., Loeffler and Behr, 1993, Meth. Enzymol. 217:599-618; Cohen et al., 1993, Meth. Enzymol. 217:618-644; Cline, 1985, Pharmac. Ther. 29:69-92) and may be used in accordance with the present invention, provided that the necessary developmental and physiological functions of the recipient cells are not disrupted. The technique should provide for the stable transfer of the nucleic acid to the cell, so that the nucleic acid is expressible by the cell and preferably, is heritable and expressible by its cell progeny.

The resulting recombinant cells can be delivered to a patient by various methods known in the art. In a preferred embodiment, epithelial cells are injected, e.g., subcutaneously. In another embodiment, recombinant skin cells may be applied as a skin graft onto the patient. Recombinant blood cells (e.g., hematopoietic stem or progenitor cells) are preferably administered intravenously. The amount of cells envisioned for use depends on the desired effect, patient state, etc., and can be determined by one skilled in the art.

Cells into which a nucleic acid can be introduced for purposes of gene therapy encompass any desired, available cell type, and include but are not limited to epithelial cells, endothelial cells, keratinocytes, fibroblasts, muscle cells, hepatocytes, blood cells such as T lymphocytes, B lymphocytes, monocytes, macrophages, neutrophils, eosinophils, megakaryocytes, and granulocytes, various stem or progenitor cells, in particular hematopoietic stem or progenitor cells, e.g., as obtained from bone marrow, umbilical cord blood, peripheral blood, fetal liver, etc.

In a preferred embodiment, the cell used for gene therapy is autologous to the patient.

In an embodiment in which recombinant cells are used in gene therapy, a component protein encoding nucleic acid is/are introduced into the cells such that the gene or genes are expressible by the cells or their progeny, and the recombinant cells are then administered *in vivo* for therapeutic effect. In a specific embodiment, stem or progenitor cells are used. Any stem and/or progenitor cells which can be isolated and maintained *in vitro* can potentially be used in accordance with this embodiment of the present invention. Such stem cells include but are not limited to hematopoietic stem cells (HSCs), stem cells of epithelial tissues such as the skin and the lining of the gut,

embryonic heart muscle cells, liver stem cells (International Patent Publication WO 94/08598), and neural stem cells (Stemple and Anderson, 1992, Cell 71:973-985).

Epithelial stem cells (ESCs), or keratinocytes, can be obtained from tissues such as the skin and the lining of the gut by known procedures (Rheinwald, 1980, Meth. Cell Biol. 2A:229). In stratified epithelial tissue such as the skin, renewal occurs by mitosis of stem cells within the germinal layer, the layer closest to the basal lamina. Similarly, stem cells within the lining of the gut provide for a rapid renewal rate of this tissue. ESCs or keratinocytes obtained from the skin or lining of the gut of a patient or donor can be grown in tissue culture (Rheinwald, 1980, Meth. Cell Bio. 2A:229; Pittelkow and Scott, 1986, Mayo Clinic Proc. 61:771). If the ESCs are provided by a donor, a method for suppression of host versus graft reactivity (e.g., irradiation, or drug or antibody administration to promote moderate immunosuppression) can also be used.

With respect to hematopoietic stem cells (HSCs), any technique that provides for the isolation, propagation, and maintenance in vitro of HSCs can be used in this embodiment of the invention. Techniques by which this may be accomplished include (a) the isolation and establishment of HSC cultures from bone marrow cells isolated from the future host, or a donor, or (b) the use of previously established long-term HSC cultures, which may be allogeneic or xenogeneic. Non-autologous HSCs are used preferably in conjunction with a method of suppressing transplantation immune reactions between the future host and patient. In a particular embodiment of the present invention, human bone marrow cells can be obtained from the posterior iliac crest by needle aspiration (see, e.g., Kodo et al., 1984, J. Clin. Invest. 73: 1377-1384). In a preferred embodiment of the present invention, the HSCs can be made highly enriched or in substantially pure form. This enrichment can be accomplished before, during, or after long-term culturing, and can be done by any technique known in the art. Long-term cultures of bone marrow cells can be established and maintained by using, for example, modified Dexter cell culture techniques (Dexter et al., 1977, J. Cell Physiol. 91:335) or Witlock-Witte culture techniques (Witlock and Witte, 1982, Proc. Natl. Acad. Sci. USA 79:3608-3612).

In a specific embodiment, the nucleic acid to be introduced for purposes of gene therapy comprises an inducible promoter operably linked to the coding region, such that expression of the nucleic acid is controllable by controlling the presence or absence of the appropriate inducer of transcription.

Additional methods can be adapted for use to deliver a nucleic acid encoding the component proteins, or functional derivatives thereof, e.g., as described in Section 4.1, *supra*.

4.4.2 USE OF ANTISENSE OLIGONUCLEOTIDES FOR SUPPRESSION OF PROTEIN COMPLEX FORMATION OR PROTEIN COMPLEX/PROTEIN ACTIVITY

In a specific embodiment of the present invention, protein complex activity and formation and protein activity is inhibited by use of antisense nucleic acids for the component proteins of the complex, that inhibit transcription and/or translation of their complementary sequence. The present invention provides the therapeutic or prophylactic use of nucleic acids of at least six nucleotides that are antisense to a gene or cDNA encoding a component protein, or a portion thereof. An "antisense" nucleic acid as used herein refers to a nucleic acid capable of hybridizing to a sequence-specific portion of a component protein RNA (preferably mRNA) by virtue of some sequence complementarity. The antisense nucleic acid may be complementary to a coding and/or noncoding region of a component protein mRNA. Such antisense nucleic acids that inhibit complex formation or activity have utility as therapeutics, and can be used in the treatment or prevention of disorders as described *supra*.

The antisense nucleic acids of the invention can be oligonucleotides that are double-stranded or single-stranded, RNA or DNA, or a modification or derivative thereof, which can be directly administered to a cell, or which can be produced intracellularly by transcription of exogenous, introduced sequences.

In another embodiment, the present invention is directed to a method for inhibiting the expression of component protein nucleic acid sequences, in a prokaryotic or eukaryotic cell, comprising providing the cell with an effective amount of a composition comprising an antisense nucleic acid of the component protein, or a derivative thereof, of the invention.

The antisense nucleic acids are of at least six nucleotides and are preferably oligonucleotides, ranging from 6 to about 200 nucleotides. In specific aspects, the oligonucleotide is at least 10 nucleotides, at least 15 nucleotides, at least 100 nucleotides, or at least 200 nucleotides. The oligonucleotides can be DNA or RNA or chimeric mixtures, or derivatives or modified versions thereof, and either single-stranded

or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone. The oligonucleotide may include other appending groups such as peptides, agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. USA 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. USA 84:648-652; International Patent Publication No. WO 88/09810) or blood-brain barrier (see, e.g., International Patent Publication No. WO 89/10134), hybridization-triggered cleavage agents (see, e.g., Krol et al., 1988, BioTechniques 6:958-976), or intercalating agents (see, e.g., Zon, 1988, Pharm. Res. 5:539-549).

In a preferred aspect of the invention, an antisense oligonucleotide is provided, preferably as single-stranded DNA. The oligonucleotide may be modified at any position in its structure with constituents generally known in the art.

The antisense oligonucleotides may comprise at least one modified base moiety which is selected from the group including but not limited to 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl)uracil, 5-carboxymethylaminomethyl-2-thio-uridine, 5-carboxymethylaminomethyluracil, dihydrouracil, β -D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, β -D-mannosylqueosine, 5N-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methyl-thio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

In another embodiment, the oligonucleotide comprises at least one modified sugar moiety selected from the group including, but not limited to, arabinose, 2-fluoroarabinose, xylulose, and hexose.

In yet another embodiment, the oligonucleotide comprises at least one modified phosphate backbone selected from the group consisting of a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal, or an analog of the foregoing.

In yet another embodiment, the oligonucleotide is a 2'- α -anomeric oligonucleotide. An α -anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gautier et al., 1987, Nucl. Acids Res. 15:6625-6641).

The oligonucleotide may be conjugated to another molecule, e.g., a peptide, hybridization-triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

Oligonucleotides of the invention may be synthesized by standard methods known in the art, e.g., by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein et al. (1988, Nucl. Acids Res. 16:3209), methylphosphonate oligonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin et al., 1988, Proc. Natl. Acad. Sci. USA 85:7448-7451), etc.

In a specific embodiment, the antisense oligonucleotides comprise catalytic RNAs, or ribozymes (see, e.g., International Patent Publication No. WO 90/11364; Sarver et al., 1990, Science 247:1222-1225). In another embodiment, the oligonucleotide is a 2'-O-methylribonucleotide (Inoue et al., 1987, Nucl. Acids Res. 15:6131-6148), or a chimeric RNA-DNA analog (Inoue et al., 1987, FEBS Lett. 215:327-330).

In an alternative embodiment, the antisense nucleic acids of the invention are produced intracellularly by transcription from an exogenous sequence. For example, a vector can be introduced in vivo such that it is taken up by a cell, within which cell the vector or a portion thereof is transcribed, producing an antisense nucleic acid (RNA) of the invention. Such a vector would contain a sequence encoding the component protein. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art to be capable of replication and expression in mammalian cells. Expression of the sequences encoding the antisense RNAs can be by any promoter known in the art to act in mammalian, preferably human, cells. Such promoters can be inducible or constitutive. Such promoters include, but are not limited to, the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto

et al., 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner et al., 1981, Proc. Natl. Acad. Sci. USA 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster et al., 1982, Nature 296:39-42), etc.

The antisense nucleic acids of the invention comprise a sequence complementary to at least a portion of an RNA transcript of a component protein gene, preferably a human gene. However, absolute complementarity, although preferred, is not required. A sequence "complementary to at least a portion of an RNA," as referred to herein, means a sequence having sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with a component protein RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

The component protein antisense nucleic acids can be used to treat (or prevent) disorders of a cell type that expresses, or preferably overexpresses, a protein complex.

Cell types that express or overexpress component protein RNA can be identified by various methods known in the art. Such methods include, but are not limited to, hybridization with component protein-specific nucleic acids (e.g., by Northern blot hybridization, dot blot hybridization, or in situ hybridization), or by observing the ability of RNA from the cell type to be translated in vitro into the component protein by immunohistochemistry, Western blot analysis, ELISA, etc. In a preferred aspect, primary tissue from a patient can be assayed for protein expression prior to treatment, e.g., by immunocytochemistry, in situ hybridization, or any number of methods to detect protein or mRNA expression.

Pharmaceutical compositions of the invention (see Section 4.7, *infra*), comprising an effective amount of a protein component antisense nucleic acid in a pharmaceutically acceptable carrier can be administered to a patient having a disease or disorder that is of a type that expresses or overexpresses a protein complex of the present invention.

The amount of antisense nucleic acid that will be effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques. Where possible, it is desirable to

determine the antisense cytotoxicity in vitro, and then in useful animal model systems, prior to testing and use in humans.

In a specific embodiment, pharmaceutical compositions comprising antisense nucleic acids are administered via liposomes, microparticles, or microcapsules. In various embodiments of the invention, it may be useful to use such compositions to achieve sustained release of the antisense nucleic acids. In a specific embodiment, it may be desirable to utilize liposomes targeted via antibodies to specific identifiable central nervous system cell types (Leonetti et al., 1990, Proc. Natl. Acad. Sci. U.S.A. 87:2448-2451; Renneisen et al., 1990, J. Biol. Chem. 265:16337-16342).

4.5 ASSAYS OF PROTEIN COMPLEXES/PROTEINS OF THE INVENTION AND DERIVATIVES AND ANALOGS THEREOF

The functional activity of a protein complex of the present invention, or a derivative, fragment or analog thereof or protein component thereof, can be assayed by various methods. Potential modulators (e.g., agonists and antagonists) of complex activity or formation, e.g., anti-complex antibodies and antisense nucleic acids, can be assayed for the ability to modulate complex activity or formation.

In one embodiment of the present invention, where one is assaying for the ability to bind or compete with a wild-type complex for binding to an anti-complex antibody, various immunoassays known in the art can be used, including but not limited to competitive and non-competitive assay systems using techniques such as radioimmunoassay, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitin reactions, immunodiffusion assays, in situ immunoassays (using colloidal gold, enzyme or radioisotope labels), western blot analysis, precipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, immunoelectrophoresis assays, etc. In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labeled. Many means are known in the art for detecting binding in an immunoassay and are within the scope of the present invention.

The expression of the component protein genes (both endogenous and those expressed from cloned DNA containing the genes) can be detected using techniques known in the art, including but not limited to Southern hybridization (Southern, 1975, J. Mol. Biol. 98:503-517), northern hybridization (see, e.g., Freeman et al., 1983, Proc. Natl. Acad. Sci. USA 80:4094-4098), restriction endonuclease mapping (Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2nd Ed. Cold Spring Harbor Laboratory Press, New York), RNase protection assays (Current Protocols in Molecular Biology, John Wiley and Sons, New York, 1997), DNA sequence analysis, and polymerase chain reaction amplification (PCR; U.S. Patent Nos. 4,683,202, 4,683,195, and 4,889,818; Gyllenstein et al., 1988, Proc. Natl. Acad. Sci. USA 85:7652-7657; Ochman et al., 1988, Genetics 120:621-623; Loh et al., 1989, Science 243:217-220) followed by Southern hybridization with probes specific for the component protein genes, in various cell types. Methods of amplification other than PCR commonly known in the art can be employed. In one embodiment, Southern hybridization can be used to detect genetic linkage of component protein gene mutations to physiological or pathological states. Various cell types, at various stages of development, can be characterized for their expression of component proteins at the same time and in the same cells. The stringency of the hybridization conditions for northern or Southern blot analysis can be manipulated to ensure detection of nucleic acids with the desired degree of relatedness to the specific probes used. Modifications to these methods and other methods commonly known in the art can be used.

Derivatives (e.g., fragments), homologs and analogs of one component protein can be assayed for binding to another component protein in the same complex by any method known in the art, for example the modified yeast matrix mating test described in Section 4.6.1 *infra*, immunoprecipitation with an antibody that binds to the component protein complexed with other component proteins in the same complex, followed by size fractionation of the immunoprecipitated proteins (e.g., by denaturing or nondenaturing polyacrylamide gel electrophoresis), Western blot analysis, etc.

One embodiment of the invention provides a method for screening a derivative, homolog or analog of a component protein for biological activity comprising contacting said derivative, homolog or analog of the component protein with the other component proteins in the same complex; and detecting the formation of a complex between said derivative, homolog or analog of the component protein and the other component

proteins; wherein detecting formation of said complex indicates that said derivative, homolog or analog of has biological (e.g., binding) activity.

The invention also provides methods of modulating the activity of a component protein that can participate in a protein complex by administration of a binding partner of that protein or derivative, homolog or analog thereof.

In a specific embodiment of the present invention, a protein complex of the present invention is administered to treat or prevent a disease or disorder, since the complex and/or component proteins have been implicated in the disease and disorder. Accordingly, a protein complex or a derivative, homolog, analog or fragment thereof, nucleic acids encoding the component proteins, anti-complex antibodies, and other modulators of protein complex activity, can be tested for activity in treating or preventing a disease or disorder in in vitro and in vivo assays.

In one embodiment, a therapeutic of the invention can be assayed for activity in treating or preventing a disease by contacting cultured cells that exhibit an indicator of the disease in vitro, with the therapeutic, and comparing the level of said indicator in the cells contacted with the therapeutic, with said level of said indicator in cells not so contacted, wherein a lower level in said contacted cells indicates that the therapeutic has activity in treating or preventing the disease.

In another embodiment of the invention, a therapeutic of the invention can be assayed for activity in treating or preventing a disease by administering the therapeutic to a test animal that is predisposed to develop symptoms of a disease, and measuring the change in said symptoms of the disease after administration of said therapeutic, wherein a reduction in the severity of the symptoms of the disease or prevention of the symptoms of the disease indicates that the therapeutic has activity in treating or preventing the disease. Such a test animal can be any one of a number of animal models known in the art for disease. These animal models are well known in the art. These animal models include, but are not limited to those which are listed in the section 4.6 (supra) as exemplary animal models to study any of the complexes provided in the invention.

4.6 SCREENING FOR MODULATORS OF THE PROTEIN COMPLEXES/PROTEINS OF THE INVENTION

A complex of the present invention, the component proteins of the complex and nucleic acids encoding the component proteins, as well as derivatives and fragments of the amino and nucleic acids, can be used to screen for compounds that bind to, or modulate the amount of, activity of, or protein component composition of, said complex, and thus, have potential use as modulators, i.e., agonists or antagonists, of complex activity, and/or complex formation, i.e., the amount of complex formed, and/or protein component composition of the complex.

Thus, the present invention is also directed to methods for screening for molecules that bind to, or modulate the function of, amount of, activity of, formation of, or protein component composition of, a complex of the present invention. In one embodiment of the invention, the method for screening for a molecule that modulates directly or indirectly the function, activity or formation of a complex of the present invention comprises exposing said complex, or a cell or organism containing the complex machinery, to one or more candidate molecules under conditions conducive to modulation; and determining the amount of, the biochemical activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependend on the complex and/or the abundance and/or activity of a protein or protein complex dependend on the function of the complex and/or product of a gene dependend on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependend on the complex and/or the abundance and/or activity of a protein or protein complex dependend on the function of the complex and/or product of a gene dependend on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

In a further specific embodiment, a modulation of the formation process of a complex can be determined.

Such a modulation can either be a change in the typical time course of its formation or a change in the typical steps leading to the formation of the complete complex.

Such changes can for example be detected by analysing and comparing the process of complex formation in untreated wild type cells of a particular type and/or cells showing or

having the predisposition to develop a certain disease phenotype and/or cells which have been treated with particular conditions and/or particular agents in a particular situation. Methods to study such changes in time course are well known in the art and include for example Western-blot analysis of the proteins in the complex isolated at different steps of its formation.

Furthermore an aberrant intracellular localization of the protein complex and/or an aberrant transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or a gene dependent on the complex can serve as a marker for a disease and thus have diagnostic utility for any disease which is caused by an aberrant activity, function, composition or formation of the complex of the invention.

Methods to study the intracellular localization are well known in the art and include, but are not limited to immunofluorescence analysis using antibodies specific for components of the protein. Preferentially, double-stainings including staining of other cellular structures are being used to facilitate the detection of the intracellular localization. Methods to analyse the transcription levels of a gene dependent on the complex are also well known in the art and include Northern blot analysis, quantitative PCR etc. The abundance of proteins dependent on the protein can be analyzed as described supra. Methods to study changes in the activity of proteins dependent on complex depend on the protein. The choice of such methods will be apparent to any person skilled in the art.

In another embodiment, the present invention further relates to a process for the identification and/or preparation of an effector of the complex comprising the step of bringing into contact a product of any of claims 1 to 8 with a compound, a mixture or a library of compounds and determining whether the compound or a certain compound of the mixture or library binds to the product and/or effects the products biological activity and optionally further purifying the compound positively tested as effector.

In another embodiment, the present invention is directed to a method for screening for a molecule that binds a protein complex of the present invention comprising exposing said complex, or a cell or organism containing the complex machinery, to one or more candidate molecules; and determining whether said complex is bound by any of said candidate molecules. Such screening assays can be carried out using cell-free and cell-based methods that are commonly known in the art in vitro, in vivo or ex vivo. For example, an isolated complex can be employed, or a cell can be contacted with the candidate molecule and the complex can be isolated from such

contacted cells and the isolated complex can be assayed for activity or component composition. In another example, a cell containing the complex can be contacted with the candidate molecule and the levels of the complex in the contacted cell can be measured. Additionally, such assays can be carried out in cells recombinantly expressing a component protein from the fourth column of table 1, or a functionally active fragment or functionally active derivative thereof, and a component protein from fifth column of table 1, or a functionally active fragment or functionally active derivative thereof. Additionally, such assays can also be carried out in cells recombinantly expressing all component proteins from the group of proteins in the fifth column of table 1.

For example, assays can be carried out using recombinant cells expressing the protein components of a complex, to screen for molecules that bind to, or interfere with, or promote complex activity or formation. In preferred embodiments, polypeptide derivatives that have superior stabilities but retain the ability to form a complex (e.g., one or more component proteins modified to be resistant to proteolytic degradation in the binding assay buffers, or to be resistant to oxidative degradation), are used to screen for modulators of complex activity or formation. Such resistant molecules can be generated, e.g., by substitution of amino acids at proteolytic cleavage sites, the use of chemically derivatized amino acids at proteolytic susceptible sites, and the replacement of amino acid residues subject to oxidation, i.e. methionine and cysteine.

A particular aspect of the present invention relates to identifying molecules that inhibit or promote formation or degradation of a complex of the present invention, e.g., using the method described for isolating the complex and identifying members of the complex using the TAP assay described in Section 4, *infra*, and in WO 00/09716 and Rigaut et al., 1999, *Nature Biotechnol.* 17:1030-1032, which are each incorporated by reference in their entirety. TNRF1

In another embodiment of the invention, a modulator is identified by administering a candidate molecule to a transgenic non-human animal expressing the complex component proteins from promoters that are not the native promoters of the respective proteins, more preferably where the candidate molecule is also recombinantly expressed in the transgenic non-human animal. Alternatively, the method for identifying such a modulator can be carried out *in vitro*, preferably with a purified complex, and a purified candidate molecule.

Agents/molecules (candidate molecules) to be screened can be provided as mixtures of a limited number of specified compounds, or as compound libraries, peptide libraries and the like. Agents/molecules to be screened may also include all forms of antisera, antisense nucleic acids, etc., that can modulate complex activity or formation. Exemplary candidate molecules and libraries for screening are set forth in Section 4.6.1, *infra*.

Screening the libraries can be accomplished by any of a variety of commonly known methods. See, e.g., the following references, which disclose screening of peptide libraries: Parmley and Smith, 1989, *Adv. Exp. Med. Biol.* 251:215-218; Scott and Smith, 1990, *Science* 249:386-390; Fowlkes et al., 1992, *BioTechniques* 13:422-427; Oldenburg et al., 1992, *Proc. Natl. Acad. Sci. USA* 89:5393-5397; Yu et al., 1994, *Cell* 76:933-945; Staudt et al., 1988, *Science* 241:577-580; Bock et al., 1992, *Nature* 355:564-566; Tuerk et al., 1992, *Proc. Natl. Acad. Sci. USA* 89:6988-6992; Ellington et al., 1992, *Nature* 355:850-852; U.S. Patent No. 5,096,815, U.S. Patent No. 5,223,409, and U.S. Patent No. 5,198,346, all to Ladner et al.; Rebar and Pabo, 1993, *Science* 263:671-673; and International Patent Publication No. WO 94/18318.

In a specific embodiment, screening can be carried out by contacting the library members with a complex immobilized on a solid phase, and harvesting those library members that bind to the protein (or encoding nucleic acid or derivative). Examples of such screening methods, termed "panning" techniques, are described by way of example in Parmley and Smith, 1988, *Gene* 73:305-318; Fowlkes et al., 1992, *BioTechniques* 13:422-427; International Patent Publication No. WO 94/18318; and in references cited hereinabove.

In a specific embodiment, fragments and/or analogs of protein components of a complex, especially peptidomimetics, are screened for activity as competitive or non-competitive inhibitors of complex formation (amount of complex or composition of complex) or activity in the cell, which thereby inhibit complex activity or formation in the cell.

In one embodiment, agents that modulate (i.e., antagonize or agonize) complex activity or formation can be screened for using a binding inhibition assay, wherein agents are screened for their ability to modulate formation of a complex under aqueous, or physiological, binding conditions in which complex formation occurs in the absence of the agent to be tested. Agents that interfere with the formation of complexes of the invention are identified as antagonists of complex formation. Agents that promote the formation of

complexes are identified as agonists of complex formation. Agents that completely block the formation of complexes are identified as inhibitors of complex formation.

Methods for screening may involve labeling the component proteins of the complex with radioligands (e.g., ^{125}I or ^3H), magnetic ligands (e.g., paramagnetic beads covalently attached to photobiotin acetate), fluorescent ligands (e.g., fluorescein or rhodamine), or enzyme ligands (e.g., luciferase or β -galactosidase). The reactants that bind in solution can then be isolated by one of many techniques known in the art, including but not restricted to, co-immunoprecipitation of the labeled complex moiety using antisera against the unlabeled binding partner (or labeled binding partner with a distinguishable marker from that used on the second labeled complex moiety), immunoaffinity chromatography, size exclusion chromatography, and gradient density centrifugation. In a preferred embodiment, the labeled binding partner is a small fragment or peptidomimetic that is not retained by a commercially available filter. Upon binding, the labeled species is then unable to pass through the filter, providing for a simple assay of complex formation.

Methods commonly known in the art are used to label at least one of the component members of the complex. Suitable labeling methods include, but are not limited to, radiolabeling by incorporation of radiolabeled amino acids, e.g., ^3H -leucine or ^{35}S -methionine, radiolabeling by post-translational iodination with ^{125}I or ^{131}I using the chloramine T method, Bolton-Hunter reagents, etc., or labeling with ^{32}P using phosphorylase and inorganic radiolabeled phosphorous, biotin labeling with photobiotin-acetate and sunlamp exposure, etc. In cases where one of the members of the complex is immobilized, e.g., as described infra, the free species is labeled. Where neither of the interacting species is immobilized, each can be labeled with a distinguishable marker such that isolation of both moieties can be followed to provide for more accurate quantification, and to distinguish the formation of homomeric from heteromeric complexes. Methods that utilize accessory proteins that bind to one of the modified interactants to improve the sensitivity of detection, increase the stability of the complex, etc., are provided.

Typical binding conditions are, for example, but not by way of limitation, in an aqueous salt solution of 10-250 mM NaCl, 5-50 mM Tris-HCl, pH 5-8, and 0.5% Triton X-100 or other detergent that improves specificity of interaction. Metal chelators and/or divalent cations may be added to improve binding and/or reduce proteolysis. Reaction temperatures may include 4, 10, 15, 22, 25, 35, or 42 degrees Celsius, and time of

incubation is typically at least 15 seconds, but longer times are preferred to allow binding equilibrium to occur. Particular complexes can be assayed using routine protein binding assays to determine optimal binding conditions for reproducible binding.

The physical parameters of complex formation can be analyzed by quantification of complex formation using assay methods specific for the label used, e.g., liquid scintillation counting for radioactivity detection, enzyme activity for enzyme-labeled moieties, etc. The reaction results are then analyzed utilizing Scatchard analysis, Hill analysis, and other methods commonly known in the arts (see, e.g., *Proteins, Structures, and Molecular Principles*, 2nd Edition (1993) Creighton, Ed., W.H. Freeman and Company, New York).

In a second common approach to binding assays, one of the binding species is immobilized on a filter, in a microtiter plate well, in a test tube, to a chromatography matrix, etc., either covalently or non-covalently. Proteins can be covalently immobilized using any method well known in the art, for example, but not limited to the method of Kadonaga and Tjian, 1986, *Proc. Natl. Acad. Sci. USA* 83:5889-5893, i.e., linkage to a cyanogen-bromide derivatized substrate such as CNBr-Sepharose 4B (Pharmacia). Where needed, the use of spacers can reduce steric hindrance by the substrate. Non-covalent attachment of proteins to a substrate include, but are not limited to, attachment of a protein to a charged surface, binding with specific antibodies, binding to a third unrelated interacting protein, etc.

Assays of agents (including cell extracts or a library pool) for competition for binding of one member of a complex (or derivatives thereof) with another member of the complex labeled by any means (e.g., those means described above) are provided to screen for competitors or enhancers of complex formation.

In specific embodiments, blocking agents to inhibit non-specific binding of reagents to other protein components, or absorptive losses of reagents to plastics, immobilization matrices, etc., are included in the assay mixture. Blocking agents include, but are not restricted to bovine serum albumin, β -casein, nonfat dried milk, Denhardt's reagent, Ficoll, polyvinylpyrrolidone, nonionic detergents (NP40, Triton X-100, Tween 20, Tween 80, etc.), ionic detergents (e.g., SDS, LDS, etc.), polyethylene glycol, etc. Appropriate blocking agent concentrations allow complex formation.

After binding is performed, unbound, labeled protein is removed in the supernatant, and the immobilized protein retaining any bound, labeled protein is washed

extensively. The amount of bound label is then quantified using standard methods in the art to detect the label as described, *supra*.

In another specific embodiments screening for modulators of the protein complexes/protein as provided herein can be carried out by attaching those and/or the antibodies as provided herein to a solid carrier. In a further specific embodiment, the invention relates to an array of said molecules.

The preparation of such an array containing different types of proteins, including antibodies) is well known in the art and is apparent to a person skilled in the art (see e.g. Ekins et al., 1989, *J. Pharm. Biomed. Anal.* 7:155-168; Mitchell et al. 2002, *Nature Biotechnol.* 20:225-229; Petricoin et al., 2002, *Lancet* 359:572-577; Templin et al., 2001, *Trends Biotechnol.* 20:160-166; Wilson and Nock, 2001, *Curr. Opin. Chem. Biol.* 6:81-85; Lee et al., 2002 *Science* 295:1702-1705; MacBeath and Schreiber, 2000, *Science* 289:1760; Blawas and Reichert, 1998, *Biomaterials* 19:595; Kane et al., 1999, *Biomaterials* 20:2363; Chen et al., 1997, *Science* 276:1425; Vaughan et al., 1996, *Nature Biotechnol.* 14:309-314; Mahler et al., 1997, *Immunotechnology* 3:31-43; Roberts et al., 1999, *Curr. Opin. Chem. Biol.* 3:268-273; Nord et al., 1997, *Nature Biotechnol.* 15:772-777; Nord et al., 2001, *Eur. J. Biochem.* 268:4269-4277; Brody and Gold, 2000, *Rev. Mol. Biotechnol.* 74:5-13; Karlstroem and Nygren, 2001, *Anal. Biochem.* 295:22-30; Nelson et al., 2000, *Electrophoresis* 21:1155-1163; Honore et al., 2001, *Expert Rev. Mol. Diagn.* 3:265-274; Albala, 2001, *Expert Rev. Mol. Diagn.* 2:145-152, Figeys and Pinto, 2001, *Electrophoresis* 2:208-216 and references in the publications listed here).

Complexes can be attached to an array by different means as will be apparent to a person skilled in the art. Complexes can for example be added to the array via a TAP-tag (as described in WO/0009716 and in Rigaut et al., 1999, *Nature Biotechnol.* 10:1030-1032) after the purification step or by another suitable purification scheme as will be apparent to a person skilled in the art.

Optionally, the proteins of the complex can be cross-linked to enhance the stability of the complex. Different methods to cross-link proteins are well known in the art. Reactive end-groups of cross-linking agents include but are not limited to -COOH, -SH, -NH₂ or N-oxy-succinamate.

The spacer of the cross-linking agent should be chosen with respect to the size of the complex to be cross-linked. For small protein complexes, comprising only a few proteins, relatively short spacers are preferable in order to reduce the likelihood of cross-linking separate complexes in the reaction mixture. For larger protein complexes, additional use

of larger spacers is preferable in order to facilitate cross-linking between proteins within the complex.

It is preferable to check the success-rate of cross-linking before linking the complex to the carrier.

As will be apparent to a person skilled in the art, the optimal rate of cross-linking need to be determined on a case by case basis. This can be achieved by methods well known in the art, some of which are exemplary described below.

A sufficient rate of cross-linking can be checked f.e. by analysing the cross-linked complex vs. a non-cross-linked complex on a denaturing protein gel.

If cross-linking has been performed successfully, the proteins of the complex are expected to be found in the same lane, whereas the proteins of the non-cross-linked complex are expected to be separated according to their individual characteristics. Optionally the presence of all proteins of the complex can be further checked by peptide-sequencing of proteins in the respective bands using methods well known in the art such as mass spectrometry and/or Edman degradation.

In addition, a rate of crosslinking which is too high should also be avoided. If cross-linking has been carried out too extensively, there will be an increasing amount of cross-linking of the individual protein complex, which potentially interferes with a screening for potential binding partners and/or modulators etc. using the arrays.

The presence of such structures can be determined by methods well known in the art and include e.g. gel-filtration experiments comparing the gel filtration profile solutions containing cross-linked complexes vs. uncross-linked complexes.

Optionally, functional assays as will be apparent to a person skilled in the art, some of which are exemplarily provided herein, can be performed to check the integrity of the complex.

Alternatively, members of the protein complex can be expressed as a single fusion protein and coupled to the matrix as will be apparent to a person skilled in the art.

Optionally, the attachment of the complex or proteins or antibody as outlined above can be further monitored by various methods apparent to a person skilled in the art. Those include, but are not limited to surface plasmon resonance (see e.g. McDonnel, 2001, Curr. Opin. Chem. Biol. 5:572-577; Lee, 2001, Trends Biotechnol. 19:217-222; Weinberger et al., 2000, 1:395-416; Pearson et al., 2000, Ann. Clin. Biochem. 37:119-

145; Vely et al., 2000, Methods Mol. Biol. 121:313-321; Slepak, 2000, J. Mol. Recognit. 13:20-26.

Exemplary assays useful for measuring the Bcl-2 binding activity of the Bcl2-complex include but are not limited to those described in Hanada M et al., 1995, J Biol Chem, 270:11962-9.

Exemplary assays useful for measuring the cytochrome c release activity from mitochondria of the Bcl2-complex include but are not limited to those described in Bossy-Wetzel E and ., 2000, Methods Enzymol, 322:235-42.

Exemplary assays useful for measuring the apoptosis induction activity of the Bcl2-complex include but are not limited to those described in Bossy-Wetzel E and ., 2000, Methods Enzymol, 322:15-8.

Exemplary assays useful for measuring the Cell motility activity of the Gab1 signalling complex include but are not limited to those described in Petrelli Annalisa et al., 2002, Nature, 416:187-90.

Exemplary assays useful for measuring the Focus forming activity of the Gab1 signalling complex include but are not limited to those described in Giordano S et al., 1997, Proc Natl Acad Sci U S A, 94:13868-72.

Exemplary assays useful for measuring the Tumorigenicity and experimental metastatic activity of the Gab1 signalling complex include but are not limited to those described in Giordano S et al., 1997, Proc Natl Acad Sci U S A, 94:13868-72.

Exemplary assays useful for measuring the In vitro invasion activity of the Gab1 signalling complex include but are not limited to those described in Giordano S et al., 1997, Proc Natl Acad Sci U S A, 94:13868-72.

Exemplary assays useful for measuring the Soft agar colony formation activity of the Gab1 signalling complex include but are not limited to those described in Giordano S et al., 1997, Proc Natl Acad Sci U S A, 94:13868-72.

Exemplary assays useful for measuring the Scatter activity of the Gab1 signalling complex include but are not limited to those described in Ponzetto C et al., 1996, J Biol Chem, 271:14119-23.

Exemplary assays useful for measuring the kinase activity of the Her2 complex include but are not limited to those described in Engelman J A et al., 1998, J Biol Chem, 273:20448-55.

Exemplary assays useful for measuring the diacylglycerol kinase activity of the Her2 complex include but are not limited to those described in Walsh J P et al., 1992, Methods Enzymol, 209:153-62.

Exemplary assays useful for measuring the sphingosine kinase activity of the Her2 complex include but are not limited to those described in Olivera A et al., 2000, Methods Enzymol, 311:215-23.

Exemplary assays useful for measuring the kinase activation of the Ringo 1 complex include but are not limited to those described in Karaiskou A et al., 2001, J Biol Chem, 276:36028-34.

Exemplary assays useful for measuring the DNA binding activity of the telomere capping complex include but are not limited to those described in Baumann P et al., 2001, Science, 292:1171-5.

Exemplary assays useful for measuring the TRF2 binding activity of the telomere capping complex include but are not limited to those described in Song K et al., 2000, FEBS Lett, 481:81-5.

Exemplary assays useful for measuring the RAP1 binding activity of the telomere capping complex include but are not limited to those described in Li B et al., 2000, Cell, 101:471-83.

4.6.1 CANDIDATE MOLECULES

Any molecule known in the art can be tested for its ability to modulate (increase or decrease) the amount of, activity of, or protein component composition of a complex of the present invention as detected by a change in the amount of, activity of, or protein component composition of, said complex. By way of example, a change in the amount of the complex can be detected by detecting a change in the amount of the complex that can be isolated from a cell expressing the complex machinery. For identifying a molecule that modulates complex activity, candidate molecules can be directly provided to a cell expressing the complex machinery, or, in the case of candidate proteins, can be provided by providing their encoding nucleic acids under conditions in which the nucleic acids are recombinantly expressed to produce the candidate proteins within the cell expressing the complex machinery, the complex is then isolated from the cell and the isolated complex is assayed for activity using methods well known in the art, not limited to those described, supra.

This embodiment of the invention is well suited to screen chemical libraries for molecules which modulate, e.g., inhibit, antagonize, or agonize, the amount of, activity of, or protein component composition of the complex. The chemical libraries can be peptide libraries, peptidomimetic libraries, chemically synthesized libraries, recombinant, e.g., phage display libraries, and in vitro translation-based libraries, other non-peptide synthetic organic libraries, etc.

Exemplary libraries are commercially available from several sources (ArQule, Tripos/PanLabs, ChemDesign, Pharmacopoeia). In some cases, these chemical libraries are generated using combinatorial strategies that encode the identity of each member of the library on a substrate to which the member compound is attached, thus allowing direct and immediate identification of a molecule that is an effective modulator. Thus, in many combinatorial approaches, the position on a plate of a compound specifies that compound's composition. Also, in one example, a single plate position may have from 1-20 chemicals that can be screened by administration to a well containing the

interactions of interest. Thus, if modulation is detected, smaller and smaller pools of interacting pairs can be assayed for the modulation activity. By such methods, many candidate molecules can be screened.

Many diversity libraries suitable for use are known in the art and can be used to provide compounds to be tested according to the present invention. Alternatively, libraries can be constructed using standard methods. Chemical (synthetic) libraries, recombinant expression libraries, or polysome-based libraries are exemplary types of libraries that can be used.

The libraries can be constrained or semirigid (having some degree of structural rigidity), or linear or nonconstrained. The library can be a cDNA or genomic expression library, random peptide expression library or a chemically synthesized random peptide library, or non-peptide library. Expression libraries are introduced into the cells in which the assay occurs, where the nucleic acids of the library are expressed to produce their encoded proteins.

In one embodiment, peptide libraries that can be used in the present invention may be libraries that are chemically synthesized *in vitro*. Examples of such libraries are given in Houghten et al., 1991, *Nature* 354:84-86, which describes mixtures of free hexapeptides in which the first and second residues in each peptide were individually and specifically defined; Lam et al., 1991, *Nature* 354:82-84, which describes a "one bead, one peptide" approach in which a solid phase split synthesis scheme produced a library of peptides in which each bead in the collection had immobilized thereon a single, random sequence of amino acid residues; Medynski, 1994, *Bio/Technology* 12:709-710, which describes split synthesis and T-bag synthesis methods; and Gallop et al., 1994, *J. Med. Chem.* 37:1233-1251. Simply by way of other examples, a combinatorial library may be prepared for use, according to the methods of Ohlmeyer et al., 1993, *Proc. Natl. Acad. Sci. USA* 90:10922-10926; Erb et al., 1994, *Proc. Natl. Acad. Sci. USA* 91:11422-11426; Houghten et al., 1992, *Biotechniques* 13:412; Jayawickreme et al., 1994, *Proc. Natl. Acad. Sci. USA* 91:1614-1618; or Salmon et al., 1993, *Proc. Natl. Acad. Sci. USA* 90:11708-11712. PCT Publication No. WO 93/20242 and Brenner and Lerner, 1992, *Proc. Natl. Acad. Sci. USA* 89:5381-5383 describe "encoded combinatorial chemical libraries," that contain oligonucleotide identifiers for each chemical polymer library member.

In a preferred embodiment, the library screened is a biological expression library that is a random peptide phage display library, where the random peptides are constrained (e.g., by virtue of having disulfide bonding).

Further, more general, structurally constrained, organic diversity (e.g., nonpeptide) libraries, can also be used. By way of example, a benzodiazepine library (see e.g., Bunin et al., 1994, Proc. Natl. Acad. Sci. USA 91:4708-4712) may be used.

Conformationally constrained libraries that can be used include but are not limited to those containing invariant cysteine residues which, in an oxidizing environment, cross-link by disulfide bonds to form cystines, modified peptides (e.g., incorporating fluorine, metals, isotopic labels, are phosphorylated, etc.), peptides containing one or more non-naturally occurring amino acids, non-peptide structures, and peptides containing a significant fraction of γ -carboxyglutamic acid.

Libraries of non-peptides, e.g., peptide derivatives (for example, that contain one or more non-naturally occurring amino acids) can also be used. One example of these are peptoid libraries (Simon et al., 1992, Proc. Natl. Acad. Sci. USA 89:9367-9371). Peptoids are polymers of non-natural amino acids that have naturally occurring side chains attached not to the α carbon but to the backbone amino nitrogen. Since peptoids are not easily degraded by human digestive enzymes, they are advantageously more easily adaptable to drug use. Another example of a library that can be used, in which the amide functionalities in peptides have been permethylated to generate a chemically transformed combinatorial library, is described by Ostresh et al., 1994, Proc. Natl. Acad. Sci. USA 91:11138-11142).

The members of the peptide libraries that can be screened according to the invention are not limited to containing the 20 naturally occurring amino acids. In particular, chemically synthesized libraries and polysome based libraries allow the use of amino acids in addition to the 20 naturally occurring amino acids (by their inclusion in the precursor pool of amino acids used in library production). In specific embodiments, the library members contain one or more non-natural or non-classical amino acids or cyclic peptides. Non-classical amino acids include but are not limited to the D-isomers of the common amino acids, γ -amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid; γ -Abu, γ -Ahx, 6-amino hexanoic acid; Aib, 2-amino isobutyric acid; 3-amino propionic acid; ornithine; norleucine; norvaline, hydroxyproline, sarcosine, citrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, β -alanine, designer amino acids such as β -methyl amino acids, γ -methyl amino acids, N-methyl amino acids,

GAMMA CATALYTIC SUBUNIT" nucleic acid or its complement under low stringency conditions,

(xliv) "SIMILAR TO OROSOMUCOID 1" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIMILAR TO OROSOMUCOID 1" encoded by a nucleic acid that hybridizes to the "SIMILAR TO OROSOMUCOID 1" nucleic acid or its complement under low stringency conditions,

(xlv) "SMC5 PROTEIN" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SMC5 PROTEIN" encoded by a nucleic acid that hybridizes to the "SMC5 PROTEIN" nucleic acid or its complement under low stringency conditions,

(xlvi) "SQUAMOUS CELL CARCINOMA ANTIGEN 1" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SQUAMOUS CELL CARCINOMA ANTIGEN 1" encoded by a nucleic acid that hybridizes to the "SQUAMOUS CELL CARCINOMA ANTIGEN 1" nucleic acid or its complement under low stringency conditions,

(xlvii) "SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG" encoded by a nucleic acid that hybridizes to the "SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG" nucleic acid or its complement under low stringency conditions,

(xlviii) "Serine/threonine protein phosphatase 2A, catalytic subunit, beta isoform" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Serine/threonine protein phosphatase 2A, catalytic subunit, beta isoform" encoded by a nucleic acid that hybridizes to the "Serine/threonine protein phosphatase 2A, catalytic subunit, beta isoform" nucleic acid or its complement under low stringency conditions,

(xlix) "Similar to diacylglycerol kinase delta" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Similar to diacylglycerol kinase delta" encoded by a nucleic acid that hybridizes to the "Similar to diacylglycerol kinase delta" nucleic acid or its complement under low stringency conditions,

(l) "TELOMERASE-BINDING PROTEIN P23" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a

variant of "TELOMERASE-BINDING PROTEIN P23" encoded by a nucleic acid that hybridizes to the "TELOMERASE-BINDING PROTEIN P23" nucleic acid or its complement under low stringency conditions,

(li) "TELOMERIC REPEAT BINDING FACTOR 2" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TELOMERIC REPEAT BINDING FACTOR 2" encoded by a nucleic acid that hybridizes to the "TELOMERIC REPEAT BINDING FACTOR 2" nucleic acid or its complement under low stringency conditions,

(lii) "TERF1 (TRF1)-INTERACTING NUCLEAR FACTOR 2" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TERF1 (TRF1)-INTERACTING NUCLEAR FACTOR 2" encoded by a nucleic acid that hybridizes to the "TERF1 (TRF1)-INTERACTING NUCLEAR FACTOR 2" nucleic acid or its complement under low stringency conditions,

(liii) "TRF1" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TRF1" encoded by a nucleic acid that hybridizes to the "TRF1" nucleic acid or its complement under low stringency conditions,

(liv) "TRF2-INTERACTING TELOMERIC RAP1 PROTEIN" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TRF2-INTERACTING TELOMERIC RAP1 PROTEIN" encoded by a nucleic acid that hybridizes to the "TRF2-INTERACTING TELOMERIC RAP1 PROTEIN" nucleic acid or its complement under low stringency conditions,

(lv) "TRICARBOXYLATE TRANSPORT PROTEIN, MITOCHONDRIAL PRECURSOR" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TRICARBOXYLATE TRANSPORT PROTEIN, MITOCHONDRIAL PRECURSOR" encoded by a nucleic acid that hybridizes to the "TRICARBOXYLATE TRANSPORT PROTEIN, MITOCHONDRIAL PRECURSOR" nucleic acid or its complement under low stringency conditions,

(lvi) "U5 SMALL NUCLEAR RIBONUCLEOPROTEIN 200 KDA HELICASE (FRAGMENT)" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "U5 SMALL NUCLEAR RIBONUCLEOPROTEIN 200 KDA HELICASE (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "U5 SMALL NUCLEAR RIBONUCLEOPROTEIN 200

KDA HELICASE (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(lvii) "WD-REPEAT PROTEIN AN11 HOMOLOG" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "WD-REPEAT PROTEIN AN11 HOMOLOG" encoded by a nucleic acid that hybridizes to the "WD-REPEAT PROTEIN AN11 HOMOLOG" nucleic acid or its complement under low stringency conditions,

and a protein complex selected from complex (II) and comprising the following proteins:

(i) "38 KDA FK-506 BINDING PROTEIN HOMOLOG" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "38 KDA FK-506 BINDING PROTEIN HOMOLOG" encoded by a nucleic acid that hybridizes to the "38 KDA FK-506 BINDING PROTEIN HOMOLOG" nucleic acid or its complement under low stringency conditions,

(ii) "ANTIGEN NY-CO-7" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ANTIGEN NY-CO-7" encoded by a nucleic acid that hybridizes to the "ANTIGEN NY-CO-7" nucleic acid or its complement under low stringency conditions,

(iii) "ATP-BINDING CASSETTE, SUB-FAMILY D, MEMBER 3" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-BINDING CASSETTE, SUB-FAMILY D, MEMBER 3" encoded by a nucleic acid that hybridizes to the "ATP-BINDING CASSETTE, SUB-FAMILY D, MEMBER 3" nucleic acid or its complement under low stringency conditions,

(iv) "ATP-DEPENDENT DNA HELICASE II, 80 KDA SUBUNIT" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-DEPENDENT DNA HELICASE II, 80 KDA SUBUNIT" encoded by a nucleic acid that hybridizes to the "ATP-DEPENDENT DNA HELICASE II, 80 KDA SUBUNIT" nucleic acid or its complement under low stringency conditions,

(v) "BAF180" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BAF180" encoded by a nucleic acid that hybridizes to the "BAF180" nucleic acid or its complement under low stringency conditions,

(vi) "CASEIN KINASE II, ALPHA CHAIN" (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a

variant of "CASEIN KINASE II, ALPHA CHAIN" encoded by a nucleic acid that hybridizes to the "CASEIN KINASE II, ALPHA CHAIN" nucleic acid or its complement under low stringency conditions,

(vii) "CDNA FLJ13664 FIS, CLONE PLACE1011649" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ13664 FIS, CLONE PLACE1011649" encoded by a nucleic acid that hybridizes to the "CDNA FLJ13664 FIS, CLONE PLACE1011649" nucleic acid or its complement under low stringency conditions,

(viii) "CDNA FLJ13998 FIS, CLONE Y79AA1002229" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ13998 FIS, CLONE Y79AA1002229" encoded by a nucleic acid that hybridizes to the "CDNA FLJ13998 FIS, CLONE Y79AA1002229" nucleic acid or its complement under low stringency conditions,

(ix) "CDNA FLJ20643 FIS, CLONE KAT02633" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ20643 FIS, CLONE KAT02633" encoded by a nucleic acid that hybridizes to the "CDNA FLJ20643 FIS, CLONE KAT02633" nucleic acid or its complement under low stringency conditions,

(x) "CDNA FLJ25320 FIS, CLONE TST00267 (FRAGMENT)" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ25320 FIS, CLONE TST00267 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "CDNA FLJ25320 FIS, CLONE TST00267 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xi) "CDNA FLJ31741 FIS, CLONE NT2RI2007148" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ31741 FIS, CLONE NT2RI2007148" encoded by a nucleic acid that hybridizes to the "CDNA FLJ31741 FIS, CLONE NT2RI2007148" nucleic acid or its complement under low stringency conditions,

(xii) "CDNA: FLJ21908 FIS, CLONE HEP03830" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA: FLJ21908 FIS, CLONE HEP03830" encoded by a nucleic acid that hybridizes to the "CDNA: FLJ21908 FIS, CLONE HEP03830" nucleic acid or its complement under low stringency conditions,

- (xiii) "CENP-F KINETOCHORE PROTEIN" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CENP-F KINETOCHORE PROTEIN" encoded by a nucleic acid that hybridizes to the "CENP-F KINETOCHORE PROTEIN" nucleic acid or its complement under low stringency conditions,
- (xiv) "CHROMATIN ASSEMBLY FACTOR 1 SUBUNIT C" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CHROMATIN ASSEMBLY FACTOR 1 SUBUNIT C" encoded by a nucleic acid that hybridizes to the "CHROMATIN ASSEMBLY FACTOR 1 SUBUNIT C" nucleic acid or its complement under low stringency conditions,
- (xv) "DNA MISMATCH REPAIR PROTEIN MSH6" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DNA MISMATCH REPAIR PROTEIN MSH6" encoded by a nucleic acid that hybridizes to the "DNA MISMATCH REPAIR PROTEIN MSH6" nucleic acid or its complement under low stringency conditions,
- (xvi) "DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT" encoded by a nucleic acid that hybridizes to the "DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT" nucleic acid or its complement under low stringency conditions,
- (xvii) "DNA-DIRECTED RNA POLYMERASE II 23 KDA POLYPEPTIDE" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DNA-DIRECTED RNA POLYMERASE II 23 KDA POLYPEPTIDE" encoded by a nucleic acid that hybridizes to the "DNA-DIRECTED RNA POLYMERASE II 23 KDA POLYPEPTIDE" nucleic acid or its complement under low stringency conditions,
- (xviii) "ELONGATION FACTOR 2 KINASE" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ELONGATION FACTOR 2 KINASE" encoded by a nucleic acid that hybridizes to the "ELONGATION FACTOR 2 KINASE" nucleic acid or its complement under low stringency conditions,
- (xix) "FK506-BINDING PROTEIN 4" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"FK506-BINDING PROTEIN 4" encoded by a nucleic acid that hybridizes to the "FK506-BINDING PROTEIN 4" nucleic acid or its complement under low stringency conditions,

(xx) "GLIAL FIBRILLARY ACIDIC PROTEIN, ASTROCYTE" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GLIAL FIBRILLARY ACIDIC PROTEIN, ASTROCYTE" encoded by a nucleic acid that hybridizes to the "GLIAL FIBRILLARY ACIDIC PROTEIN, ASTROCYTE" nucleic acid or its complement under low stringency conditions,

(xxi) "HDCMD34P" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HDCMD34P" encoded by a nucleic acid that hybridizes to the "HDCMD34P" nucleic acid or its complement under low stringency conditions,

(xxii) "HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H'" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H'" encoded by a nucleic acid that hybridizes to the "HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H'" nucleic acid or its complement under low stringency conditions,

(xxiii) "HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2" encoded by a nucleic acid that hybridizes to the "HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2" nucleic acid or its complement under low stringency conditions,

(xxiv) "HSPC029" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC029" encoded by a nucleic acid that hybridizes to the "HSPC029" nucleic acid or its complement under low stringency conditions,

(xxv) "HYPOTHETICAL PROTEIN KIAA0310 (FRAGMENT)" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN KIAA0310 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN KIAA0310 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxvi) "INCOMPATIBILITY PROTEIN HET-E-1 (FRAGMENT)" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "INCOMPATIBILITY PROTEIN HET-E-1 (FRAGMENT)"

encoded by a nucleic acid that hybridizes to the "INCOMPATIBILITY PROTEIN HET-E-1 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxvii) "KIAA0792 PROTEIN" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0792 PROTEIN" encoded by a nucleic acid that hybridizes to the "KIAA0792 PROTEIN" nucleic acid or its complement under low stringency conditions,

(xxviii) "KIAA1284 PROTEIN (FRAGMENT)" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1284 PROTEIN (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1284 PROTEIN (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxix) "MEPRIN A BETA-SUBUNIT PRECURSOR" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MEPRIN A BETA-SUBUNIT PRECURSOR" encoded by a nucleic acid that hybridizes to the "MEPRIN A BETA-SUBUNIT PRECURSOR" nucleic acid or its complement under low stringency conditions,

(xxx) "MUTS" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MUTS" encoded by a nucleic acid that hybridizes to the "MUTS" nucleic acid or its complement under low stringency conditions,

(xxxi) "MYELOID LEUKEMIA FACTOR 2" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MYELOID LEUKEMIA FACTOR 2" encoded by a nucleic acid that hybridizes to the "MYELOID LEUKEMIA FACTOR 2" nucleic acid or its complement under low stringency conditions,

(xxxii) "NEIGHBOR OF A-KINASE ANCHORING PROTEIN 95" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NEIGHBOR OF A-KINASE ANCHORING PROTEIN 95" encoded by a nucleic acid that hybridizes to the "NEIGHBOR OF A-KINASE ANCHORING PROTEIN 95" nucleic acid or its complement under low stringency conditions,

(xxxiii) "P30 DBC" (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "P30 DBC"

encoded by a nucleic acid that hybridizes to the "P30 DBC" nucleic acid or its complement under low stringency conditions,

(xxxiv) "PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-X" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-X" encoded by a nucleic acid that hybridizes to the "PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-X" nucleic acid or its complement under low stringency conditions,

(xxxv) "PROGRAMED CELL DEATH PROTEIN 2" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PROGRAMED CELL DEATH PROTEIN 2" encoded by a nucleic acid that hybridizes to the "PROGRAMED CELL DEATH PROTEIN 2" nucleic acid or its complement under low stringency conditions,

(xxxvi) "PROLIFERATING CELL NUCLEAR ANTIGEN" (SEQ ID No:36) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PROLIFERATING CELL NUCLEAR ANTIGEN" encoded by a nucleic acid that hybridizes to the "PROLIFERATING CELL NUCLEAR ANTIGEN" nucleic acid or its complement under low stringency conditions,

(xxxvii) "PROTEASOME SUBUNIT BETA TYPE 3" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PROTEASOME SUBUNIT BETA TYPE 3" encoded by a nucleic acid that hybridizes to the "PROTEASOME SUBUNIT BETA TYPE 3" nucleic acid or its complement under low stringency conditions,

(xxxviii) "Pot1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pot1" encoded by a nucleic acid that hybridizes to the "Pot1" nucleic acid or its complement under low stringency conditions,

(xxxix) "RAD50 HOMOLOGUE HSRAD50" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAD50 HOMOLOGUE HSRAD50" encoded by a nucleic acid that hybridizes to the "RAD50 HOMOLOGUE HSRAD50" nucleic acid or its complement under low stringency conditions,

(xl) "RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a

homolog thereof, or a variant of "RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP2" encoded by a nucleic acid that hybridizes to the "RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP2" nucleic acid or its complement under low stringency conditions,

(xli) "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-ALPHA 1 CATALYTIC SUBUNIT" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-ALPHA 1 CATALYTIC SUBUNIT" encoded by a nucleic acid that hybridizes to the "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-ALPHA 1 CATALYTIC SUBUNIT" nucleic acid or its complement under low stringency conditions,

(xlii) "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT" encoded by a nucleic acid that hybridizes to the "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT" nucleic acid or its complement under low stringency conditions,

(xliii) "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-GAMMA CATALYTIC SUBUNIT" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-GAMMA CATALYTIC SUBUNIT" encoded by a nucleic acid that hybridizes to the "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-GAMMA CATALYTIC SUBUNIT" nucleic acid or its complement under low stringency conditions,

(xliv) "SIMILAR TO OROSOMUCOID 1" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIMILAR TO OROSOMUCOID 1" encoded by a nucleic acid that hybridizes to the "SIMILAR TO OROSOMUCOID 1" nucleic acid or its complement under low stringency conditions,

(xlv) "SMC5 PROTEIN" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SMC5 PROTEIN" encoded by a nucleic acid that hybridizes to the "SMC5 PROTEIN" nucleic acid or its complement under low stringency conditions,

- (xlvii) "SQUAMOUS CELL CARCINOMA ANTIGEN 1" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SQUAMOUS CELL CARCINOMA ANTIGEN 1" encoded by a nucleic acid that hybridizes to the "SQUAMOUS CELL CARCINOMA ANTIGEN 1" nucleic acid or its complement under low stringency conditions,
- (xlviii) "SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG" encoded by a nucleic acid that hybridizes to the "SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG" nucleic acid or its complement under low stringency conditions,
- (xlix) "Serine/threonine protease phosphatase 2A, catalytic subunit, beta isoform" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Serine/threonine protease phosphatase 2A, catalytic subunit, beta isoform" encoded by a nucleic acid that hybridizes to the "Serine/threonine protease phosphatase 2A, catalytic subunit, beta isoform" nucleic acid or its complement under low stringency conditions,
- (l) "Similar to diacylglycerol kinase delta" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Similar to diacylglycerol kinase delta" encoded by a nucleic acid that hybridizes to the "Similar to diacylglycerol kinase delta" nucleic acid or its complement under low stringency conditions,
- (ii) "TELOMERASE-BINDING PROTEIN P23" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TELOMERASE-BINDING PROTEIN P23" encoded by a nucleic acid that hybridizes to the "TELOMERASE-BINDING PROTEIN P23" nucleic acid or its complement under low stringency conditions,
- (iii) "TELOMERIC REPEAT BINDING FACTOR 2" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TELOMERIC REPEAT BINDING FACTOR 2" encoded by a nucleic acid that hybridizes to the "TELOMERIC REPEAT BINDING FACTOR 2" nucleic acid or its complement under low stringency conditions,
- (iv) "TERF1 (TRF1)-INTERACTING NUCLEAR FACTOR 2" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TERF1 (TRF1)-INTERACTING NUCLEAR FACTOR 2"

encoded by a nucleic acid that hybridizes to the "TERF1 (TRF1)-INTERACTING NUCLEAR FACTOR 2" nucleic acid or its complement under low stringency conditions,

(liii) "TRF1" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TRF1" encoded by a nucleic acid that hybridizes to the "TRF1" nucleic acid or its complement under low stringency conditions,

(liv) "TRF2-INTERACTING TELOMERIC RAP1 PROTEIN" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TRF2-INTERACTING TELOMERIC RAP1 PROTEIN" encoded by a nucleic acid that hybridizes to the "TRF2-INTERACTING TELOMERIC RAP1 PROTEIN" nucleic acid or its complement under low stringency conditions,

(lv) "TRICARBOXYLATE TRANSPORT PROTEIN, MITOCHONDRIAL PRECURSOR" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TRICARBOXYLATE TRANSPORT PROTEIN, MITOCHONDRIAL PRECURSOR" encoded by a nucleic acid that hybridizes to the "TRICARBOXYLATE TRANSPORT PROTEIN, MITOCHONDRIAL PRECURSOR" nucleic acid or its complement under low stringency conditions,

(lvi) "U5 SMALL NUCLEAR RIBONUCLEOPROTEIN 200 KDA HELICASE (FRAGMENT)" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "U5 SMALL NUCLEAR RIBONUCLEOPROTEIN 200 KDA HELICASE (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "U5 SMALL NUCLEAR RIBONUCLEOPROTEIN 200 KDA HELICASE (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(lvii) "WD-REPEAT PROTEIN AN11 HOMOLOG" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "WD-REPEAT PROTEIN AN11 HOMOLOG" encoded by a nucleic acid that hybridizes to the "WD-REPEAT PROTEIN AN11 HOMOLOG" nucleic acid or its complement under low stringency conditions,

and a protein complex selected from complex (III) and comprising the following proteins:

(i) "38 KDA FK-506 BINDING PROTEIN HOMOLOG" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "38 KDA FK-506 BINDING PROTEIN HOMOLOG" encoded by a nucleic

acid that hybridizes to the "38 KDA FK-506 BINDING PROTEIN HOMOLOG" nucleic acid or its complement under low stringency conditions,

(ii) "ANTIGEN NY-CO-7" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ANTIGEN NY-CO-7" encoded by a nucleic acid that hybridizes to the "ANTIGEN NY-CO-7" nucleic acid or its complement under low stringency conditions,

(iii) "ATP-BINDING CASSETTE, SUB-FAMILY D, MEMBER 3" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-BINDING CASSETTE, SUB-FAMILY D, MEMBER 3" encoded by a nucleic acid that hybridizes to the "ATP-BINDING CASSETTE, SUB-FAMILY D, MEMBER 3" nucleic acid or its complement under low stringency conditions,

(iv) "ATP-DEPENDENT DNA HELICASE II, 80 KDA SUBUNIT" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-DEPENDENT DNA HELICASE II, 80 KDA SUBUNIT" encoded by a nucleic acid that hybridizes to the "ATP-DEPENDENT DNA HELICASE II, 80 KDA SUBUNIT" nucleic acid or its complement under low stringency conditions,

(v) "CASEIN KINASE II, ALPHA CHAIN" (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CASEIN KINASE II, ALPHA CHAIN" encoded by a nucleic acid that hybridizes to the "CASEIN KINASE II, ALPHA CHAIN" nucleic acid or its complement under low stringency conditions,

(vi) "CDNA FLJ13664 FIS, CLONE PLACE1011649" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ13664 FIS, CLONE PLACE1011649" encoded by a nucleic acid that hybridizes to the "CDNA FLJ13664 FIS, CLONE PLACE1011649" nucleic acid or its complement under low stringency conditions,

(vii) "CDNA FLJ13998 FIS, CLONE Y79AA1002229" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ13998 FIS, CLONE Y79AA1002229" encoded by a nucleic acid that hybridizes to the "CDNA FLJ13998 FIS, CLONE Y79AA1002229" nucleic acid or its complement under low stringency conditions,

(viii) "CDNA FLJ20643 FIS, CLONE KAT02633" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a

variant of "CDNA FLJ20643 FIS, CLONE KAT02633" encoded by a nucleic acid that hybridizes to the "CDNA FLJ20643 FIS, CLONE KAT02633" nucleic acid or its complement under low stringency conditions,

(ix) "CDNA FLJ31741 FIS, CLONE NT2RI2007148" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ31741 FIS, CLONE NT2RI2007148" encoded by a nucleic acid that hybridizes to the "CDNA FLJ31741 FIS, CLONE NT2RI2007148" nucleic acid or its complement under low stringency conditions,

(x) "CDNA: FLJ21908 FIS, CLONE HEP03830" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA: FLJ21908 FIS, CLONE HEP03830" encoded by a nucleic acid that hybridizes to the "CDNA: FLJ21908 FIS, CLONE HEP03830" nucleic acid or its complement under low stringency conditions,

(xi) "CHROMATIN ASSEMBLY FACTOR 1 SUBUNIT C" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CHROMATIN ASSEMBLY FACTOR 1 SUBUNIT C" encoded by a nucleic acid that hybridizes to the "CHROMATIN ASSEMBLY FACTOR 1 SUBUNIT C" nucleic acid or its complement under low stringency conditions,

(xii) "DNA MISMATCH REPAIR PROTEIN MSH6" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DNA MISMATCH REPAIR PROTEIN MSH6" encoded by a nucleic acid that hybridizes to the "DNA MISMATCH REPAIR PROTEIN MSH6" nucleic acid or its complement under low stringency conditions,

(xiii) "DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT" encoded by a nucleic acid that hybridizes to the "DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT" nucleic acid or its complement under low stringency conditions,

(xiv) "DNA-DIRECTED RNA POLYMERASE II 23 KDA POLYPEPTIDE" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DNA-DIRECTED RNA POLYMERASE II 23 KDA POLYPEPTIDE" encoded by a nucleic acid that hybridizes to the "DNA-DIRECTED RNA

POLYMERASE II 23 KDA POLYPEPTIDE" nucleic acid or its complement under low stringency conditions,

(xv) "GLIAL FIBRILLARY ACIDIC PROTEIN, ASTROCYTE" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GLIAL FIBRILLARY ACIDIC PROTEIN, ASTROCYTE" encoded by a nucleic acid that hybridizes to the "GLIAL FIBRILLARY ACIDIC PROTEIN, ASTROCYTE" nucleic acid or its complement under low stringency conditions,

(xvi) "HDCMD34P" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HDCMD34P" encoded by a nucleic acid that hybridizes to the "HDCMD34P" nucleic acid or its complement under low stringency conditions,

(xvii) "HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2" encoded by a nucleic acid that hybridizes to the "HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2" nucleic acid or its complement under low stringency conditions,

(xviii) "KIAA1284 PROTEIN (FRAGMENT)" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1284 PROTEIN (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1284 PROTEIN (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xix) "MUTS" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MUTS" encoded by a nucleic acid that hybridizes to the "MUTS" nucleic acid or its complement under low stringency conditions,

(xx) "NEIGHBOR OF A-KINASE ANCHORING PROTEIN 95" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NEIGHBOR OF A-KINASE ANCHORING PROTEIN 95" encoded by a nucleic acid that hybridizes to the "NEIGHBOR OF A-KINASE ANCHORING PROTEIN 95" nucleic acid or its complement under low stringency conditions,

(xxi) "PROGRAMED CELL DEATH PROTEIN 2" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PROGRAMED CELL DEATH PROTEIN 2" encoded by a nucleic acid that

hybridizes to the "PROGRAMED CELL DEATH PROTEIN 2" nucleic acid or its complement under low stringency conditions,

(xxii) "Pot1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pot1" encoded by a nucleic acid that hybridizes to the "Pot1" nucleic acid or its complement under low stringency conditions,

(xxiii) "RAD50 HOMOLOGUE HSRAD50" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAD50 HOMOLOGUE HSRAD50" encoded by a nucleic acid that hybridizes to the "RAD50 HOMOLOGUE HSRAD50" nucleic acid or its complement under low stringency conditions,

(xxiv) "RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP2" encoded by a nucleic acid that hybridizes to the "RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP2" nucleic acid or its complement under low stringency conditions,

(xxv) "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-ALPHA 1 CATALYTIC SUBUNIT" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-ALPHA 1 CATALYTIC SUBUNIT" encoded by a nucleic acid that hybridizes to the "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-ALPHA 1 CATALYTIC SUBUNIT" nucleic acid or its complement under low stringency conditions,

(xxvi) "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT" encoded by a nucleic acid that hybridizes to the "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT" nucleic acid or its complement under low stringency conditions,

(xxvii) "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-GAMMA CATALYTIC SUBUNIT" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-GAMMA CATALYTIC SUBUNIT" encoded by a nucleic

acid that hybridizes to the "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-GAMMA CATALYTIC SUBUNIT" nucleic acid or its complement under low stringency conditions,

(xxviii) "SQUAMOUS CELL CARCINOMA ANTIGEN 1" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SQUAMOUS CELL CARCINOMA ANTIGEN 1" encoded by a nucleic acid that hybridizes to the "SQUAMOUS CELL CARCINOMA ANTIGEN 1" nucleic acid or its complement under low stringency conditions,

(xxix) "SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG" encoded by a nucleic acid that hybridizes to the "SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG" nucleic acid or its complement under low stringency conditions,

(xxx) "Serine/threonine proteine phosphatase 2A, catalytic subunit, beta isoform" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Serine/threonine proteine phosphatase 2A, catalytic subunit, beta isoform" encoded by a nucleic acid that hybridizes to the "Serine/threonine proteine phosphatase 2A, catalytic subunit, beta isoform" nucleic acid or its complement under low stringency conditions,

(xxxi) "TELOMERASE-BINDING PROTEIN P23" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TELOMERASE-BINDING PROTEIN P23" encoded by a nucleic acid that hybridizes to the "TELOMERASE-BINDING PROTEIN P23" nucleic acid or its complement under low stringency conditions,

(xxxii) "TELOMERIC REPEAT BINDING FACTOR 2" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TELOMERIC REPEAT BINDING FACTOR 2" encoded by a nucleic acid that hybridizes to the "TELOMERIC REPEAT BINDING FACTOR 2" nucleic acid or its complement under low stringency conditions,

(xxxiii) "TERF1 (TRF1)-INTERACTING NUCLEAR FACTOR 2" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TERF1 (TRF1)-INTERACTING NUCLEAR FACTOR 2" encoded by a nucleic acid that hybridizes to the "TERF1 (TRF1)-INTERACTING NUCLEAR FACTOR 2" nucleic acid or its complement under low stringency conditions,

(xxxiv) "TRF1" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TRF1" encoded by a nucleic acid that hybridizes to the "TRF1" nucleic acid or its complement under low stringency conditions,

(xxxv) "TRF2-INTERACTING TELOMERIC RAP1 PROTEIN" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TRF2-INTERACTING TELOMERIC RAP1 PROTEIN" encoded by a nucleic acid that hybridizes to the "TRF2-INTERACTING TELOMERIC RAP1 PROTEIN" nucleic acid or its complement under low stringency conditions,

(xxxvi) "WD-REPEAT PROTEIN AN11 HOMOLOG" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "WD-REPEAT PROTEIN AN11 HOMOLOG" encoded by a nucleic acid that hybridizes to the "WD-REPEAT PROTEIN AN11 HOMOLOG" nucleic acid or its complement under low stringency conditions,

4. The protein complex according to No. 1 comprising all but 1 - 55 of the following proteins:

(i) "38 KDA FK-506 BINDING PROTEIN HOMOLOG" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "38 KDA FK-506 BINDING PROTEIN HOMOLOG" encoded by a nucleic acid that hybridizes to the "38 KDA FK-506 BINDING PROTEIN HOMOLOG" nucleic acid or its complement under low stringency conditions,

(ii) "ANTIGEN NY-CO-7" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ANTIGEN NY-CO-7" encoded by a nucleic acid that hybridizes to the "ANTIGEN NY-CO-7" nucleic acid or its complement under low stringency conditions,

(iii) "ATP-BINDING CASSETTE, SUB-FAMILY D, MEMBER 3" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-BINDING CASSETTE, SUB-FAMILY D, MEMBER 3" encoded by a nucleic acid that hybridizes to the "ATP-BINDING CASSETTE, SUB-FAMILY D, MEMBER 3" nucleic acid or its complement under low stringency conditions,

(iv) "ATP-DEPENDENT DNA HELICASE II, 80 KDA SUBUNIT" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a

homolog thereof, or a variant of "ATP-DEPENDENT DNA HELICASE II, 80 KDA SUBUNIT" encoded by a nucleic acid that hybridizes to the "ATP-DEPENDENT DNA HELICASE II, 80 KDA SUBUNIT" nucleic acid or its complement under low stringency conditions,

(v) "BAF180" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BAF180" encoded by a nucleic acid that hybridizes to the "BAF180" nucleic acid or its complement under low stringency conditions,

(vi) "CASEIN KINASE II, ALPHA CHAIN" (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CASEIN KINASE II, ALPHA CHAIN" encoded by a nucleic acid that hybridizes to the "CASEIN KINASE II, ALPHA CHAIN" nucleic acid or its complement under low stringency conditions,

(vii) "CDNA FLJ13664 FIS, CLONE PLACE1011649" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ13664 FIS, CLONE PLACE1011649" encoded by a nucleic acid that hybridizes to the "CDNA FLJ13664 FIS, CLONE PLACE1011649" nucleic acid or its complement under low stringency conditions,

(viii) "CDNA FLJ13998 FIS, CLONE Y79AA1002229" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ13998 FIS, CLONE Y79AA1002229" encoded by a nucleic acid that hybridizes to the "CDNA FLJ13998 FIS, CLONE Y79AA1002229" nucleic acid or its complement under low stringency conditions,

(ix) "CDNA FLJ20643 FIS, CLONE KAT02633" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ20643 FIS, CLONE KAT02633" encoded by a nucleic acid that hybridizes to the "CDNA FLJ20643 FIS, CLONE KAT02633" nucleic acid or its complement under low stringency conditions,

(x) "CDNA FLJ25320 FIS, CLONE TST00267 (FRAGMENT)" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ25320 FIS, CLONE TST00267 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "CDNA FLJ25320 FIS, CLONE TST00267 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

- (xi) "CDNA FLJ31741 FIS, CLONE NT2RI2007148" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ31741 FIS, CLONE NT2RI2007148" encoded by a nucleic acid that hybridizes to the "CDNA FLJ31741 FIS, CLONE NT2RI2007148" nucleic acid or its complement under low stringency conditions,
- (xii) "CDNA: FLJ21908 FIS, CLONE HEP03830" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA: FLJ21908 FIS, CLONE HEP03830" encoded by a nucleic acid that hybridizes to the "CDNA: FLJ21908 FIS, CLONE HEP03830" nucleic acid or its complement under low stringency conditions,
- (xiii) "CENP-F KINETOCHORE PROTEIN" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CENP-F KINETOCHORE PROTEIN" encoded by a nucleic acid that hybridizes to the "CENP-F KINETOCHORE PROTEIN" nucleic acid or its complement under low stringency conditions,
- (xiv) "CHROMATIN ASSEMBLY FACTOR 1 SUBUNIT C" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CHROMATIN ASSEMBLY FACTOR 1 SUBUNIT C" encoded by a nucleic acid that hybridizes to the "CHROMATIN ASSEMBLY FACTOR 1 SUBUNIT C" nucleic acid or its complement under low stringency conditions,
- (xv) "DNA MISMATCH REPAIR PROTEIN MSH6" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DNA MISMATCH REPAIR PROTEIN MSH6" encoded by a nucleic acid that hybridizes to the "DNA MISMATCH REPAIR PROTEIN MSH6" nucleic acid or its complement under low stringency conditions,
- (xvi) "DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT" encoded by a nucleic acid that hybridizes to the "DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT" nucleic acid or its complement under low stringency conditions,
- (xvii) "DNA-DIRECTED RNA POLYMERASE II 23 KDA POLYPEPTIDE" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DNA-DIRECTED RNA POLYMERASE II 23 KDA

POLYPEPTIDE" encoded by a nucleic acid that hybridizes to the "DNA-DIRECTED RNA POLYMERASE II 23 KDA POLYPEPTIDE" nucleic acid or its complement under low stringency conditions,

(xviii) "ELONGATION FACTOR 2 KINASE" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ELONGATION FACTOR 2 KINASE" encoded by a nucleic acid that hybridizes to the "ELONGATION FACTOR 2 KINASE" nucleic acid or its complement under low stringency conditions,

(xix) "FK506-BINDING PROTEIN 4" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FK506-BINDING PROTEIN 4" encoded by a nucleic acid that hybridizes to the "FK506-BINDING PROTEIN 4" nucleic acid or its complement under low stringency conditions,

(xx) "GLIAL FIBRILLARY ACIDIC PROTEIN, ASTROCYTE" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GLIAL FIBRILLARY ACIDIC PROTEIN, ASTROCYTE" encoded by a nucleic acid that hybridizes to the "GLIAL FIBRILLARY ACIDIC PROTEIN, ASTROCYTE" nucleic acid or its complement under low stringency conditions,

(xxi) "HDCMD34P" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HDCMD34P" encoded by a nucleic acid that hybridizes to the "HDCMD34P" nucleic acid or its complement under low stringency conditions,

(xxii) "HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H" encoded by a nucleic acid that hybridizes to the "HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H" nucleic acid or its complement under low stringency conditions,

(xxiii) "HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2" encoded by a nucleic acid that hybridizes to the "HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2" nucleic acid or its complement under low stringency conditions,

(xxiv) "HSPC029" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC029"

encoded by a nucleic acid that hybridizes to the "HSPC029" nucleic acid or its complement under low stringency conditions,

(xxv) "HYPOTHETICAL PROTEIN KIAA0310 (FRAGMENT)" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN KIAA0310 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN KIAA0310 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxvi) "INCOMPATIBILITY PROTEIN HET-E-1 (FRAGMENT)" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "INCOMPATIBILITY PROTEIN HET-E-1 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "INCOMPATIBILITY PROTEIN HET-E-1 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxvii) "KIAA0792 PROTEIN" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0792 PROTEIN" encoded by a nucleic acid that hybridizes to the "KIAA0792 PROTEIN" nucleic acid or its complement under low stringency conditions,

(xxviii) "KIAA1284 PROTEIN (FRAGMENT)" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1284 PROTEIN (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1284 PROTEIN (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxix) "MEPRIN A BETA-SUBUNIT PRECURSOR" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MEPRIN A BETA-SUBUNIT PRECURSOR" encoded by a nucleic acid that hybridizes to the "MEPRIN A BETA-SUBUNIT PRECURSOR" nucleic acid or its complement under low stringency conditions,

(xxx) "MUTS" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MUTS" encoded by a nucleic acid that hybridizes to the "MUTS" nucleic acid or its complement under low stringency conditions,

(xxxi) "MYELOID LEUKEMIA FACTOR 2" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MYELOID LEUKEMIA FACTOR 2" encoded by a nucleic acid that hybridizes

to the "MYELOID LEUKEMIA FACTOR 2" nucleic acid or its complement under low stringency conditions,

(xxxii) "NEIGHBOR OF A-KINASE ANCHORING PROTEIN 95" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NEIGHBOR OF A-KINASE ANCHORING PROTEIN 95" encoded by a nucleic acid that hybridizes to the "NEIGHBOR OF A-KINASE ANCHORING PROTEIN 95" nucleic acid or its complement under low stringency conditions,

(xxxiii) "P30 DBC" (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "P30 DBC" encoded by a nucleic acid that hybridizes to the "P30 DBC" nucleic acid or its complement under low stringency conditions,

(xxxiv) "PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-X" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-X" encoded by a nucleic acid that hybridizes to the "PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-X" nucleic acid or its complement under low stringency conditions,

(xxxv) "PROGRAMED CELL DEATH PROTEIN 2" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PROGRAMED CELL DEATH PROTEIN 2" encoded by a nucleic acid that hybridizes to the "PROGRAMED CELL DEATH PROTEIN 2" nucleic acid or its complement under low stringency conditions,

(xxxvi) "PROLIFERATING CELL NUCLEAR ANTIGEN" (SEQ ID No:36) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PROLIFERATING CELL NUCLEAR ANTIGEN" encoded by a nucleic acid that hybridizes to the "PROLIFERATING CELL NUCLEAR ANTIGEN" nucleic acid or its complement under low stringency conditions,

(xxxvii) "PROTEASOME SUBUNIT BETA TYPE 3" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PROTEASOME SUBUNIT BETA TYPE 3" encoded by a nucleic acid that hybridizes to the "PROTEASOME SUBUNIT BETA TYPE 3" nucleic acid or its complement under low stringency conditions,

(xxxviii) "Pot1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pot1" encoded by a nucleic acid that hybridizes to the "Pot1" nucleic acid or its complement under low stringency conditions,

(xxxix) "RAD50 HOMOLOGUE HSRAD50" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAD50 HOMOLOGUE HSRAD50" encoded by a nucleic acid that hybridizes to the "RAD50 HOMOLOGUE HSRAD50" nucleic acid or its complement under low stringency conditions,

(xl) "RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP2" encoded by a nucleic acid that hybridizes to the "RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP2" nucleic acid or its complement under low stringency conditions,

(xli) "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-ALPHA 1 CATALYTIC SUBUNIT" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-ALPHA 1 CATALYTIC SUBUNIT" encoded by a nucleic acid that hybridizes to the "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-ALPHA 1 CATALYTIC SUBUNIT" nucleic acid or its complement under low stringency conditions,

(xlii) "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT" encoded by a nucleic acid that hybridizes to the "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT" nucleic acid or its complement under low stringency conditions,

(xliii) "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-GAMMA CATALYTIC SUBUNIT" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-GAMMA CATALYTIC SUBUNIT" encoded by a nucleic acid that hybridizes to the "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-

GAMMA CATALYTIC SUBUNIT" nucleic acid or its complement under low stringency conditions,

(xliv) "SIMILAR TO OROSOMUCOID 1" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIMILAR TO OROSOMUCOID 1" encoded by a nucleic acid that hybridizes to the "SIMILAR TO OROSOMUCOID 1" nucleic acid or its complement under low stringency conditions,

(xlv) "SMC5 PROTEIN" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SMC5 PROTEIN" encoded by a nucleic acid that hybridizes to the "SMC5 PROTEIN" nucleic acid or its complement under low stringency conditions,

(xlvi) "SQUAMOUS CELL CARCINOMA ANTIGEN 1" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SQUAMOUS CELL CARCINOMA ANTIGEN 1" encoded by a nucleic acid that hybridizes to the "SQUAMOUS CELL CARCINOMA ANTIGEN 1" nucleic acid or its complement under low stringency conditions,

(xlvii) "SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG" encoded by a nucleic acid that hybridizes to the "SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG" nucleic acid or its complement under low stringency conditions,

(xlviii) "Serine/threonine protein phosphatase 2A, catalytic subunit, beta isoform" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Serine/threonine protein phosphatase 2A, catalytic subunit, beta isoform" encoded by a nucleic acid that hybridizes to the "Serine/threonine protein phosphatase 2A, catalytic subunit, beta isoform" nucleic acid or its complement under low stringency conditions,

(xlix) "Similar to diacylglycerol kinase delta" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Similar to diacylglycerol kinase delta" encoded by a nucleic acid that hybridizes to the "Similar to diacylglycerol kinase delta" nucleic acid or its complement under low stringency conditions,

(l) "TELOMERASE-BINDING PROTEIN P23" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a

variant of "TELOMERASE-BINDING PROTEIN P23" encoded by a nucleic acid that hybridizes to the "TELOMERASE-BINDING PROTEIN P23" nucleic acid or its complement under low stringency conditions,

(li) "TELOMERIC REPEAT BINDING FACTOR 2" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TELOMERIC REPEAT BINDING FACTOR 2" encoded by a nucleic acid that hybridizes to the "TELOMERIC REPEAT BINDING FACTOR 2" nucleic acid or its complement under low stringency conditions,

(lii) "TERF1 (TRF1)-INTERACTING NUCLEAR FACTOR 2" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TERF1 (TRF1)-INTERACTING NUCLEAR FACTOR 2" encoded by a nucleic acid that hybridizes to the "TERF1 (TRF1)-INTERACTING NUCLEAR FACTOR 2" nucleic acid or its complement under low stringency conditions,

(liii) "TRF1" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TRF1" encoded by a nucleic acid that hybridizes to the "TRF1" nucleic acid or its complement under low stringency conditions,

(liv) "TRF2-INTERACTING TELOMERIC RAP1 PROTEIN" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TRF2-INTERACTING TELOMERIC RAP1 PROTEIN" encoded by a nucleic acid that hybridizes to the "TRF2-INTERACTING TELOMERIC RAP1 PROTEIN" nucleic acid or its complement under low stringency conditions,

(lv) "TRICARBOXYLATE TRANSPORT PROTEIN, MITOCHONDRIAL PRECURSOR" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TRICARBOXYLATE TRANSPORT PROTEIN, MITOCHONDRIAL PRECURSOR" encoded by a nucleic acid that hybridizes to the "TRICARBOXYLATE TRANSPORT PROTEIN, MITOCHONDRIAL PRECURSOR" nucleic acid or its complement under low stringency conditions,

(lvi) "U5 SMALL NUCLEAR RIBONUCLEOPROTEIN 200 KDA HELICASE (FRAGMENT)" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "U5 SMALL NUCLEAR RIBONUCLEOPROTEIN 200 KDA HELICASE (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "U5 SMALL NUCLEAR RIBONUCLEOPROTEIN 200

KDA HELICASE (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(lvii) "WD-REPEAT PROTEIN AN11 HOMOLOG" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "WD-REPEAT PROTEIN AN11 HOMOLOG" encoded by a nucleic acid that hybridizes to the "WD-REPEAT PROTEIN AN11 HOMOLOG" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.

6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.

7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.

8. The complex of any of No. 1 - 7 that is involved in the DNA binding activity, TRF2 binding activity or RAP1 binding activity.

9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps: expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.

10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.

11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.

12. Component of the telomere capping complex obtainable by a process according to any of No. 9 - 11.

13. Protein of the telomere capping complex selected from

(i) "CDNA FLJ13664 FIS, CLONE PLACE1011649" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ13664 FIS, CLONE PLACE1011649" encoded by a nucleic acid that hybridizes to the "CDNA FLJ13664 FIS, CLONE PLACE1011649" nucleic acid or its complement under low stringency conditions,

(ii) "CDNA FLJ13998 FIS, CLONE Y79AA1002229" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ13998 FIS, CLONE Y79AA1002229" encoded by a nucleic acid that hybridizes to the "CDNA FLJ13998 FIS, CLONE Y79AA1002229" nucleic acid or its complement under low stringency conditions,

(iii) "CDNA FLJ20643 FIS, CLONE KAT02633" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ20643 FIS, CLONE KAT02633" encoded by a nucleic acid that hybridizes to the "CDNA FLJ20643 FIS, CLONE KAT02633" nucleic acid or its complement under low stringency conditions,

(iv) "CDNA FLJ25320 FIS, CLONE TST00267 (FRAGMENT)" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ25320 FIS, CLONE TST00267 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "CDNA FLJ25320 FIS, CLONE TST00267 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(v) "CDNA FLJ31741 FIS, CLONE NT2RI2007148" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ31741 FIS, CLONE NT2RI2007148" encoded by a nucleic acid that hybridizes to the "CDNA FLJ31741 FIS, CLONE NT2RI2007148" nucleic acid or its complement under low stringency conditions,

- (vi) "CDNA: FLJ21908 FIS, CLONE HEP03830" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA: FLJ21908 FIS, CLONE HEP03830" encoded by a nucleic acid that hybridizes to the "CDNA: FLJ21908 FIS, CLONE HEP03830" nucleic acid or its complement under low stringency conditions,
- (vii) "HSPC029" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC029" encoded by a nucleic acid that hybridizes to the "HSPC029" nucleic acid or its complement under low stringency conditions,
- (viii) "HYPOTHETICAL PROTEIN KIAA0310 (FRAGMENT)" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN KIAA0310 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN KIAA0310 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (ix) "KIAA0792 PROTEIN" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0792 PROTEIN" encoded by a nucleic acid that hybridizes to the "KIAA0792 PROTEIN" nucleic acid or its complement under low stringency conditions,
- (x) "KIAA1284 PROTEIN (FRAGMENT)" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1284 PROTEIN (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1284 PROTEIN (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and
- (xi) "P30 DBC" (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "P30 DBC" encoded by a nucleic acid that hybridizes to the "P30 DBC" nucleic acid or its complement under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

14. Nucleic acid encoding a protein according to No. 13.

15. Construct, preferably a vector construct, comprising (a) a nucleic acid according to No. 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or

(b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).

16. Host cell, containing a vector comprising at least one of the nucleic acid of No. 14 and/or a construct of No. 15 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).

17. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and an antibody or a fragment of said antibody which binds to any of the proteins according to No. 13.

18. A kit comprising in one or more container the complex of any of No. 1 - 8 and/or the proteins of No. 13 optionally together with an antibody according to No. 17 and/or further components such as reagents and working instructions.

19. The kit according to No. 18 for processing a substrate of said complex.

20. The kit according to No. 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as cancer such as solid tumours such as breast cancer, prostate cancer, lung cancer, colon cancer; cancer such as haematological cancers such as leukemia.

21. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one protein according to No. 14 and/or at least one antibody according to No. 17 is attached to a solid carrier.

22. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.

23. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:

(i) "CDNA FLJ13664 FIS, CLONE PLACE1011649" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ13664 FIS, CLONE PLACE1011649" encoded by a nucleic acid that hybridizes to the "CDNA FLJ13664 FIS, CLONE PLACE1011649" nucleic acid or its complement under low stringency conditions,

(ii) "CDNA FLJ13998 FIS, CLONE Y79AA1002229" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ13998 FIS, CLONE Y79AA1002229" encoded by a nucleic acid that hybridizes to the "CDNA FLJ13998 FIS, CLONE Y79AA1002229" nucleic acid or its complement under low stringency conditions,

(iii) "CDNA FLJ20643 FIS, CLONE KAT02633" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ20643 FIS, CLONE KAT02633" encoded by a nucleic acid that hybridizes to the "CDNA FLJ20643 FIS, CLONE KAT02633" nucleic acid or its complement under low stringency conditions,

(iv) "CDNA FLJ25320 FIS, CLONE TST00267 (FRAGMENT)" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ25320 FIS, CLONE TST00267 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "CDNA FLJ25320 FIS,

CLONE TST00267 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(v) "CDNA FLJ31741 FIS, CLONE NT2RI2007148" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ31741 FIS, CLONE NT2RI2007148" encoded by a nucleic acid that hybridizes to the "CDNA FLJ31741 FIS, CLONE NT2RI2007148" nucleic acid or its complement under low stringency conditions,

(vi) "CDNA: FLJ21908 FIS, CLONE HEP03830" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA: FLJ21908 FIS, CLONE HEP03830" encoded by a nucleic acid that hybridizes to the "CDNA: FLJ21908 FIS, CLONE HEP03830" nucleic acid or its complement under low stringency conditions,

(vii) "HSPC029" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC029" encoded by a nucleic acid that hybridizes to the "HSPC029" nucleic acid or its complement under low stringency conditions,

(viii) "HYPOTHETICAL PROTEIN KIAA0310 (FRAGMENT)" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN KIAA0310 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN KIAA0310 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(ix) "KIAA0792 PROTEIN" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0792 PROTEIN" encoded by a nucleic acid that hybridizes to the "KIAA0792 PROTEIN" nucleic acid or its complement under low stringency conditions,

(x) "KIAA1284 PROTEIN (FRAGMENT)" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1284 PROTEIN (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1284 PROTEIN (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(xi) "P30 DBC" (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "P30 DBC" encoded by a nucleic acid that hybridizes to the "P30 DBC" nucleic acid or its complement under low stringency conditions, and a pharmaceutical acceptable carrier.

24. A pharmaceutical composition according to No. 23 for the treatment of diseases and disorders such as cancer such as solid tumours such as breast cancer, prostate cancer, lung cancer, colon cancer; cancer such as haematological cancers such as leukemia.

25. A method for screening for a molecule that binds to the complex of anyone of No. 1 - 8 and/or any of the following the proteins:

(i) "CDNA FLJ13664 FIS, CLONE PLACE1011649" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ13664 FIS, CLONE PLACE1011649" encoded by a nucleic acid that hybridizes to the "CDNA FLJ13664 FIS, CLONE PLACE1011649" nucleic acid or its complement under low stringency conditions,

(ii) "CDNA FLJ13998 FIS, CLONE Y79AA1002229" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ13998 FIS, CLONE Y79AA1002229" encoded by a nucleic acid that hybridizes to the "CDNA FLJ13998 FIS, CLONE Y79AA1002229" nucleic acid or its complement under low stringency conditions,

(iii) "CDNA FLJ20643 FIS, CLONE KAT02633" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ20643 FIS, CLONE KAT02633" encoded by a nucleic acid that hybridizes to the "CDNA FLJ20643 FIS, CLONE KAT02633" nucleic acid or its complement under low stringency conditions,

(iv) "CDNA FLJ25320 FIS, CLONE TST00267 (FRAGMENT)" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ25320 FIS, CLONE TST00267 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "CDNA FLJ25320 FIS, CLONE TST00267 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(v) "CDNA FLJ31741 FIS, CLONE NT2RI2007148" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ31741 FIS, CLONE NT2RI2007148" encoded by a nucleic acid

that hybridizes to the "CDNA FLJ31741 FIS, CLONE NT2RI2007148" nucleic acid or its complement under low stringency conditions,

(vi) "CDNA: FLJ21908 FIS, CLONE HEP03830" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA: FLJ21908 FIS, CLONE HEP03830" encoded by a nucleic acid that hybridizes to the "CDNA: FLJ21908 FIS, CLONE HEP03830" nucleic acid or its complement under low stringency conditions,

(vii) "HSPC029" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC029" encoded by a nucleic acid that hybridizes to the "HSPC029" nucleic acid or its complement under low stringency conditions,

(viii) "HYPOTHETICAL PROTEIN KIAA0310 (FRAGMENT)" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN KIAA0310 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN KIAA0310 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(ix) "KIAA0792 PROTEIN" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0792 PROTEIN" encoded by a nucleic acid that hybridizes to the "KIAA0792 PROTEIN" nucleic acid or its complement under low stringency conditions,

(x) "KIAA1284 PROTEIN (FRAGMENT)" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1284 PROTEIN (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1284 PROTEIN (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(xi) "P30 DBC" (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "P30 DBC" encoded by a nucleic acid that hybridizes to the "P30 DBC" nucleic acid or its complement under low stringency conditions, comprising the steps of

(a) exposing said complex, or a cell or organism containing same to one or more candidate molecules; and

(b) determining whether said candidate molecule is bound to the complex or protein.

26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of (a) exposing said complex, or a cell or organism containing telomere capping complex to one or more candidate molecules; and

(b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

27. The method of No. 26, wherein the amount of said complex is determined.

28. The method of No. 26, wherein the activity of said complex is determined.

29. The method of No. 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining the processing of said substrate is modified in the presence of said candidate molecule.

30. The method of No. 26, wherein the amount of the individual protein components of said complex are determined.

31. The method of No. 30, wherein said determining step comprises determining whether (i) "38 KDA FK-506 BINDING PROTEIN HOMOLOG" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "38 KDA FK-506 BINDING PROTEIN HOMOLOG" encoded by a nucleic

acid that hybridizes to the "38 KDA FK-506 BINDING PROTEIN HOMOLOG" nucleic acid or its complement under low stringency conditions, and/or

(ii) "ANTIGEN NY-CO-7" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ANTIGEN NY-CO-7" encoded by a nucleic acid that hybridizes to the "ANTIGEN NY-CO-7" nucleic acid or its complement under low stringency conditions, and/or

(iii) "ATP-BINDING CASSETTE, SUB-FAMILY D, MEMBER 3" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-BINDING CASSETTE, SUB-FAMILY D, MEMBER 3" encoded by a nucleic acid that hybridizes to the "ATP-BINDING CASSETTE, SUB-FAMILY D, MEMBER 3" nucleic acid or its complement under low stringency conditions, and/or

(iv) "ATP-DEPENDENT DNA HELICASE II, 80 KDA SUBUNIT" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-DEPENDENT DNA HELICASE II, 80 KDA SUBUNIT" encoded by a nucleic acid that hybridizes to the "ATP-DEPENDENT DNA HELICASE II, 80 KDA SUBUNIT" nucleic acid or its complement under low stringency conditions, and/or

(v) "BAF180" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BAF180" encoded by a nucleic acid that hybridizes to the "BAF180" nucleic acid or its complement under low stringency conditions, and/or

(vi) "CASEIN KINASE II, ALPHA CHAIN" (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CASEIN KINASE II, ALPHA CHAIN" encoded by a nucleic acid that hybridizes to the "CASEIN KINASE II, ALPHA CHAIN" nucleic acid or its complement under low stringency conditions, and/or

(vii) "CDNA FLJ13664 FIS, CLONE PLACE1011649" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ13664 FIS, CLONE PLACE1011649" encoded by a nucleic acid that hybridizes to the "CDNA FLJ13664 FIS, CLONE PLACE1011649" nucleic acid or its complement under low stringency conditions, and/or

(viii) "CDNA FLJ13998 FIS, CLONE Y79AA1002229" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof,

or a variant of "CDNA FLJ13998 FIS, CLONE Y79AA1002229" encoded by a nucleic acid that hybridizes to the "CDNA FLJ13998 FIS, CLONE Y79AA1002229" nucleic acid or its complement under low stringency conditions, and/or

(ix) "CDNA FLJ20643 FIS, CLONE KAT02633" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ20643 FIS, CLONE KAT02633" encoded by a nucleic acid that hybridizes to the "CDNA FLJ20643 FIS, CLONE KAT02633" nucleic acid or its complement under low stringency conditions, and/or

(x) "CDNA FLJ25320 FIS, CLONE TST00267 (FRAGMENT)" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ25320 FIS, CLONE TST00267 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "CDNA FLJ25320 FIS, CLONE TST00267 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(xi) "CDNA FLJ31741 FIS, CLONE NT2RI2007148" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ31741 FIS, CLONE NT2RI2007148" encoded by a nucleic acid that hybridizes to the "CDNA FLJ31741 FIS, CLONE NT2RI2007148" nucleic acid or its complement under low stringency conditions, and/or

(xii) "CDNA: FLJ21908 FIS, CLONE HEP03830" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA: FLJ21908 FIS, CLONE HEP03830" encoded by a nucleic acid that hybridizes to the "CDNA: FLJ21908 FIS, CLONE HEP03830" nucleic acid or its complement under low stringency conditions, and/or

(xiii) "CENP-F KINETOCHORE PROTEIN" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CENP-F KINETOCHORE PROTEIN" encoded by a nucleic acid that hybridizes to the "CENP-F KINETOCHORE PROTEIN" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "CHROMATIN ASSEMBLY FACTOR 1 SUBUNIT C" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CHROMATIN ASSEMBLY FACTOR 1 SUBUNIT C" encoded by a nucleic acid that hybridizes to the "CHROMATIN ASSEMBLY FACTOR 1 SUBUNIT C" nucleic acid or its complement under low stringency conditions, and/or

- (xv) "DNA MISMATCH REPAIR PROTEIN MSH6" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DNA MISMATCH REPAIR PROTEIN MSH6" encoded by a nucleic acid that hybridizes to the "DNA MISMATCH REPAIR PROTEIN MSH6" nucleic acid or its complement under low stringency conditions, and/or
- (xvi) "DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT" encoded by a nucleic acid that hybridizes to the "DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT" nucleic acid or its complement under low stringency conditions, and/or
- (xvii) "DNA-DIRECTED RNA POLYMERASE II 23 KDA POLYPEPTIDE" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DNA-DIRECTED RNA POLYMERASE II 23 KDA POLYPEPTIDE" encoded by a nucleic acid that hybridizes to the "DNA-DIRECTED RNA POLYMERASE II 23 KDA POLYPEPTIDE" nucleic acid or its complement under low stringency conditions, and/or
- (xviii) "ELONGATION FACTOR 2 KINASE" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ELONGATION FACTOR 2 KINASE" encoded by a nucleic acid that hybridizes to the "ELONGATION FACTOR 2 KINASE" nucleic acid or its complement under low stringency conditions, and/or
- (xix) "FK506-BINDING PROTEIN 4" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FK506-BINDING PROTEIN 4" encoded by a nucleic acid that hybridizes to the "FK506-BINDING PROTEIN 4" nucleic acid or its complement under low stringency conditions, and/or
- (xx) "GLIAL FIBRILLARY ACIDIC PROTEIN, ASTROCYTE" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GLIAL FIBRILLARY ACIDIC PROTEIN, ASTROCYTE" encoded by a nucleic acid that hybridizes to the "GLIAL FIBRILLARY ACIDIC PROTEIN, ASTROCYTE" nucleic acid or its complement under low stringency conditions, and/or
- (xxi) "HDCMD34P" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HDCMD34P"

encoded by a nucleic acid that hybridizes to the "HDCMD34P" nucleic acid or its complement under low stringency conditions, and/or

(xxii) "HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H" encoded by a nucleic acid that hybridizes to the "HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2" encoded by a nucleic acid that hybridizes to the "HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "HSPC029" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC029" encoded by a nucleic acid that hybridizes to the "HSPC029" nucleic acid or its complement under low stringency conditions, and/or

(xxv) "HYPOTHETICAL PROTEIN KIAA0310 (FRAGMENT)" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN KIAA0310 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN KIAA0310 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "INCOMPATIBILITY PROTEIN HET-E-1 (FRAGMENT)" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "INCOMPATIBILITY PROTEIN HET-E-1 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "INCOMPATIBILITY PROTEIN HET-E-1 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "KIAA0792 PROTEIN" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0792 PROTEIN" encoded by a nucleic acid that hybridizes to the "KIAA0792 PROTEIN" nucleic acid or its complement under low stringency conditions, and/or

(xxviii) "KIAA1284 PROTEIN (FRAGMENT)" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a

variant of "KIAA1284 PROTEIN (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1284 PROTEIN (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(xxix) "MEPRIN A BETA-SUBUNIT PRECURSOR" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MEPRIN A BETA-SUBUNIT PRECURSOR" encoded by a nucleic acid that hybridizes to the "MEPRIN A BETA-SUBUNIT PRECURSOR" nucleic acid or its complement under low stringency conditions, and/or

(xxx) "MUTS" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MUTS" encoded by a nucleic acid that hybridizes to the "MUTS" nucleic acid or its complement under low stringency conditions, and/or

(xxxi) "MYELOID LEUKEMIA FACTOR 2" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MYELOID LEUKEMIA FACTOR 2" encoded by a nucleic acid that hybridizes to the "MYELOID LEUKEMIA FACTOR 2" nucleic acid or its complement under low stringency conditions, and/or

(xxxii) "NEIGHBOR OF A-KINASE ANCHORING PROTEIN 95" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NEIGHBOR OF A-KINASE ANCHORING PROTEIN 95" encoded by a nucleic acid that hybridizes to the "NEIGHBOR OF A-KINASE ANCHORING PROTEIN 95" nucleic acid or its complement under low stringency conditions, and/or

(xxxiii) "P30 DBC" (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "P30 DBC" encoded by a nucleic acid that hybridizes to the "P30 DBC" nucleic acid or its complement under low stringency conditions, and/or

(xxxiv) "PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-X" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-X" encoded by a nucleic acid that hybridizes to the "PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-X" nucleic acid or its complement under low stringency conditions, and/or

(xxxv) "PROGRAMED CELL DEATH PROTEIN 2" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PROGRAMED CELL DEATH PROTEIN 2" encoded by a nucleic acid that hybridizes to the "PROGRAMED CELL DEATH PROTEIN 2" nucleic acid or its complement under low stringency conditions, and/or

(xxxvi) "PROLIFERATING CELL NUCLEAR ANTIGEN" (SEQ ID No:36) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PROLIFERATING CELL NUCLEAR ANTIGEN" encoded by a nucleic acid that hybridizes to the "PROLIFERATING CELL NUCLEAR ANTIGEN" nucleic acid or its complement under low stringency conditions, and/or

(xxxvii) "PROTEASOME SUBUNIT BETA TYPE 3" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PROTEASOME SUBUNIT BETA TYPE 3" encoded by a nucleic acid that hybridizes to the "PROTEASOME SUBUNIT BETA TYPE 3" nucleic acid or its complement under low stringency conditions, and/or

(xxxviii) "Pot1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pot1" encoded by a nucleic acid that hybridizes to the "Pot1" nucleic acid or its complement under low stringency conditions, and/or

(xxxix) "RAD50 HOMOLOGUE HSRAD50" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAD50 HOMOLOGUE HSRAD50" encoded by a nucleic acid that hybridizes to the "RAD50 HOMOLOGUE HSRAD50" nucleic acid or its complement under low stringency conditions, and/or

(xl) "RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP2" encoded by a nucleic acid that hybridizes to the "RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP2" nucleic acid or its complement under low stringency conditions, and/or

(xli) "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-ALPHA 1 CATALYTIC SUBUNIT" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-ALPHA 1 CATALYTIC SUBUNIT" encoded by a nucleic

acid that hybridizes to the "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-ALPHA 1 CATALYTIC SUBUNIT" nucleic acid or its complement under low stringency conditions, and/or

(xlii) "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT" encoded by a nucleic acid that hybridizes to the "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT" nucleic acid or its complement under low stringency conditions, and/or

(xliii) "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-GAMMA CATALYTIC SUBUNIT" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-GAMMA CATALYTIC SUBUNIT" encoded by a nucleic acid that hybridizes to the "SERINE/THREONINE PROTEIN PHOSPHATASE PP1-GAMMA CATALYTIC SUBUNIT" nucleic acid or its complement under low stringency conditions, and/or

(xliv) "SIMILAR TO OROSOMUCOID 1" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIMILAR TO OROSOMUCOID 1" encoded by a nucleic acid that hybridizes to the "SIMILAR TO OROSOMUCOID 1" nucleic acid or its complement under low stringency conditions, and/or

(xlv) "SMC5 PROTEIN" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SMC5 PROTEIN" encoded by a nucleic acid that hybridizes to the "SMC5 PROTEIN" nucleic acid or its complement under low stringency conditions, and/or

(xlii) "SQUAMOUS CELL CARCINOMA ANTIGEN 1" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SQUAMOUS CELL CARCINOMA ANTIGEN 1" encoded by a nucleic acid that hybridizes to the "SQUAMOUS CELL CARCINOMA ANTIGEN 1" nucleic acid or its complement under low stringency conditions, and/or

(xlvii) "SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG"

encoded by a nucleic acid that hybridizes to the "SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG" nucleic acid or its complement under low stringency conditions, and/or

(xlviii) "Serine/threonine protein phosphatase 2A, catalytic subunit, beta isoform" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Serine/threonine protein phosphatase 2A, catalytic subunit, beta isoform" encoded by a nucleic acid that hybridizes to the "Serine/threonine protein phosphatase 2A, catalytic subunit, beta isoform" nucleic acid or its complement under low stringency conditions, and/or

(xlix) "Similar to diacylglycerol kinase delta" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Similar to diacylglycerol kinase delta" encoded by a nucleic acid that hybridizes to the "Similar to diacylglycerol kinase delta" nucleic acid or its complement under low stringency conditions, and/or

(l) "TELOMERASE-BINDING PROTEIN P23" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TELOMERASE-BINDING PROTEIN P23" encoded by a nucleic acid that hybridizes to the "TELOMERASE-BINDING PROTEIN P23" nucleic acid or its complement under low stringency conditions, and/or

(li) "TELOMERIC REPEAT BINDING FACTOR 2" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TELOMERIC REPEAT BINDING FACTOR 2" encoded by a nucleic acid that hybridizes to the "TELOMERIC REPEAT BINDING FACTOR 2" nucleic acid or its complement under low stringency conditions, and/or

(lii) "TERF1 (TRF1)-INTERACTING NUCLEAR FACTOR 2" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TERF1 (TRF1)-INTERACTING NUCLEAR FACTOR 2" encoded by a nucleic acid that hybridizes to the "TERF1 (TRF1)-INTERACTING NUCLEAR FACTOR 2" nucleic acid or its complement under low stringency conditions, and/or

(liii) "TRF1" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TRF1" encoded by a nucleic acid that hybridizes to the "TRF1" nucleic acid or its complement under low stringency conditions, and/or

(liv) "TRF2-INTERACTING TELOMERIC RAP1 PROTEIN" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TRF2-INTERACTING TELOMERIC RAP1 PROTEIN" encoded by a nucleic acid that hybridizes to the "TRF2-INTERACTING TELOMERIC RAP1 PROTEIN" nucleic acid or its complement under low stringency conditions, and/or

(lv) "TRICARBOXYLATE TRANSPORT PROTEIN, MITOCHONDRIAL PRECURSOR" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TRICARBOXYLATE TRANSPORT PROTEIN, MITOCHONDRIAL PRECURSOR" encoded by a nucleic acid that hybridizes to the "TRICARBOXYLATE TRANSPORT PROTEIN, MITOCHONDRIAL PRECURSOR" nucleic acid or its complement under low stringency conditions, and/or

(lvi) "U5 SMALL NUCLEAR RIBONUCLEOPROTEIN 200 KDA HELICASE (FRAGMENT)" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "U5 SMALL NUCLEAR RIBONUCLEOPROTEIN 200 KDA HELICASE (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "U5 SMALL NUCLEAR RIBONUCLEOPROTEIN 200 KDA HELICASE (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(lvii) "WD-REPEAT PROTEIN AN11 HOMOLOG" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "WD-REPEAT PROTEIN AN11 HOMOLOG" encoded by a nucleic acid that hybridizes to the "WD-REPEAT PROTEIN AN11 HOMOLOG" nucleic acid or its complement under low stringency conditions, is present in the complex.

32. The method of any of No. 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as cancer such as solid tumours such as breast cancer, prostate cancer, lung cancer, colon cancer; cancer such as haematological cancers such as leukemia.

33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder such as cancer such as solid tumours such as breast cancer, prostate cancer, lung cancer, colon cancer; cancer such as haematological cancers such as leukemia.

34. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

36. The method of No. 35, wherein the amount of said complex is determined.

37. The method of No. 35, wherein the activity of said complex is determined.

38. The method of No. 37, wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

39. The method of No. 35, wherein the amount of the individual protein components of said complex is determined.

40. The method of No. 39, wherein said determining step comprises determining whether

- (i) "38 KDA FK-506 BINDING PROTEIN HOMOLOG" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "38 KDA FK-506 BINDING PROTEIN HOMOLOG" encoded by a nucleic acid that hybridizes to the "38 KDA FK-506 BINDING PROTEIN HOMOLOG" nucleic acid or its complement under low stringency conditions, and/or
- (ii) "ANTIGEN NY-CO-7" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ANTIGEN NY-CO-7" encoded by a nucleic acid that hybridizes to the "ANTIGEN NY-CO-7" nucleic acid or its complement under low stringency conditions, and/or
- (iii) "ATP-BINDING CASSETTE, SUB-FAMILY D, MEMBER 3" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-BINDING CASSETTE, SUB-FAMILY D, MEMBER 3" encoded by a nucleic acid that hybridizes to the "ATP-BINDING CASSETTE, SUB-FAMILY D, MEMBER 3" nucleic acid or its complement under low stringency conditions, and/or
- (iv) "ATP-DEPENDENT DNA HELICASE II, 80 KDA SUBUNIT" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-DEPENDENT DNA HELICASE II, 80 KDA SUBUNIT" encoded by a nucleic acid that hybridizes to the "ATP-DEPENDENT DNA HELICASE II, 80 KDA SUBUNIT" nucleic acid or its complement under low stringency conditions, and/or
- (v) "BAF180" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BAF180" encoded by a nucleic acid that hybridizes to the "BAF180" nucleic acid or its complement under low stringency conditions, and/or
- (vi) "CASEIN KINASE II, ALPHA CHAIN" (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CASEIN KINASE II, ALPHA CHAIN" encoded by a nucleic acid that hybridizes to the "CASEIN KINASE II, ALPHA CHAIN" nucleic acid or its complement under low stringency conditions, and/or
- (vii) "CDNA FLJ13664 FIS, CLONE PLACE1011649" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ13664 FIS, CLONE PLACE1011649" encoded by a nucleic

acid that hybridizes to the "CDNA FLJ13664 FIS, CLONE PLACE1011649" nucleic acid or its complement under low stringency conditions, and/or

(viii) "CDNA FLJ13998 FIS, CLONE Y79AA1002229" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ13998 FIS, CLONE Y79AA1002229" encoded by a nucleic acid that hybridizes to the "CDNA FLJ13998 FIS, CLONE Y79AA1002229" nucleic acid or its complement under low stringency conditions, and/or

(ix) "CDNA FLJ20643 FIS, CLONE KAT02633" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ20643 FIS, CLONE KAT02633" encoded by a nucleic acid that hybridizes to the "CDNA FLJ20643 FIS, CLONE KAT02633" nucleic acid or its complement under low stringency conditions, and/or

(x) "CDNA FLJ25320 FIS, CLONE TST00267 (FRAGMENT)" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ25320 FIS, CLONE TST00267 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "CDNA FLJ25320 FIS, CLONE TST00267 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(xi) "CDNA FLJ31741 FIS, CLONE NT2RI2007148" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA FLJ31741 FIS, CLONE NT2RI2007148" encoded by a nucleic acid that hybridizes to the "CDNA FLJ31741 FIS, CLONE NT2RI2007148" nucleic acid or its complement under low stringency conditions, and/or

(xii) "CDNA: FLJ21908 FIS, CLONE HEP03830" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDNA: FLJ21908 FIS, CLONE HEP03830" encoded by a nucleic acid that hybridizes to the "CDNA: FLJ21908 FIS, CLONE HEP03830" nucleic acid or its complement under low stringency conditions, and/or

(xiii) "CENP-F KINETOCHORE PROTEIN" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CENP-F KINETOCHORE PROTEIN" encoded by a nucleic acid that hybridizes to the "CENP-F KINETOCHORE PROTEIN" nucleic acid or its complement under low stringency conditions, and/or

variant of "HYPOTHETICAL 68.1 KDA PROTEIN" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL 68.1 KDA PROTEIN" nucleic acid or its complement under low stringency conditions,

(xxv) "HYPOTHETICAL PROTEIN XP_058906" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN XP_058906" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN XP_058906" nucleic acid or its complement under low stringency conditions,

(xxvi) "Heat shock protein 90, alpha" (SEQ ID No:83) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Heat shock protein 90, alpha" encoded by a nucleic acid that hybridizes to the "Heat shock protein 90, alpha" nucleic acid or its complement under low stringency conditions,

(xxvii) "Her2" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Her2" encoded by a nucleic acid that hybridizes to the "Her2" nucleic acid or its complement under low stringency conditions,

(xxviii) "Her4" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Her4" encoded by a nucleic acid that hybridizes to the "Her4" nucleic acid or its complement under low stringency conditions,

(xxix) "INSULIN RECEPTOR SUBSTRATE 4" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "INSULIN RECEPTOR SUBSTRATE 4" encoded by a nucleic acid that hybridizes to the "INSULIN RECEPTOR SUBSTRATE 4" nucleic acid or its complement under low stringency conditions,

(xxx) "KIAA0667 PROTEIN (FRAGMENT)" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0667 PROTEIN (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0667 PROTEIN (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxxi) "KIAA0792 PROTEIN" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0792 PROTEIN" encoded by a nucleic acid that hybridizes to the "KIAA0792 PROTEIN" nucleic acid or its complement under low stringency conditions,

(xxxii) "KIAA0887 PROTEIN (FRAGMENT)" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0887 PROTEIN (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0887 PROTEIN (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxxiii) "PALMITOYL-PROTEIN THIOESTERASE 1 PRECURSOR" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PALMITOYL-PROTEIN THIOESTERASE 1 PRECURSOR" encoded by a nucleic acid that hybridizes to the "PALMITOYL-PROTEIN THIOESTERASE 1 PRECURSOR" nucleic acid or its complement under low stringency conditions,

(xxxiv) "PI3 kinase regulatory subunit p55 gamma" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PI3 kinase regulatory subunit p55 gamma" encoded by a nucleic acid that hybridizes to the "PI3 kinase regulatory subunit p55 gamma" nucleic acid or its complement under low stringency conditions,

(xxxv) "PI3 kinase regulatory subunit p85 alpha" (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PI3 kinase regulatory subunit p85 alpha" encoded by a nucleic acid that hybridizes to the "PI3 kinase regulatory subunit p85 alpha" nucleic acid or its complement under low stringency conditions,

(xxxvi) "PI3 kinase regulatory subunit p85 beta" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PI3 kinase regulatory subunit p85 beta" encoded by a nucleic acid that hybridizes to the "PI3 kinase regulatory subunit p85 beta" nucleic acid or its complement under low stringency conditions,

(xxxvii) "PROCOLLAGEN-PROLINE, 2-OXOGLUTARATE 4-DIOXYGENASE (PROLINE 4- HYDROXYLASE), ALPHA POLYPEPTIDE I" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PROCOLLAGEN-PROLINE, 2-OXOGLUTARATE 4-DIOXYGENASE (PROLINE 4- HYDROXYLASE), ALPHA POLYPEPTIDE I" encoded by a nucleic acid that hybridizes to the "PROCOLLAGEN-PROLINE, 2-OXOGLUTARATE 4-DIOXYGENASE (PROLINE 4- HYDROXYLASE), ALPHA POLYPEPTIDE I" nucleic acid or its complement under low stringency conditions,

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Val Asn Thr Lys Pro Glu Lys Thr Glu Glu Asp Ser Glu Glu Val Arg
 130 135 140

Glu Gln Lys His Lys Thr Phe Val Glu Lys Tyr Glu Lys Gln Ile Lys
 145 150 155 160

His Phe Gly Met Leu Arg Arg Trp Asp Asp Ser Gln Lys Tyr Leu Ser
 165 170 175

Asp Asn Val His Leu Val Cys Glu Glu Thr Ala Asn Tyr Leu Val Ile
 180 185 190

Trp Cys Ile Asp Leu Glu Val Glu Glu Lys Cys Ala Leu Met Glu Gln
 195 200 205

Val Ala His Gln Thr Ile Val Met Gln Phe Ile Leu Glu Leu Ala Lys
 210 215 220

Ser Leu Lys Val Asp Pro Arg Ala Cys Phe Arg Gln Phe Phe Thr Lys
 225 230 235 240

Ile Lys Thr Ala Asp Arg Gln Tyr Met Glu Gly Phe Asn Asp Glu Leu
 245 250 255

Glu Ala Phe Lys Glu Arg Val Arg Gly Arg Ala Lys Leu Arg Ile Glu
 260 265 270

Lys Ala Met Lys Glu Tyr Glu Glu Glu Glu Arg Lys Lys Arg Leu Gly
 275 280 285

Pro Gly Gly Leu Asp Pro Val Glu Val Tyr Glu Ser Leu Pro Glu Glu
 290 295 300

Leu Gln Lys Cys Phe Asp Val Lys Asp Val Gln Met Leu Gln Asp Ala
 305 310 315 320

Ile Ser Lys Met Asp Pro Thr Asp Ala Lys Tyr His Met Gln Arg Cys
 325 330 335

Ile Asp Ser Gly Leu Trp Val Pro Asn Ser Lys Ala Ser Glu Ala Lys
 340 345 350

Glu Gly Glu Glu Ala Gly Pro Gly Asp Pro Leu Leu Glu Ala Val Pro
 355 360 365

Lys Thr Gly Asp Glu Lys Asp Val Ser Val
 370 375

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 <211> 237
 <212> PRT
 <213> HOMO sapiens

<400> 63

Met Ala Glu Ala Leu Gly Val Ser Val Thr Asp Tyr Thr Phe Glu Asp
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Cys Gln Leu Ala Leu Ala Glu Gly Gln Leu Arg Leu Pro Ala Asp Thr
 20 25 30

Cys Leu Leu Glu Phe Ala Arg Leu Val Arg Gly Leu Gly Leu Lys Pro
 35 40 45

Glu Lys Leu Glu Lys Asp Leu Asp Arg Tyr Ser Glu Arg Ala Arg Met
 50 55 60

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Lys Gly Gly Glu Lys Ile Gly Ile Ala Glu Phe Ala Ala Ser Leu Glu
65 70 75 80

Val Pro Val Ser Asp Leu Leu Glu Asp Met Phe Ser Leu Phe Asp Glu
85 90 95

Ser Gly Ser Gly Glu Val Asp Leu Arg Glu Cys Val Val Ala Leu Ser
100 105 110

Val Val Cys Arg Pro Ala Arg Thr Leu Asp Thr Ile Gln Leu Ala Phe
115 120 125

Lys Thr Tyr Gly Ala Gln Glu Asp Gly Ser Val Gly Glu Gly Asp Leu
130 135 140

Ser Cys Ile Leu Lys Thr Ala Leu Gly Val Ala Glu Leu Thr Val Thr
145 150 155 160

Asp Leu Phe Arg Ala Ile Asp Gln Glu Glu Lys Gly Lys Ile Thr Phe
165 170 175

Ala Asp Phe His Arg Phe Ala Glu Met Tyr Pro Ala Phe Ala Glu Glu
180 185 190

Tyr Leu Tyr Pro Asp Gln Thr His Phe Glu Ser Cys Ala Glu Thr Ser
195 200 205

Pro Ala Pro Ile Pro Asn Gly Phe Cys Ala Asp Phe Ser Pro Glu Asn
210 215 220

Ser Asp Ala Gly Arg Lys Pro Val Arg Lys Lys Leu Asp
225 230 235

<210> 64
<211> 568
<212> PRT
<213> Homo sapiens

<400> 64

Met Arg Pro Asp Ser Pro Thr Met Ala Ala Pro Ala Glu Ser Leu Arg
1 5 10 15

Arg Arg Lys Thr Gly Tyr Ser Asp Pro Glu Pro Glu Ser Pro Pro Ala
20 25 30

Pro Gly Arg Gly Pro Ala Gly Ser Pro Ala His Leu His Thr Gly Thr
35 40 45

Phe Trp Leu Thr Arg Ile Val Leu Leu Lys Ala Leu Ala Phe Val Tyr
50 55 60

Phe Val Ala Phe Leu Val Ala Phe His Gln Asn Lys Gln Leu Ile Gly
65 70 75 80

Asp Arg Gly Leu Leu Pro Cys Arg Val Phe Leu Lys Asn Phe Gln Gln
85 90 95

Tyr Phe Gln Asp Arg Thr Ser Trp Glu Val Phe Ser Tyr Met Pro Thr
100 105 110

Ile Leu Trp Leu Met Asp Trp Ser Asp Met Asn Ser Asn Leu Asp Leu
115 120 125

Leu Ala Leu Leu Gly Leu Gly Ile Ser Ser Phe Val Leu Ile Thr Gly

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 130 135 140

Cys Ala Asn Met Leu Leu Met Ala Ala Leu Trp Gly Leu Tyr Met Ser
 145 150 155 160

Leu Val Asn Val Gly His Val Trp Glu Ala Glu Ala Arg Trp Glu Ser
 165 170 175

Gln Leu Leu Glu Thr Gly Phe Leu Gly Ile Phe Leu Cys Pro Leu Trp
 180 185 190

Thr Leu Ser Arg Leu Pro Gln His Thr Pro Thr Ser Arg Ile Val Leu
 195 200 205

Trp Gly Phe Arg Trp Leu Ile Phe Arg Ile Met Leu Gly Ala Gly Leu
 210 215 220

Ile Lys Ile Arg Gly Asp Arg Cys Trp Arg Asp Leu Thr Cys Met Asp
 225 230 235 240

Phe His Tyr Glu Thr Gln Pro Met Pro Asn Pro Val Ala Tyr Tyr Leu
 245 250 255

His His Ser Pro Trp Trp Phe His Arg Phe Glu Thr Leu Ser Asn His
 260 265 270

Phe Ile Glu Leu Leu Val Pro Phe Phe Leu Phe Leu Gly Arg Arg Ala
 275 280 285

Cys Ile Ile His Gly Val Leu Gln Ile Leu Phe Gln Ala Val Leu Ile
 290 295 300

Val Ser Gly Asn Leu Ser Phe Leu Asn Trp Leu Thr Met Val Pro Ser
 305 310 315 320

Leu Ala Cys Phe Asp Asp Ala Thr Leu Gly Phe Leu Phe Pro Ser Gly
 325 330 335

Pro Gly Ser Leu Lys Asp Arg Val Leu Gln Met Gln Arg Asp Ile Arg
 340 345 350

Gly Ala Arg Pro Glu Pro Arg Phe Gly Ser Val Val Arg Arg Ala Ala
 355 360 365

Asn Val Ser Leu Gly Val Leu Leu Ala Trp Leu Ser Val Pro Val Val
 370 375 380

Leu Asn Leu Leu Ser Ser Arg Gln Val Met Asn Thr His Phe Asn Ser
 385 390 395 400

Leu His Ile Val Asn Thr Tyr Gly Ala Phe Gly Ser Ile Thr Lys Glu
 405 410 415

Arg Ala Glu Val Ile Leu Gln Gly Thr Ala Ser Ser Asn Ala Ser Ala
 420 425 430

Pro Asp Ala Met Trp Glu Asp Tyr Glu Phe Lys Cys Lys Pro Gly Asp
 435 440 445

Pro Ser Arg Arg Pro Cys Leu Ile Ser Pro Tyr His Tyr Arg Leu Asp
 450 455 460

Trp Leu Met Trp Phe Ala Ala Phe Gln Thr Tyr Glu His Asn Asp Trp
 465 470 475 480

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ile Ile His Leu Ala Gly Lys Leu Leu Ala Ser Asp Ala Glu Ala Leu
485 490 495

Ser Leu Leu Ala His Asn Pro Phe Ala Gly Arg Pro Pro Pro Arg Trp
500 505 510

Val Arg Gly Glu His Tyr Arg Tyr Lys Phe Ser Arg Pro Gly Gly Arg
515 520 525

His Ala Ala Glu Gly Lys Trp Trp Val Arg Lys Arg Ile Gly Ala Tyr
530 535 540

Phe Pro Pro Leu Ser Leu Glu Glu Leu Arg Pro Tyr Phe Arg Asp Arg
545 550 555 560

Gly Trp Pro Leu Pro Gly Pro Leu
565

<210> 65
<211> 764
<212> PRT
<213> Homo sapiens

<400> 65

Met Ala Ala Thr Leu Lys Ser Leu Lys Leu Val Arg Tyr Arg Ala Phe
1 5 10 15

Cys Ser Pro Ser Ala Phe Gly Ala Val Arg Ser Val Ser Tyr Trp Asn
20 25 30

Val Ser Ser Thr Gln His Gly Gly Gln Asp Pro Pro Glu His Ile Ser
35 40 45

Leu Cys His Ser Ala Lys Lys Val Lys Asn Ile Cys Ser Thr Phe Ser
50 55 60

Ser Arg Arg Ile Leu Thr Thr Ser Ser Ala His Pro Gly Leu Glu Phe
65 70 75 80

Ser Lys Thr Ser Ser Ser Lys Ala Ser Thr Leu Gln Leu Gly Ser Pro
85 90 95

Arg Ala Thr Gly Val Asp Glu Glu Asp Val Glu Val Phe Asp Ser Phe
100 105 110

Glu Asn Met Arg Val Phe Leu Gln Leu Arg Pro Glu Tyr Arg Val His
115 120 125

Ser Tyr Asn Ala Ser Glu Thr Ser Gln Leu Leu Ser Val Ser Glu Gly
130 135 140

Glu Leu Ile Leu His Lys Val Arg Val Asn Gln Asn Asn Leu Gln Ala
145 150 155 160

Gln Val Ile Val Asp Tyr Leu Cys Lys Leu Ser Ser Leu Pro Ala Glu
165 170 175

Gln His Pro Val Leu Leu Gly Ser Thr Ser Phe Ala Leu Leu Cys Gln
180 185 190

Leu Ser Val Lys Lys Ile Gln Leu Phe Asp Thr Gln Asp Leu Ile Asn
195 200 205

Val Leu Lys Ala Phe Val Ile Leu Gly Ile Pro His Ser His Ser Met
210 215 220

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Leu Asp Val Tyr Glu Thr Lys Cys Cys His Gln Val Trp Glu Met Asn
 225 230 235 240
 Met Asp Gln Leu Leu Leu Val Ala Asp Leu Trp Arg Tyr Leu Gly Arg
 245 250 255
 Lys Val Pro Arg Phe Leu Asn Ile Phe Ser Ser Tyr Leu Asn Leu His
 260 265 270
 Trp Lys Asp Leu Ser Leu Ser Gln Leu Val His Leu Ile Tyr Val Ile
 275 280 285
 Gly Glu Asn Arg Gln Val Ser Gln Asp Leu Met Gln Lys Leu Glu Ser
 290 295 300
 Leu Ile Leu Lys Tyr Ile Asp Leu Ile Asn Leu Glu Glu Val Gly Thr
 305 310 315 320
 Ile Cys Leu Gly Phe Phe Lys Ser Ser Thr Asn Leu Ser Glu Phe Val
 325 330 335
 Met Arg Lys Ile Gly Asp Leu Ala Cys Ala Asn Ile Gln His Leu Ser
 340 345 350
 Ser Arg Ser Leu Val Asn Ile Val Lys Met Phe Arg Phe Thr His Val
 355 360 365
 Asp His Ile Asn Phe Met Lys Gln Ile Gly Glu Ile Ala Pro Gln Arg
 370 375 380
 Ile Pro Ser Leu Gly Val Gln Gly Val Met His Leu Thr Leu Tyr Cys
 385 390 395 400
 Ser Ala Leu Arg Phe Leu Asn Glu Gly Val Met Asn Ala Val Ala Ala
 405 410 415
 Ser Leu Pro Pro Arg Val Ala His Cys Arg Ser Lys Asp Val Ala Lys
 420 425 430
 Ile Leu Trp Ser Phe Gly Thr Leu Asn Tyr Lys Pro Pro Asn Ala Glu
 435 440 445
 Glu Phe Tyr Ser Ser Leu Ile Ser Glu Ile His Arg Lys Met Pro Glu
 450 455 460
 Phe Asn Gln Tyr Pro Glu His Leu Pro Thr Cys Leu Leu Gly Leu Ala
 465 470 475 480
 Phe Leu Glu Tyr Phe Pro Val Glu Leu Ile Asp Phe Ala Leu Ser Pro
 485 490 495
 Gly Phe Val Arg Leu Ala Gln Glu Arg Thr Lys Phe Asp Leu Leu Lys
 500 505 510
 Glu Leu Tyr Thr Leu Asp Gly Thr Val Gly Ile Glu Cys Pro Asp Tyr
 515 520 525
 Arg Gly Asn Arg Leu Ser Thr His Leu Gln Gln Glu Gly Ser Glu Leu
 530 535 540
 Leu Trp Tyr Leu Ala Glu Lys Asp Met Asn Ser Lys Pro Glu Phe Leu
 545 550 555 560

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Glu Thr Val Phe Leu Leu Glu Thr Met Leu Gly Gly Pro Gln Tyr Val
 565 570 575

Lys His His Met Ile Leu Pro His Thr Arg Ser Ser Asp Leu Glu Val
 580 585 590

Gln Leu Asp Val Asn Leu Lys Pro Leu Pro Phe Asn Arg Glu Ala Thr
 595 600 605

Pro Ala Glu Asn Val Ala Lys Leu Arg Leu Glu His Val Gly Val Ser
 610 615 620

Leu Thr Asp Asp Leu Met Asn Lys Leu Leu Lys Gly Lys Ala Arg Gly
 625 630 635 640

His Phe Gln Gly Lys Thr Glu Ser Glu Pro Gly Gln Gln Pro Met Glu
 645 650 655

Leu Glu Asn Lys Ala Ala Val Pro Leu Gly Gly Phe Leu Cys Asn Val
 660 665 670

Ala Asp Lys Ser Gly Ala Met Glu Met Ala Gly Leu Cys Pro Ala Ala
 675 680 685

Cys Met Gln Thr Pro Arg Met Lys Leu Ala Val Gln Phe Thr Asn Arg
 690 695 700

Asn Gln Tyr Cys Tyr Gly Ser Arg Asp Leu Leu Gly Leu His Asn Met
 705 710 715 720

Lys Arg Arg Gln Leu Ala Arg Leu Gly Tyr Arg Val Val Glu Leu Ser
 725 730 735

Tyr Trp Glu Trp Leu Pro Leu Leu Lys Arg Thr Arg Leu Glu Lys Leu
 740 745 750

Ala Phe Leu His Glu Lys Val Phe Thr Ser Ala Leu
 755 760

<210> 66
 <211> 355
 <212> PRT
 <213> Homo sapiens

<400> 66

Met Ser Thr Asn Gly Val Ser Asn Gly Val Ser Asn Gly Leu His Leu
 1 5 10 15

His Ser Asn Gly Phe Arg Leu Pro Glu Ser Arg Gly His Val Ser Pro
 20 25 30

Gln Val Glu Leu Pro Pro Tyr Leu Glu Arg Val Lys Gln Gln Ala Asn
 35 40 45

Glu Ala Phe Ala Cys Gln Gln Trp Thr Gln Ala Ile Gln Leu Tyr Ser
 50 55 60

Lys Ala Val Gln Arg Ala Pro His Asn Ala Met Leu Tyr Gly Asn Arg
 65 70 75 80

Ala Ala Ala Tyr Met Lys Arg Lys Trp Asp Gly Asp His Tyr Asp Ala
 85 90 95

Leu Arg Asp Cys Leu Lys Ala Ile Ser Leu Asn Pro Cys His Leu Lys
 100 105 110

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ala His Phe Arg Leu Ala Arg Cys Leu Phe Glu Leu Lys Tyr Val Ala
115 120 125

Glu Ala Leu Glu Cys Leu Asp Asp Phe Lys Gly Lys Phe Pro Glu Gln
130 135 140

Ala His Ser Ser Ala Cys Asp Ala Leu Gly Arg Ala Ile Thr Ala Ala
145 150 155 160

Leu Phe Ser Lys Asn Asp Gly Glu Glu Lys Lys Gly Pro Gly Gly Gly
165 170 175

Ala Pro Val Arg Leu Arg Ser Thr Ser Arg Lys Asp Ser Ile Ser Glu
180 185 190

Asp Glu Met Ala Leu Arg Glu Arg Ser Tyr Asp Tyr Gln Phe Arg Tyr
195 200 205

Cys Gly His Cys Asn Thr Thr Thr Asp Ile Lys Glu Ala Asn Phe Phe
210 215 220

Gly Ser Asn Ala Gln Tyr Ile Val Ser Gly Ser Asp Asp Gly Ser Phe
225 230 235 240

Phe Ile Trp Glu Lys Glu Thr Thr Asn Leu Val Arg Val Leu Gln Gly
245 250 255

Asp Glu Ser Ile Val Asn Cys Leu Gln Pro His Pro Ser Tyr Cys Phe
260 265 270

Leu Ala Thr Ser Gly Ile Asp Pro Val Val Arg Leu Trp Asn Pro Arg
275 280 285

Pro Glu Ser Glu Asp Leu Thr Gly Arg Val Val Glu Asp Met Glu Gly
290 295 300

Ala Ser Gln Ala Asn Gln Arg Arg Met Asn Ala Asp Pro Leu Glu Val
305 310 315 320

Met Leu Leu Asn Met Gly Tyr Arg Ile Thr Gly Leu Ser Ser Gly Gly
325 330 335

Ala Gly Ala Ser Asp Asp Glu Asp Ser Ser Glu Gly Gln Val Gln Cys
340 345 350

Arg Pro Ser
355

<210> 67
<211> 774
<212> PRT
<213> Homo sapiens

<400> 67

Met Gln Ser Lys Met Arg Ser Tyr Gln Ala Lys Val Arg Gln Gly Ala
1 5 10 15

Leu Val Cys Phe Leu Ser Thr Ile Lys Ser Ile Glu Lys Lys Val Leu
20 25 30

Tyr Gly Tyr Trp Ser Ala Phe Ile Pro Asp Thr Pro Glu Leu Gly Ser
35 40 45

Pro Gln Ser Val Ser Leu Met Thr Leu Thr Leu Lys Asp Pro Ser Pro
50 55 60

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Lys Thr Arg Ala Cys Ala Leu Gln Val Leu Ser Ala Ile Leu Glu Gly
65 70 75 80

Ser Lys Gln Phe Leu Ser Val Ala Glu Asp Thr Ser Asp His Arg Arg
85 90 95

Ala Phe Thr Pro Phe Ser Val Met Ile Ala Cys Ser Ile Arg Glu Leu
100 105 110

His Arg Cys Leu Leu Leu Ala Leu Val Ala Glu Ser Ser Ser Gln Thr
115 120 125

Val Thr Gln Ile Ile Lys Cys Leu Ala Asn Leu Val Ser Asn Ala Pro
130 135 140

Tyr Asp Arg Leu Lys Leu Ser Leu Leu Thr Lys Val Trp Asn Gln Ile
145 150 155 160

Lys Pro Tyr Ile Arg His Lys Asp Val Asn Val Arg Val Ser Ser Leu
165 170 175

Thr Leu Leu Gly Ala Ile Val Ser Thr His Ala Pro Leu Pro Glu Val
180 185 190

Gln Leu Leu Leu Gln Gln Pro Cys Ser Ser Gly Leu Gly Asn Ser Asn
195 200 205

Ser Ala Thr Pro His Leu Ser Pro Pro Asp Trp Trp Lys Lys Thr Pro
210 215 220

Ala Gly Pro Ser Leu Glu Glu Thr Ser Val Ser Ser Pro Lys Gly Ser
225 230 235 240

Ser Glu Pro Cys Trp Leu Ile Arg Leu Cys Ile Ser Ile Val Val Leu
245 250 255

Pro Lys Glu Asp Ser Cys Ser Gly Ser Asp Ala Gly Ser Ala Ala Gly
260 265 270

Ser Thr Tyr Glu Pro Ser Pro Met Arg Leu Glu Ala Leu Gln Val Leu
275 280 285

Thr Leu Leu Ala Arg Gly Tyr Phe Ser Met Thr Gln Ala Tyr Leu Met
290 295 300

Glu Leu Gly Glu Val Ile Cys Lys Cys Met Gly Glu Ala Asp Pro Ser
305 310 315 320

Ile Gln Leu His Gly Ala Lys Leu Leu Glu Glu Leu Gly Thr Gly Leu
325 330 335

Ile Gln Gln Tyr Lys Pro Asp Ser Thr Ala Ala Pro Asp Gln Arg Ala
340 345 350

Pro Val Phe Leu Val Val Met Phe Trp Thr Met Met Leu Asn Gly Pro
355 360 365

Leu pro Arg Ala Leu Gln Asn Ser Glu His Pro Thr Leu Gln Ala Ser
370 375 380

Ala Cys Asp Ala Leu Ser Ser Ile Leu Pro Glu Ala Phe Ser Asn Leu
385 390 395 400

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 Pro Asn Asp Arg Gln Met Leu Cys Ile Thr Val Leu Leu Gly Leu Asn
 405 410 415

Asp Ser Lys Asn Arg Leu Val Lys Ala Ala Thr Ser Arg Ala Leu Gly
 420 425 430

Val Tyr Val Leu Phe Pro Cys Leu Arg Gln Asp Val Ile Phe Val Ala
 435 440 445

Asp Ala Ala Asn Ala Ile Leu Met Ser Leu Glu Asp Lys Ser Leu Asn
 450 455 460

Val Arg Ala Lys Ala Ala Trp Ser Leu Gly Asn Leu Thr Asp Thr Leu
 465 470 475 480

Ile Val Asn Met Glu Thr Pro Asp Pro Ser Phe Gln Glu Glu Phe Ser
 485 490 495

Gly Leu Leu Leu Leu Lys Met Leu Arg Ser Ala Ile Glu Ala Ser Lys
 500 505 510

Asp Lys Asp Lys Val Lys Ser Asn Ala Val Arg Ala Leu Gly Asn Leu
 515 520 525

Leu His Phe Leu Gln Pro Ser His Ile Glu Lys Pro Thr Phe Ala Glu
 530 535 540

Ile Ile Glu Glu Ser Ile Gln Ala Leu Ile Ser Thr Val Leu Thr Glu
 545 550 555 560

Ala Ala Met Lys Val Arg Trp Asn Ala Cys Tyr Ala Met Gly Asn Val
 565 570 575

Phe Lys Asn Pro Ala Leu Pro Leu Gly Thr Ala Pro Trp Thr Ser Gln
 580 585 590

Ala Tyr Asn Ala Leu Thr Ser Val Val Thr Ser Cys Lys Asn Phe Lys
 595 600 605

Val Arg Ile Arg Ser Ala Ala Ala Leu Ser Val Pro Gly Lys Arg Glu
 610 615 620

Gln Tyr Gly Ser Val Asp Gln Tyr Ala Arg Ile Trp Asn Ala Leu Val
 625 630 635 640

Thr Ala Leu Gln Lys Ser Glu Asp Thr Ile Asp Phe Leu Glu Phe Lys
 645 650 655

Tyr Cys Val Ser Leu Arg Thr Gln Ile Cys Gln Ala Leu Ile His Leu
 660 665 670

Leu Ser Leu Ala Ser Ala Ser Asp Leu Pro Cys Met Lys Glu Thr Leu
 675 680 685

Glu Leu Ser Gly Asn Met Val Gln Ser Tyr Ile Leu Gln Phe Leu Lys
 690 695 700

Ser Gly Ala Glu Gly Asp Asp Thr Gly Ala Pro His Ser Pro Gln Glu
 705 710 715 720

Arg Asp Gln Met Val Arg Met Ala Leu Lys His Met Gly Ser Ile Gln
 725 730 735

Ala Pro Thr Gly Asp Thr Ala Arg Arg Ala Ile Met Gly Phe Leu Glu
 740 745 750

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Glu Ile Leu Ala Val Cys Phe Asp Ser Ser Gly Ser Gln Gly Ala Leu
755 760 765

Pro Gly Leu Thr Asn Gln
770

<210> 68
<211> 213
<212> PRT
<213> Homo sapiens

<400> 68

Met Pro Asp Glu Asn Ile Phe Leu Phe Val Pro Asn Leu Ile Gly Tyr
1 5 10 15

Ala Arg Ile Val Phe Ala Ile Ile Ser Phe Tyr Phe Met Pro Cys Cys
20 25 30

Pro Leu Thr Ala Ser Ser Phe Tyr Leu Leu Ser Gly Leu Leu Asp Ala
35 40 45

Phe Asp Gly His Ala Ala Arg Ala Leu Asn Gln Gly Thr Arg Phe Gly
50 55 60

Ala Met Leu Asp Met Leu Thr Asp Arg Cys Ser Thr Met Cys Leu Leu
65 70 75 80

Val Asn Leu Ala Leu Leu Tyr Pro Gly Ala Thr Leu Phe Phe Gln Ile
85 90 95

Ser Met Ser Leu Asp Val Ala Ser His Trp Leu His Leu His Ser Ser
100 105 110

Val Val Arg Gly Ser Glu Ser His Lys Met Ile Asp Leu Ser Gly Asn
115 120 125

Pro Val Leu Arg Ile Tyr Tyr Thr Ser Arg Pro Ala Leu Phe Thr Leu
130 135 140

Cys Ala Gly Asn Glu Leu Phe Tyr Cys Leu Leu Tyr Leu Phe His Phe
145 150 155 160

Ser Glu Gly Pro Leu Val Gly Ser Val Gly Leu Phe Arg Met Gly Leu
165 170 175

Trp Val Thr Ala Pro Ile Ala Leu Leu Lys Ser Leu Ile Ser Val Ile
180 185 190

His Leu Ile Thr Ala Ala Arg Asn Met Ala Ala Leu Asp Ala Ala Asp
195 200 205

Arg Ala Lys Lys Lys
210

<210> 69
<211> 1047
<212> PRT
<213> Homo sapiens

<400> 69

Met Ala Val Thr Leu Asp Lys Asp Ala Tyr Tyr Arg Arg Val Lys Arg
1 5 10 15

Leu Tyr Ser Asn Trp Arg Lys Gly Glu Asp Glu Tyr Ala Asn Val Asp
20 25 30

protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ala Ile Val Val Ser Val Gly Val Asp Glu Glu Ile Val Tyr Ala Lys
 35 40 45

Ser Thr Ala Leu Gln Thr Trp Leu Phe Gly Tyr Glu Leu Thr Asp Thr
 50 55 60

Ile Met Val Phe Cys Asp Asp Lys Ile Ile Phe Met Ala Ser Lys Lys
 65 70 75 80

Lys Val Glu Phe Leu Lys Gln Ile Ala Asn Thr Lys Gly Asn Glu Asn
 85 90 95

Ala Asn Gly Ala Pro Ala Ile Thr Leu Leu Ile Arg Glu Lys Asn Glu
 100 105 110

Ser Asn Lys Ser Ser Phe Asp Lys Met Ile Glu Ala Ile Lys Glu Ser
 115 120 125

Lys Asn Gly Lys Lys Ile Gly Val Phe Ser Lys Asp Lys Phe Pro Gly
 130 135 140

Glu Phe Met Lys Ser Trp Asn Asp Cys Leu Asn Lys Glu Gly Phe Asp
 145 150 155 160

Lys Ile Asp Ile Ser Ala Val Val Ala Tyr Thr Ile Ala Val Lys Glu
 165 170 175

Asp Gly Glu Leu Asn Leu Met Lys Lys Ala Ala Ser Ile Thr Ser Glu
 180 185 190

Val Phe Asn Lys Phe Phe Lys Glu Arg Val Met Glu Ile Val Asp Ala
 195 200 205

Asp Glu Lys Val Arg His Ser Lys Leu Ala Glu Ser Val Glu Lys Ala
 210 215 220

Ile Glu Glu Lys Lys Tyr Leu Ala Gly Ala Asp Pro Ser Thr Val Glu
 225 230 235 240

Met Cys Tyr Pro Pro Ile Ile Gln Ser Gly Gly Asn Tyr Asn Leu Lys
 245 250 255

Phe Ser Val Val Ser Asp Lys Asn His Met His Phe Gly Ala Ile Thr
 260 265 270

Cys Ala Met Gly Ile Arg Phe Lys Ser Tyr Cys Ser Asn Leu Val Arg
 275 280 285

Thr Leu Met Val Asp Pro Ser Gln Glu Val Gln Glu Asn Tyr Asn Phe
 290 295 300

Leu Leu Gln Leu Gln Glu Glu Leu Leu Lys Glu Leu Arg His Gly Val
 305 310 315 320

Lys Ile Cys Asp Val Tyr Asn Ala Val Met Asp Val Val Lys Lys Gln
 325 330 335

Lys Pro Glu Leu Leu Asn Lys Ile Thr Lys Asn Leu Gly Phe Gly Met
 340 345 350

Gly Ile Glu Phe Arg Glu Gly Ser Leu Val Ile Asn Ser Lys Asn Gln
 355 360 365

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Tyr Lys Leu Lys Lys Gly Met Val Phe Ser Ile Asn Leu Gly Phe Ser
370 375 380

Asp Leu Thr Asn Lys Glu Gly Lys Lys Pro Glu Glu Lys Thr Tyr Ala
385 390 395 400

Leu Phe Ile Gly Asp Thr Val Leu Val Asp Glu Asp Gly Pro Ala Thr
405 410 415

Val Leu Thr Ser Val Lys Lys Lys Val Lys Asn Val Gly Ile Phe Leu
420 425 430

Lys Asn Glu Asp Glu Glu Glu Glu Glu Glu Lys Asp Glu Ala Glu
435 440 445

Asp Leu Leu Gly Arg Gly Ser Arg Ala Ala Leu Leu Thr Glu Arg Thr
450 455 460

Arg Asn Glu Met Thr Ala Glu Glu Lys Arg Arg Ala His Gln Lys Glu
465 470 475 480

Leu Ala Ala Gln Leu Asn Glu Glu Ala Lys Arg Arg Leu Thr Glu Gln
485 490 495

Lys Gly Glu Gln Gln Ile Gln Lys Ala Arg Lys Ser Asn Val Ser Tyr
500 505 510

Lys Asn Pro Ser Leu Met Pro Lys Glu Pro His Ile Arg Glu Met Lys
515 520 525

Ile Tyr Ile Asp Lys Lys Tyr Glu Thr Val Ile Met Pro Val Phe Gly
530 535 540

Ile Ala Thr Pro Phe His Ile Ala Thr Ile Lys Asn Ile Ser Met Ser
545 550 555 560

Val Glu Gly Asp Tyr Thr Tyr Leu Arg Ile Asn Phe Tyr Cys Pro Gly
565 570 575

Ser Ala Leu Gly Arg Asn Glu Gly Asn Ile Phe Pro Asn Pro Glu Ala
580 585 590

Thr Phe Val Lys Glu Ile Thr Tyr Arg Ala Ser Asn Ile Lys Ala Pro
595 600 605

Gly Glu Gln Thr Val Pro Ala Leu Asn Leu Gln Asn Ala Phe Arg Ile
610 615 620

Ile Lys Glu Val Gln Lys Arg Tyr Lys Thr Arg Glu Ala Glu Glu Lys
625 630 635 640

Glu Lys Glu Gly Ile Val Lys Gln Asp Ser Leu Val Ile Asn Leu Asn
645 650 655

Arg Ser Asn Pro Lys Leu Lys Asp Leu Tyr Ile Arg Pro Asn Ile Ala
660 665 670

Gln Lys Arg Met Gln Gly Ser Leu Glu Ala His Val Asn Gly Phe Arg
675 680 685

Phe Thr Ser Val Arg Gly Asp Lys Val Asp Ile Leu Tyr Asn Asn Ile
690 695 700

Lys His Ala Leu Phe Gln Pro Cys Asp Gly Glu Met Ile Ile Val Leu
705 710 715 720

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

His Phe His Leu Lys Asn Ala Ile Met Phe Gly Lys Lys Arg His Thr
 725 730 735
 Asp Val Gln Phe Tyr Thr Glu Val Gly Glu Ile Thr Thr Asp Leu Gly
 740 745 750
 Lys His Gln His Met His Asp Arg Asp Asp Leu Tyr Ala Glu Gln Met
 755 760 765
 Glu Arg Glu Met Arg His Lys Leu Lys Thr Ala Phe Lys Asn Phe Ile
 770 775 780
 Glu Lys Val Glu Ala Leu Thr Lys Glu Glu Leu Glu Phe Glu Val Pro
 785 790 795 800
 Phe Arg Asp Leu Gly Phe Asn Gly Ala Pro Tyr Arg Ser Thr Cys Leu
 805 810 815
 Leu Gln Pro Thr Ser Ser Ala Leu Val Asn Ala Thr Glu Trp Pro Pro
 820 825 830
 Phe Val Val Thr Leu Asp Glu Val Glu Leu Ile His Phe Glu Arg Val
 835 840 845
 Gln Phe His Leu Lys Asn Phe Asp Met Val Ile Val Tyr Lys Asp Tyr
 850 855 860
 Ser Lys Lys Val Thr Met Ile Asn Ala Ile Pro Val Ala Ser Leu Asp
 865 870 875 880
 Pro Ile Lys Glu Trp Leu Asn Ser Cys Asp Leu Lys Tyr Thr Glu Gly
 885 890 895
 Val Gln Ser Leu Asn Trp Thr Lys Ile Met Lys Thr Ile Val Asp Asp
 900 905 910
 Pro Glu Gly Phe Phe Glu Gln Gly Gly Trp Ser Phe Leu Glu Pro Glu
 915 920 925
 Gly Glu Gly Ser Asp Ala Glu Glu Gly Asp Ser Glu Ser Glu Ile Glu
 930 935 940
 Asp Glu Thr Phe Asn Pro Ser Glu Asp Asp Tyr Glu Glu Glu Glu Glu
 945 950 955 960
 Asp Ser Asp Glu Asp Tyr Ser Ser Glu Ala Glu Glu Ser Asp Tyr Ser
 965 970 975
 Lys Glu Ser Leu Gly Ser Glu Glu Glu Ser Gly Lys Asp Trp Asp Glu
 980 985 990
 Leu Glu Glu Glu Ala Arg Lys Ala Asp Arg Glu Ser Arg Tyr Glu Glu
 995 1000 1005
 Glu Glu Glu Gln Ser Arg Ser Met Ser Arg Lys Arg Lys Ala Ser
 1010 1015 1020
 Val His Ser Ser Gly Arg Gly Ser Asn Arg Gly Ser Arg His Ser
 1025 1030 1035
 Ser Ala Pro Pro Lys Lys Lys Arg Lys
 1040 1045

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

<210> 70

<211> 564

<212> PRT

<213> Homo sapiens

<400> 70

Met Leu Ala Asn Ser Ala Ser Val Arg Ile Leu Ile Lys Gly Gly Lys
1 5 10 15Val Val Asn Asp Asp Cys Thr His Glu Ala Asp Val Tyr Ile Glu Asn
20 25 30Gly Ile Ile Gln Gln Val Gly Arg Glu Leu Met Ile Pro Gly Gly Ala
35 40 45Lys Val Ile Asp Ala Thr Gly Lys Leu Val Ile Pro Gly Gly Ile Asp
50 55 60Thr Ser Thr His Phe His Gln Thr Phe Met Asn Ala Thr Cys Val Asp
65 70 75 80Asp Phe Tyr His Gly Thr Lys Ala Ala Leu Val Gly Gly Thr Thr Met
85 90 95Ile Ile Gly His Val Leu Pro Asp Lys Glu Thr Ser Leu Val Asp Ala
100 105 110Tyr Glu Lys Cys Arg Gly Leu Ala Asp Pro Lys Val Cys Cys Asp Tyr
115 120 125Ala Leu His Val Gly Ile Thr Trp Trp Ala Pro Lys Val Lys Ala Glu
130 135 140Met Glu Thr Leu Val Arg Glu Lys Gly Val Asn Ser Phe Gln Met Phe
145 150 155 160Met Thr Tyr Lys Asp Leu Tyr Met Leu Arg Asp Ser Glu Leu Tyr Gln
165 170 175Val Leu His Ala Cys Lys Asp Ile Gly Ala Ile Ala Arg Val His Ala
180 185 190Glu Asn Gly Glu Leu Val Ala Glu Gly Ala Lys Glu Ala Leu Asp Leu
195 200 205Gly Ile Thr Gly Pro Glu Gly Ile Glu Ile Ser Arg Pro Glu Glu Leu
210 215 220Glu Ala Glu Ala Thr His Arg Val Ile Thr Ile Ala Asn Arg Thr His
225 230 235 240Cys Pro Ile Tyr Leu Val Asn Val Ser Ser Ile Ser Ala Gly Asp Val
245 250 255Ile Ala Ala Ala Lys Met Gln Gly Lys Val Val Leu Ala Glu Thr Thr
260 265 270Thr Ala His Ala Thr Leu Thr Gly Leu His Tyr Tyr His Gln Asp Trp
275 280 285Ser His Ala Ala Ala Tyr Val Thr Val Pro Pro Leu Arg Leu Asp Thr
290 295 300Asn Thr Ser Thr Tyr Leu Met Ser Leu Leu Ala Asn Asp Thr Leu Asn
305 310 315 320

protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ile Val Ala Ser Asp His Arg Pro Phe Thr Thr Lys Gln Lys Ala Met
325 330 335

Gly Lys Glu Asp Phe Thr Lys Ile Pro His Gly Val Ser Gly Val Gln
340 345 350

Asp Arg Met Ser Val Ile Trp Glu Arg Gly Val Val Gly Gly Lys Met
355 360 365

Asp Glu Asn Arg Phe Val Ala Val Thr Ser Ser Asn Ala Ser Lys Leu
370 375 380

Leu Asn Leu Tyr Pro Arg Lys Gly Arg Ile Ile Pro Gly Ala His Ala
385 390 395 400

Asp Val Val Val Trp Asp Pro Glu Ala Thr Lys Thr Ile Ser Ala Ser
405 410 415

Thr Gln Val Gln Gly Gly Asp Phe Asn Leu Tyr Glu Asn Met Arg Cys
420 425 430

His Gly Val Pro Leu Val Thr Ile Ser Arg Gly Arg Val Val Tyr Glu
435 440 445

Asn Gly Val Phe Met Cys Ala Glu Gly Thr Gly Lys Phe Cys Pro Leu
450 455 460

Arg Ser Phe Pro Asp Thr Val Tyr Lys Lys Leu Val Gln Arg Glu Lys
465 470 475 480

Thr Leu Lys Val Arg Gly Val Asp Arg Thr Pro Tyr Leu Gly Asp Val
485 490 495

Ala Val Val Val His Pro Gly Lys Lys Glu Met Gly Thr Pro Leu Ala
500 505 510

Asp Thr Pro Thr Arg Pro Val Thr Arg His Gly Gly Met Arg Asp Leu
515 520 525

His Glu Ser Ser Phe Ser Leu Ser Gly Ser Gln Ile Asp Asp His Val
530 535 540

Pro Lys Arg Ala Ser Ala Arg Ile Leu Ala Pro Pro Gly Gly Arg Ser
545 550 555 560

ser Gly Ile Trp

<210> 71
<211> 564
<212> PRT
<213> Homo sapiens

<400> 71

Met Leu Ala Asn Ser Ala Ser Val Arg Ile Leu Ile Lys Gly Gly Lys
1 5 10 15

Val Val Asn Asp Asp Cys Thr His Glu Ala Asp Val Tyr Ile Glu Asn
20 25 30

Gly Ile Ile Gln Gln Val Gly Arg Glu Leu Met Ile Pro Gly Gly Ala
35 40 45

Lys Val Ile Asp Ala Thr Gly Lys Leu Val Ile Pro Gly Gly Ile Asp
50 55 60

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Thr Ser Thr His Phe His Gln Thr Phe Met Asn Ala Thr Cys Val Asp
65 70 75 80

Asp Phe Tyr His Gly Thr Lys Ala Ala Leu Val Gly Gly Thr Thr Met
85 90 95

Ile Ile Gly His Val Leu Pro Asp Lys Glu Thr Ser Leu Val Asp Ala
100 105 110

Tyr Glu Lys Cys Arg Gly Leu Ala Asp Pro Lys Val Cys Cys Asp Tyr
115 120 125

Ala Leu His Val Gly Ile Thr Trp Trp Ala Pro Lys Val Lys Ala Glu
130 135 140

Met Glu Thr Leu Val Arg Glu Lys Gly Val Asn Ser Phe Gln Met Phe
145 150 155 160

Met Thr Tyr Lys Asp Leu Tyr Met Leu Arg Asp Ser Glu Leu Tyr Gln
165 170 175

Val Leu His Ala Cys Lys Asp Ile Gly Ala Ile Ala Arg Val His Ala
180 185 190

Glu Asn Gly Glu Leu Val Ala Glu Gly Ala Lys Glu Ala Leu Asp Leu
195 200 205

Gly Ile Thr Gly Pro Glu Gly Ile Glu Ile Ser Arg Pro Glu Glu Leu
210 215 220

Glu Ala Glu Ala Thr His Arg Val Ile Thr Ile Ala Asn Arg Thr His
225 230 235 240

Cys Pro Ile Tyr Leu Val Asn Val Ser Ser Ile Ser Ala Gly Asp Val
245 250 255

Ile Ala Ala Ala Lys Met Gln Gly Lys Val Val Leu Ala Glu Thr Thr
260 265 270

Thr Ala His Ala Thr Leu Thr Gly Leu His Tyr Tyr His Gln Asp Trp
275 280 285

Ser His Ala Ala Ala Tyr Val Thr Val Pro Pro Leu Arg Leu Asp Thr
290 295 300

Asn Thr Ser Thr Tyr Leu Met Ser Leu Leu Ala Asn Asp Thr Leu Asn
305 310 315 320

Ile Val Ala Ser Asp His Arg Pro Phe Thr Thr Lys Gln Lys Ala Met
325 330 335

Gly Lys Glu Asp Phe Thr Lys Ile Pro His Gly Val Ser Gly Val Gln
340 345 350

Asp Arg Met Ser Val Ile Trp Glu Arg Gly Val Val Gly Gly Lys Met
355 360 365

Asp Glu Asn Arg Phe Val Ala Val Thr Ser Ser Asn Ala Ala Lys Leu
370 375 380

Leu Asn Leu Tyr Pro Arg Lys Gly Arg Ile Ile Pro Gly Ala Asp Ala
385 390 395 400

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Asp Val Val Val Trp Asp Pro Glu Ala Thr Lys Thr Ile Ser Ala Ser
405 410 415

Thr Gln Val Gln Gly Gly Asp Phe Asn Leu Tyr Glu Asn Met Arg Cys
420 425 430

His Gly Val Pro Leu Val Thr Ile Ser Arg Gly Arg Val Val Tyr Glu
435 440 445

Asn Gly Val Phe Met Cys Ala Glu Gly Thr Gly Lys Phe Cys Pro Leu
450 455 460

Arg Ser Phe Pro Asp Thr Val Tyr Lys Lys Leu Val Gln Arg Glu Lys
465 470 475 480

Thr Leu Lys Val Arg Gly Val Asp Arg Thr Pro Tyr Leu Gly Asp Val
485 490 495

Ala Val Val Val His Pro Gly Lys Lys Glu Met Gly Thr Pro Leu Ala
500 505 510

Asp Thr Pro Thr Arg Pro Val Thr Arg His Gly Gly Met Arg Asp Leu
515 520 525

His Glu Ser Ser Phe Ser Leu Ser Gly Ser Gln Ile Asp Asp His Val
530 535 540

Pro Lys Arg Ala Ser Ala Arg Ile Leu Ala Pro Pro Gly Gly Arg Ser
545 550 555 560

Ser Gly Ile Trp

<210> 72
<211> 395
<212> PRT
<213> Homo sapiens

<400> 72

Met Leu Pro Ala Val Gly Ser Ala Asp Glu Glu Glu Asp Pro Ala Glu
1 5 10 15

Glu Asp Cys Pro Glu Leu Val Pro Ile Glu Thr Thr Gln Ser Glu Glu
20 25 30

Glu Glu Lys Ser Gly Leu Gly Ala Lys Ile Pro Val Thr Ile Ile Thr
35 40 45

Gly Tyr Leu Gly Ala Gly Lys Thr Thr Leu Leu Asn Tyr Ile Leu Thr
50 55 60

Glu Gln His Ser Lys Arg Val Ala Val Ile Leu Asn Glu Phe Gly Glu
65 70 75 80

Gly Ser Ala Leu Glu Lys Ser Leu Ala Val Ser Gln Gly Gly Glu Leu
85 90 95

Tyr Glu Glu Trp Leu Glu Leu Arg Asn Gly Cys Leu Cys Cys Ser Val
100 105 110

Lys Asp Ser Gly Leu Arg Ala Ile Glu Asn Leu Met Gln Lys Lys Gly
115 120 125

Lys Phe Asp Tyr Ile Leu Leu Glu Thr Thr Gly Leu Ala Asp Pro Gly
130 135 140

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ala val Ala Ser Met Phe Trp Val Asp Ala Glu Leu Gly Ser Asp Ile
145 150 155 160

Tyr Leu Asp Gly Ile Ile Thr Ile Val Asp Ser Lys Tyr Gly Leu Lys
165 170 175

His Leu Thr Glu Glu Lys Pro Asp Gly Leu Ile Asn Glu Ala Thr Arg
180 185 190

Gln Val Ala Leu Ala Asp Ala Ile Leu Ile Asn Lys Thr Asp Leu Val
195 200 205

Pro Glu Glu Asp Val Lys Lys Leu Arg Thr Thr Ile Arg Ser Ile Asn
210 215 220

Gly Leu Gly Gln Ile Leu Glu Thr Gln Arg Ser Arg Val Asp Leu Ser
225 230 235 240

Asn Val Leu Asp Leu His Ala Phe Asp Ser Leu Ser Gly Ile Ser Leu
245 250 255

Gln Lys Lys Leu Gln His Val Pro Gly Thr Gln Pro His Leu Asp Gln
260 265 270

Ser Ile Val Thr Ile Thr Phe Glu Val Pro Gly Asn Ala Lys Glu Glu
275 280 285

His Leu Asn Met Phe Ile Gln Asn Leu Leu Trp Glu Lys Asn Val Arg
290 295 300

Asn Lys Asp Asn His Cys Met Glu Val Ile Arg Leu Lys Gly Leu Val
305 310 315 320

Ser Ile Lys Asp Lys Ser Gln Gln Val Ile Val Gln Gly Val His Glu
325 330 335

Leu Tyr Asp Leu Glu Glu Thr Pro Val Ser Trp Lys Asp Asp Thr Glu
340 345 350

Arg Thr Asn Arg Leu Val Leu Leu Gly Arg Asn Leu Asp Lys Asp Ile
355 360 365

Leu Lys Gln Leu Phe Ile Ala Thr Val Thr Glu Thr Glu Lys Gln Trp
370 375 380

Thr Thr Arg Phe Gln Glu Asp Gln Val Cys Thr
385 390 395

<210> 73
<211> 567
<212> PRT
<213> Homo sapiens

<400> 73

Met Glu Ala Glu Arg Arg Pro Ala Pro Gly Ser Pro Ser Glu Gly Leu
1 5 10 15

Phe Ala Asp Gly His Leu Ile Leu Trp Thr Leu Cys Ser Val Leu Leu
20 25 30

Pro val Phe Ile Thr Phe Trp Cys Ser Leu Gln Arg Ser Arg Arg Gln
35 40 45

Leu His Arg Arg Asp Ile Phe Arg Lys Ser Lys His Gly Trp Arg Asp
50 55 60

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Thr Asp Leu Phe Ser Gln Pro Thr Tyr Cys Cys Val Cys Ala Gln His
 65 70 75 80
 Ile Leu Gln Gly Ala Phe Cys Asp Cys Cys Gly Leu Arg Val Asp Glu
 85 90 95
 Gly Cys Leu Arg Lys Ala Asp Lys Arg Phe Gln Cys Lys Glu Ile Met
 100 105 110
 Leu Lys Asn Asp Thr Lys Val Leu Asp Ala Met Pro His His Trp Ile
 115 120 125
 Arg Gly Asn Val Pro Leu Cys Ser Tyr Cys Met Val Cys Lys Gln Gln
 130 135 140
 Cys Gly Cys Gln Pro Lys Leu Cys Asp Tyr Arg Cys Ile Trp Cys Gln
 145 150 155 160
 Lys Thr Val His Asp Glu Cys Met Lys Asn Ser Leu Lys Asn Glu Lys
 165 170 175
 Cys Asp Phe Gly Glu Phe Lys Asn Leu Ile Ile Pro Pro Ser Tyr Leu
 180 185 190
 Thr Ser Ile Asn Gln Met Arg Lys Asp Lys Lys Thr Asp Tyr Glu Val
 195 200 205
 Leu Ala Ser Lys Leu Gly Lys Gln Trp Thr Pro Leu Ile Ile Leu Ala
 210 215 220
 Asn Ser Arg Ser Gly Thr Asn Met Gly Glu Gly Leu Leu Gly Glu Phe
 225 230 235 240
 Arg Ile Leu Leu Asn Pro Val Gln Val Phe Asp Val Thr Lys Thr Pro
 245 250 255
 Pro Ile Lys Ala Leu Gln Leu Cys Thr Leu Leu Pro Tyr Tyr Ser Ala
 260 265 270
 Arg Val Leu Val Cys Gly Gly Asp Gly Thr Val Gly Trp Val Leu Asp
 275 280 285
 Ala Val Asp Asp Met Lys Ile Lys Gly Gln Glu Lys Tyr Ile Pro Gln
 290 295 300
 Val Ala Val Leu Pro Leu Gly Thr Gly Asn Asp Leu Ser Asn Thr Leu
 305 310 315 320
 Gly Trp Gly Thr Gly Tyr Ala Gly Glu Ile Pro Val Ala Gln Val Leu
 325 330 335
 Arg Asn Val Met Glu Ala Asp Gly Ile Lys Leu Asp Arg Trp Lys Val
 340 345 350
 Gln Val Thr Asn Lys Gly Tyr Tyr Asn Leu Arg Lys Pro Lys Glu Phe
 355 360 365
 Thr Met Asn Asn Tyr Phe Ser Val Gly Pro Asp Ala Leu Met Ala Leu
 370 375 380
 Asn Phe His Ala His Arg Glu Lys Ala Pro Ser Leu Phe Ser Ser Arg
 385 390 395 400

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ile Leu Asn Lys Ala Val Tyr Leu Phe Tyr Gly Thr Lys Asp Cys Leu
 405 410 415

Val Gln Glu Cys Lys Asp Leu Asn Lys Lys Val Glu Leu Glu Leu Asp
 420 425 430

Gly Glu Arg Val Ala Leu Pro Ser Leu Glu Gly Ile Ile Val Leu Asn
 435 440 445

Ile Gly Tyr Trp Gly Gly Gly Cys Arg Leu Trp Glu Gly Met Gly Asp
 450 455 460

Glu Thr Tyr Pro Leu Ala Arg His Asp Asp Gly Leu Leu Glu Val Val
 465 470 475 480

Gly Val Tyr Gly Ser Phe His Cys Ala Gln Ile Gln Val Lys Leu Ala
 485 490 495

Asn Pro Phe Arg Ile Gly Gln Ala His Thr Val Arg Leu Ile Leu Lys
 500 505 510

Cys Ser Met Met Pro Met Gln Val Asp Gly Glu Pro Trp Ala Gln Gly
 515 520 525

Pro Cys Thr Val Thr Ile Thr His Lys Thr His Ala Met Met Leu Tyr
 530 535 540

Phe Ser Gly Glu Gln Thr Asp Asp Asp Ile Ser Ser Thr Ser Asp Gln
 545 550 555 560

Glu Asp Ile Lys Ala Thr Glu
 565

<210> 74
 <211> 542
 <212> PRT
 <213> Homo sapiens

<400> 74

Met Thr Lys Ser Asn Gly Glu Glu Pro Lys Met Gly Gly Arg Met Glu
 1 5 10 15

Arg Phe Gln Gln Gly Val Arg Lys Arg Thr Leu Leu Ala Lys Lys Lys
 20 25 30

Val Gln Asn Ile Thr Lys Glu Asp Val Lys Ser Tyr Leu Phe Arg Asn
 35 40 45

Ala Phe Val Leu Leu Thr Val Thr Ala Val Ile Val Gly Thr Ile Leu
 50 55 60

Gly Phe Thr Leu Arg Pro Tyr Arg Met Ser Tyr Arg Glu Val Lys Tyr
 65 70 75 80

Phe Ser Phe Pro Gly Glu Leu Leu Met Arg Met Leu Gln Met Leu Val
 85 90 95

Leu pro Leu Ile Ile Ser Ser Leu Val Thr Gly Met Ala Ala Leu Asp
 100 105 110

Ser Lys Ala Ser Gly Lys Met Gly Met Arg Ala Val Val Tyr Tyr Met
 115 120 125

Thr Thr Thr Ile Ile Ala Val Val Ile Gly Ile Ile Ile Val Ile Ile
 130 135 140

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ile His Pro Gly Lys Gly Thr Lys Glu Asn Met His Arg Glu Gly Lys
145 150 155 160

Ile Val Arg Val Thr Ala Ala Asp Ala Phe Leu Asp Leu Ile Arg Asn
165 170 175

Met Phe Pro Pro Asn Leu Val Glu Ala Cys Phe Lys Gln Phe Lys Thr
180 185 190

Asn Tyr Glu Lys Arg Ser Phe Lys Val Pro Ile Gln Ala Asn Glu Thr
195 200 205

Leu Val Gly Ala Val Ile Asn Asn Val Ser Glu Ala Met Glu Thr Leu
210 215 220

Thr Arg Ile Thr Glu Glu Leu Val Pro Val Pro Gly Ser Val Asn Gly
225 230 235 240

Val Asn Ala Leu Gly Leu Val Val Phe Ser Met Cys Phe Gly Phe Val
245 250 255

Ile Gly Asn Met Lys Glu Gln Gly Gln Ala Leu Arg Glu Phe Phe Asp
260 265 270

Ser Leu Asn Glu Ala Ile Met Arg Leu Val Ala Val Ile Met Trp Tyr
275 280 285

Ala Pro Val Gly Ile Leu Phe Leu Ile Ala Gly Lys Ile Val Glu Met
290 295 300

Glu Asp Met Gly Val Ile Gly Gly Gln Leu Ala Met Tyr Thr Val Thr
305 310 315 320

Val Ile Val Gly Leu Leu Ile His Ala Val Ile Val Leu Pro Leu Leu
325 330 335

Tyr Phe Leu Val Thr Arg Lys Asn Pro Trp Val Phe Ile Gly Gly Leu
340 345 350

Leu Gln Ala Leu Ile Thr Ala Leu Gly Thr Ser Ser Ser Ser Ala Thr
355 360 365

Leu Pro Ile Thr Phe Lys Cys Leu Glu Glu Asn Asn Gly Val Asp Lys
370 375 380

Arg Val Thr Arg Phe Val Leu Pro Val Gly Ala Thr Ile Asn Met Asp
385 390 395 400

Gly Thr Ala Leu Tyr Glu Ala Leu Ala Ala Ile Phe Ile Ala Gln Val
405 410 415

Asn Asn Phe Glu Leu Asn Phe Gly Gln Ile Ile Thr Ile Ser Ile Thr
420 425 430

Ala Thr Ala Ala Ser Ile Gly Ala Ala Gly Ile Pro Gln Ala Gly Leu
435 440 445

Val Thr Met Val Ile Val Leu Thr Ser Val Gly Leu Pro Thr Asp Asp
450 455 460

Ile Thr Leu Ile Ile Ala Val Asp Trp Phe Leu Asp Arg Leu Arg Thr
465 470 475 480

Thr Thr Asn Val Leu Gly Asp Ser Leu Gly Ala Gly Ile Val Glu His

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Leu Ser Arg His Glu Leu Lys Asn Arg Asp Val Glu Met Gly Asn Ser
485 500 505 510

Val Ile Glu Glu Asn Glu Met Lys Lys Pro Tyr Gln Leu Ile Ala Gln
515 520 525

Asp Asn Glu Thr Glu Lys Pro Ile Asp Ser Glu Thr Lys Met
530 535 540

<210> 75
<211> 2647
<212> PRT
<213> Homo sapiens

<400> 75

Met Ser Ser Ser His Ser Arg Ala Gly Gln Ser Ala Ala Gly Ala Ala
1 5 10 15

Pro Gly Gly Gly Val Asp Thr Arg Asp Ala Glu Met Pro Ala Thr Glu
20 25 30

Lys Asp Leu Ala Glu Asp Ala Pro Trp Lys Lys Ile Gln Gln Asn Thr
35 40 45

Phe Thr Arg Trp Cys Asn Glu His Leu Lys Cys Val Ser Lys Arg Ile
50 55 60

Ala Asn Leu Gln Thr Asp Leu Ser Asp Gly Leu Arg Leu Ile Ala Leu
65 70 75 80

Leu Glu Val Leu Ser Gln Lys Lys Met His Arg Lys His Asn Gln Arg
85 90 95

Pro Thr Phe Arg Gln Met Gln Leu Glu Asn Val Ser Val Ala Leu Glu
100 105 110

Phe Leu Asp Arg Glu Ser Ile Lys Leu Val Ser Ile Asp Ser Lys Ala
115 120 125

Ile Val Asp Gly Asn Leu Lys Leu Ile Leu Gly Leu Ile Trp Thr Leu
130 135 140

Ile Leu His Tyr Ser Ile Ser Met Pro Met Trp Asp Glu Glu Glu Asp
145 150 155 160

Glu Glu Ala Lys Lys Gln Thr Pro Lys Gln Arg Leu Leu Gly Trp Ile
165 170 175

Gln Asn Lys Leu Pro Gln Leu Pro Ile Thr Asn Phe Ser Arg Asp Trp
180 185 190

Gln Ser Gly Arg Ala Leu Gly Ala Leu Val Asp Ser Cys Ala Pro Gly
195 200 205

Leu Cys Pro Asp Trp Asp Ser Trp Asp Ala Ser Lys Pro Val Thr Asn
210 215 220

Ala Arg Glu Ala Met Gln Gln Ala Asp Asp Trp Leu Gly Ile Pro Gln
225 230 235 240

Val Ile Thr Pro Glu Glu Ile Val Asp Pro Asn Val Asp Glu His Ser
245 250 255

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Val Met Thr Tyr Leu Ser Gln Phe Pro Lys Ala Lys Leu Lys Pro Gly
 260 265 270

Ala Pro Leu Arg Pro Lys Leu Asn Pro Lys Lys Ala Arg Ala Tyr Gly
 275 280 285

Pro Gly Ile Glu Pro Thr Gly Asn Met Val Lys Lys Arg Ala Glu Phe
 290 295 300

Thr Val Glu Thr Arg Ser Ala Gly Gln Gly Glu Val Leu Val Tyr Val
 305 310 315 320

Glu Asp Pro Ala Gly His Gln Glu Glu Ala Lys Val Thr Ala Asn Asn
 325 330 335

Asp Lys Asn Arg Thr Phe Ser Val Trp Tyr Val Pro Glu Val Thr Gly
 340 345 350

Thr His Lys Val Thr Val Leu Phe Ala Gly Gln His Ile Ala Lys Ser
 355 360 365

Pro Phe Glu Val Tyr Val Asp Lys Ser Gln Gly Asp Ala Ser Lys Val
 370 375 380

Thr Ala Gln Gly Pro Gly Leu Glu Pro Ser Gly Asn Ile Ala Asn Lys
 385 390 395 400

Thr Thr Tyr Phe Glu Ile Phe Thr Ala Gly Ala Gly Thr Gly Glu Val
 405 410 415

Glu Val Val Ile Gln Asp Pro Met Gly Gln Lys Gly Thr Val Glu Pro
 420 425 430

Gln Leu Glu Ala Arg Gly Asp Ser Thr Tyr Arg Cys Ser Tyr Gln Pro
 435 440 445

Thr Met Glu Gly Val His Thr Val His Val Thr Phe Ala Gly Val Pro
 450 455 460

Ile Pro Arg Ser Pro Tyr Thr Val Thr Val Gly Gln Ala Cys Asn Pro
 465 470 475 480

Ser Ala Cys Arg Ala Val Gly Arg Gly Leu Gln Pro Lys Gly Val Arg
 485 490 495

Val Lys Glu Thr Ala Asp Phe Lys Val Tyr Thr Lys Gly Ala Gly Ser
 500 505 510

Gly Glu Leu Lys Val Thr Val Lys Gly Pro Lys Gly Glu Glu Arg Val
 515 520 525

Lys Gln Lys Asp Leu Gly Asp Gly Val Tyr Gly Phe Glu Tyr Tyr Pro
 530 535 540

Met Val Pro Gly Thr Tyr Ile Val Thr Ile Thr Trp Gly Gly Gln Asn
 545 550 555 560

Ile Gly Arg Ser Pro Phe Glu Val Lys Val Gly Thr Glu Cys Gly Asn
 565 570 575

Gln Lys Val Arg Ala Trp Gly Pro Gly Leu Glu Gly Gly Val Val Gly
 580 585 590

Lys Ser Ala Asp Phe Val Val Glu Ala Ile Gly Asp Asp Val Gly Thr
 595 600 605

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Leu Gly Phe Ser Val Glu Gly Pro Ser Gln Ala Lys Ile Glu Cys Asp
 610 615 620
 Asp Lys Gly Asp Gly Ser Cys Asp Val Arg Tyr Trp Pro Gln Glu Ala
 625 630 635 640
 Gly Glu Tyr Ala Val His Val Leu Cys Asn Ser Glu Asp Ile Arg Leu
 645 650 655
 Ser Pro Phe Met Ala Asp Ile Arg Asp Ala Pro Gln Asp Phe His Pro
 660 665 670
 Asp Arg Val Lys Ala Arg Gly Pro Gly Leu Glu Lys Thr Gly Val Ala
 675 680 685
 Val Asn Lys Pro Ala Glu Phe Thr Val Asp Ala Lys His Gly Gly Lys
 690 695 700
 Ala Pro Leu Arg Val Gln Val Gln Asp Asn Glu Gly Cys Pro Val Glu
 705 710 715 720
 Ala Leu Val Lys Asp Asn Gly Asn Gly Thr Tyr Ser Cys Ser Tyr Val
 725 730 735
 Pro Arg Lys Pro Val Lys His Thr Ala Met Val Ser Trp Gly Gly Val
 740 745 750
 Ser Ile Pro Asn Ser Pro Phe Arg Val Asn Val Gly Ala Gly Ser His
 755 760 765
 Pro Asn Lys Val Lys Val Tyr Gly Pro Gly Val Ala Lys Thr Gly Leu
 770 775 780
 Lys Ala His Glu Pro Thr Tyr Phe Thr Val Asp Cys Ala Glu Ala Gly
 785 790 795 800
 Gln Gly Asp Val Ser Ile Gly Ile Lys Cys Ala Pro Gly Val Val Gly
 805 810 815
 Pro Ala Glu Ala Asp Ile Asp Phe Asp Ile Ile Arg Asn Asp Asn Asp
 820 825 830
 Thr Phe Thr Val Lys Tyr Thr Pro Arg Gly Ala Gly Ser Tyr Thr Ile
 835 840 845
 Met Val Leu Phe Ala Asp Gln Ala Thr Pro Thr Ser Pro Ile Arg Val
 850 855 860
 Lys Val Glu Pro Ser His Asp Ala Ser Lys Val Lys Ala Glu Gly Pro
 865 870 875 880
 Gly Leu Ser Arg Thr Gly Val Glu Leu Gly Lys Pro Thr His Phe Thr
 885 890 895
 Val Asn Ala Lys Ala Ala Gly Lys Gly Lys Leu Asp Val Gln Phe Ser
 900 905 910
 Gly Leu Thr Lys Gly Asp Ala Val Arg Asp Val Asp Ile Ile Asp His
 915 920 925
 His Asp Asn Thr Tyr Thr Val Lys Tyr Thr Pro Val Gln Gln Gly Pro
 930 935 940

protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Val Gly Val Asn Val Thr Tyr Gly Gly Asp Pro Ile Pro Lys Ser Pro
945 950 955 960

Phe Ser Val Ala Val Ser Pro Ser Leu Asp Leu Ser Lys Ile Lys Val
965 970 975

Ser Gly Leu Gly Glu Lys Val Asp Val Gly Lys Asp Gln Glu Phe Thr
980 985 990

Val Lys Ser Lys Gly Ala Gly Gly Gln Gly Lys Val Ala Ser Lys Ile
995 1000 1005

Val Gly Pro Ser Gly Ala Ala Val Pro Cys Lys Val Glu Pro Gly
1010 1015 1020

Leu Gly Ala Asp Asn Ser Val Val Arg Phe Leu Pro Arg Glu Glu
1025 1030 1035

Gly Pro Tyr Glu Val Glu Val Thr Tyr Asp Gly Val Pro Val Pro
1040 1045 1050

Gly Ser Pro Phe Pro Leu Glu Ala Val Ala Pro Thr Lys Pro Ser
1055 1060 1065

Lys Val Lys Ala Phe Gly Pro Gly Leu Gln Gly Gly Ser Ala Gly
1070 1075 1080

Ser Pro Ala Arg Phe Thr Ile Asp Thr Lys Gly Ala Gly Thr Gly
1085 1090 1095

Gly Leu Gly Leu Thr Val Glu Gly Pro Cys Glu Ala Gln Leu Glu
1100 1105 1110

Cys Leu Asp Asn Gly Asp Gly Thr Cys Ser Val Ser Tyr Val Pro
1115 1120 1125

Thr Glu Pro Gly Asp Tyr Asn Ile Asn Ile Leu Phe Ala Asp Thr
1130 1135 1140

His Ile Pro Gly Ser Pro Phe Lys Ala His Val Val Pro Cys Phe
1145 1150 1155

Asp Ala Ser Lys Val Lys Cys Ser Gly Pro Gly Leu Glu Arg Ala
1160 1165 1170

Thr Ala Gly Glu Val Gly Gln Phe Gln Val Asp Cys Ser Ser Ala
1175 1180 1185

Gly Ser Ala Glu Leu Thr Ile Glu Ile Cys Ser Glu Ala Gly Leu
1190 1195 1200

Pro Ala Glu Val Tyr Ile Gln Asp His Gly Asp Gly Thr His Thr
1205 1210 1215

Ile Thr Tyr Ile Pro Leu Cys Pro Gly Ala Tyr Thr Val Thr Ile
1220 1225 1230

Lys Tyr Gly Gly Gln Pro Val Pro Asn Phe Pro Ser Lys Leu Gln
1235 1240 1245

Val Glu Pro Ala Val Asp Thr Ser Gly Val Gln Cys Tyr Gly Pro
1250 1255 1260

Gly Ile Glu Gly Gln Gly Val Phe Arg Glu Ala Thr Thr Glu Phe
1265 1270 1275

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ser Val Asp Ala Arg Ala Leu Thr Gln Thr Gly Gly Pro His Val
1280 1285 1290

Lys Ala Arg Val Ala Asn Pro Ser Gly Asn Leu Thr Glu Thr Tyr
1295 1300 1305

Val Gln Asp Arg Gly Asp Gly Met Tyr Lys Val Glu Tyr Thr Pro
1310 1315 1320

Tyr Glu Glu Gly Leu His Ser Val Asp Val Thr Tyr Asp Gly Ser
1325 1330 1335

Pro Val Pro Ser Ser Pro Phe Gln Val Pro Val Thr Glu Gly Cys
1340 1345 1350

Asp Pro Ser Arg Val Arg Val His Gly Pro Gly Ile Gln Ser Gly
1355 1360 1365

Thr Thr Asn Lys Pro Asn Lys Phe Thr Val Glu Thr Arg Gly Ala
1370 1375 1380

Gly Thr Gly Gly Leu Gly Leu Ala Val Glu Gly Pro Ser Glu Ala
1385 1390 1395

Lys Met Ser Cys Met Asp Asn Lys Asp Gly Ser Cys Ser Val Glu
1400 1405 1410

Tyr Ile Pro Tyr Glu Ala Gly Thr Tyr Ser Leu Asn Val Thr Tyr
1415 1420 1425

Gly Gly His Gln Val Pro Gly Ser Pro Phe Lys Val Pro Val His
1430 1435 1440

Asp Val Thr Asp Ala Ser Lys Val Lys Cys Ser Gly Pro Gly Leu
1445 1450 1455

Ser Pro Gly Met Val Arg Ala Asn Leu Pro Gln Ser Phe Gln Val
1460 1465 1470

Asp Thr Ser Lys Ala Gly Val Ala Pro Leu Gln Val Lys Val Gln
1475 1480 1485

Gly Pro Lys Gly Leu Val Glu Pro Val Asp Val Val Asp Asn Ala
1490 1495 1500

Asp Gly Thr Gln Thr Val Asn Tyr Val Pro Ser Arg Glu Gly Pro
1505 1510 1515

Tyr Ser Ile Ser Val Leu Tyr Gly Asp Glu Glu Val Pro Arg Ser
1520 1525 1530

Pro Phe Lys Val Lys Val Leu Pro Thr His Asp Ala Ser Lys Val
1535 1540 1545

Lys Ala Ser Gly Pro Gly Leu Asn Thr Thr Gly Val Pro Ala Ser
1550 1555 1560

Leu Pro Val Glu Phe Thr Ile Asp Ala Lys Asp Ala Gly Glu Gly
1565 1570 1575

Leu Leu Ala Val Gln Ile Thr Asp Pro Glu Gly Lys Pro Lys Lys
1580 1585 1590

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Thr His Ile Gln Asp Asn His Asp Gly Thr Tyr Thr Val Ala Tyr
 1595 1600 1605

Val Pro Asp Val Thr Gly Arg Tyr Thr Ile Leu Ile Lys Tyr Gly
 1610 1615 1620

Gly Asp Glu Ile Pro Phe Ser Pro Tyr Arg Val Arg Ala Val Pro
 1625 1630 1635

Thr Gly Asp Ala Ser Lys Cys Thr Val Thr Val Ser Ile Gly Gly
 1640 1645 1650

His Gly Leu Gly Ala Gly Ile Gly Pro Thr Ile Gln Ile Gly Glu
 1655 1660 1665

Glu Thr Val Ile Thr Val Asp Thr Lys Ala Ala Gly Lys Gly Lys
 1670 1675 1680

Val Thr Cys Thr Val Cys Thr Pro Asp Gly Ser Glu Val Asp Val
 1685 1690 1695

Asp Val Val Glu Asn Glu Asp Gly Thr Phe Asp Ile Phe Tyr Thr
 1700 1705 1710

Ala Pro Gln Pro Gly Lys Tyr Val Ile Cys Val Arg Phe Gly Gly
 1715 1720 1725

Glu His Val Pro Asn Ser Pro Phe Gln Val Thr Ala Leu Ala Gly
 1730 1735 1740

Asp Gln Pro Ser Val Gln Pro Pro Leu Arg Ser Gln Gln Leu Ala
 1745 1750 1755

Pro Gln Tyr Thr Tyr Ala Gln Gly Gly Gln Gln Thr Trp Ala Pro
 1760 1765 1770

Glu Arg Pro Leu Val Gly Val Asn Gly Leu Asp Val Thr Ser Leu
 1775 1780 1785

Arg Pro Phe Asp Leu Val Ile Pro Phe Thr Ile Lys Lys Gly Glu
 1790 1795 1800

Ile Thr Gly Glu Val Arg Met Pro Ser Gly Lys Val Ala Gln Pro
 1805 1810 1815

Thr Ile Thr Asp Asn Lys Asp Gly Thr Val Thr Val Arg Tyr Ala
 1820 1825 1830

Pro Ser Glu Ala Gly Leu His Glu Met Asp Ile Arg Tyr Asp Asn
 1835 1840 1845

Met His Ile Pro Gly Ser Pro Leu Gln Phe Tyr Val Asp Tyr Val
 1850 1855 1860

Asn Cys Gly His Val Thr Ala Tyr Gly Pro Gly Leu Thr His Gly
 1865 1870 1875

Val Val Asn Lys Pro Ala Thr Phe Thr Val Asn Thr Lys Asp Ala
 1880 1885 1890

Gly Glu Gly Gly Leu Ser Leu Ala Ile Glu Gly Pro Ser Lys Ala
 1895 1900 1905

Glu Ile Ser Cys Thr Asp Asn Gln Asp Gly Thr Cys Ser Val Ser
 1910 1915 1920

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Tyr Leu Pro Val Leu Pro Gly Asp Tyr Ser Ile Leu Val Lys Tyr
 1925 1930 1935
 Asn Glu Gln His Val Pro Gly Ser Pro Phe Thr Ala Arg Val Thr
 1940 1945 1950
 Gly Asp Asp Ser Met Arg Met Ser His Leu Lys Val Gly Ser Ala
 1955 1960 1965
 Ala Asp Ile Pro Ile Asn Ile Ser Glu Thr Asp Leu Ser Leu Leu
 1970 1975 1980
 Thr Ala Thr Val Val Pro Pro Ser Gly Arg Glu Glu Pro Cys Leu
 1985 1990 1995
 Leu Lys Arg Leu Arg Asn Gly His Val Gly Ile Ser Phe Val Pro
 2000 2005 2010
 Lys Glu Thr Gly Glu His Leu Val His Val Lys Lys Asn Gly Gln
 2015 2020 2025
 His Val Ala Ser Ser Pro Ile Pro Val Val Ile Ser Gln Ser Glu
 2030 2035 2040
 Ile Gly Asp Ala Ser Arg Val Arg Val Ser Gly Gln Gly Leu His
 2045 2050 2055
 Glu Gly His Thr Phe Glu Pro Ala Glu Phe Ile Ile Asp Thr Arg
 2060 2065 2070
 Asp Ala Gly Tyr Gly Gly Leu Ser Leu Ser Ile Glu Gly Pro Ser
 2075 2080 2085
 Lys Val Asp Ile Asn Thr Glu Asp Leu Glu Asp Gly Thr Cys Arg
 2090 2095 2100
 Val Thr Tyr Cys Pro Thr Glu Pro Gly Asn Tyr Ile Ile Asn Ile
 2105 2110 2115
 Lys Phe Ala Asp Gln His Val Pro Gly Ser Pro Phe Ser Val Lys
 2120 2125 2130
 Val Thr Gly Glu Gly Arg Val Lys Glu Ser Ile Thr Arg Arg Arg
 2135 2140 2145
 Arg Ala Pro Ser Val Ala Asn Val Gly Ser His Cys Asp Leu Ser
 2150 2155 2160
 Leu Lys Ile Pro Glu Ile Ser Ile Gln Asp Met Thr Ala Gln Val
 2165 2170 2175
 Thr Ser Pro Ser Gly Lys Thr His Glu Ala Glu Ile Val Glu Gly
 2180 2185 2190
 Glu Asn His Thr Tyr Cys Ile Arg Phe Val Pro Ala Glu Met Gly
 2195 2200 2205
 Thr His Thr Val Ser Val Lys Tyr Lys Gly Gln His Val Pro Gly
 2210 2215 2220
 Ser Pro Phe Gln Phe Thr Val Gly Pro Leu Gly Glu Gly Gly Ala
 2225 2230 2235

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

His Lys Val Arg Ala Gly Gly Pro Gly Leu Glu Arg Ala Glu Ala
 2240 2245 2250

 Gly Val Pro Ala Glu Phe Ser Ile Trp Thr Arg Glu Ala Gly Ala
 2255 2260 2265

 Gly Gly Leu Ala Ile Ala Val Glu Gly Pro Ser Lys Ala Glu Ile
 2270 2275 2280

 Ser Phe Glu Asp Arg Lys Asp Gly Ser Cys Gly Val Ala Tyr Val
 2285 2290 2295

 Val Gln Glu Pro Gly Asp Tyr Glu Val Ser Val Lys Phe Asn Glu
 2300 2305 2310

 Glu His Ile Pro Asp Ser Pro Phe Val Val Pro Val Ala Ser Pro
 2315 2320 2325

 Ser Gly Asp Ala Arg Arg Leu Thr Val Ser Ser Leu Gln Glu Ser
 2330 2335 2340

 Gly Leu Lys Val Asn Gln Pro Ala Ser Phe Ala Val Ser Leu Asn
 2345 2350 2355

 Gly Ala Lys Gly Ala Ile Asp Ala Lys Val His Ser Pro Ser Gly
 2360 2365 2370

 Ala Leu Glu Glu Cys Tyr Val Thr Glu Ile Asp Gln Asp Lys Tyr
 2375 2380 2385

 Ala Val Arg Phe Ile Pro Arg Glu Asn Gly Val Tyr Leu Ile Asp
 2390 2395 2400

 Val Lys Phe Asn Gly Thr His Ile Pro Gly Ser Pro Phe Lys Ile
 2405 2410 2415

 Arg Val Gly Glu Pro Gly His Gly Gly Asp Pro Gly Leu Val Ser
 2420 2425 2430

 Ala Tyr Gly Ala Gly Leu Glu Gly Gly Val Thr Gly Asn Pro Ala
 2435 2440 2445

 Glu phe Val Val Asn Thr Ser Asn Ala Gly Ala Gly Ala Leu Ser
 2450 2455 2460

 Val Thr Ile Asp Gly Pro Ser Lys Val Lys Met Asp Cys Gln Glu
 2465 2470 2475

 Cys Pro Glu Gly Tyr Arg Val Thr Tyr Thr Pro Met Ala Pro Gly
 2480 2485 2490

 Ser Tyr Leu Ile Ser Ile Lys Tyr Gly Gly Pro Tyr His Ile Gly
 2495 2500 2505

 Gly Ser Pro Phe Lys Ala Lys Val Thr Gly Pro Arg Leu Val Ser
 2510 2515 2520

 Asn His Ser Leu His Glu Thr Ser Ser Val Phe Val Asp Ser Leu
 2525 2530 2535

 Thr Lys Ala Thr Cys Ala Pro Gln His Gly Ala Pro Gly Pro Gly
 2540 2545 2550

 Pro Ala Asp Ala Ser Lys Val Val Ala Lys Gly Leu Gly Leu Ser
 2555 2560 2565

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Lys Ala Tyr Val Gly Gln Lys Ser Ser Phe Thr Val Asp Cys Ser
2570 2575 2580

Lys Ala Gly Asn Asn Met Leu Leu Val Gly Val His Gly Pro Arg
2585 2590 2595

Thr Pro Cys Glu Glu Ile Leu Val Lys His Val Gly Ser Arg Leu
2600 2605 2610

Tyr Ser Val Ser Tyr Leu Leu Lys Asp Lys Gly Glu Tyr Thr Leu
2615 2620 2625

Val Val Lys Trp Gly His Glu His Ile Pro Gly Ser Pro Tyr Arg
2630 2635 2640

Val Val Val Pro
2645

<210> 76
<211> 395
<212> PRT
<213> Homo sapiens

<400> 76

Met Ala Val Thr Asp Ser Leu Ser Arg Ala Ala Thr Val Leu Ala Thr
1 5 10 15

Val Leu Leu Leu Ser Phe Gly Ser Val Ala Ala Ser His Ile Glu Asp
20 25 30

Gln Ala Glu Gln Phe Phe Arg Ser Gly His Thr Asn Asn Trp Ala Val
35 40 45

Leu Val Cys Thr Ser Arg Phe Trp Phe Asn Tyr Arg His Val Ala Asn
50 55 60

Thr Leu Ser Val Tyr Arg Ser Val Lys Arg Leu Gly Ile Pro Asp Ser
65 70 75 80

His Ile Val Leu Met Leu Ala Asp Asp Met Ala Cys Asn Pro Arg Asn
85 90 95

Pro Lys Pro Ala Thr Val Phe Ser His Lys Asn Met Glu Leu Asn Val
100 105 110

Tyr Gly Asp Asp Val Glu Val Asp Tyr Arg Ser Tyr Glu Val Thr Val
115 120 125

Glu Asn Phe Leu Arg Val Leu Thr Gly Arg Ile Pro Pro Ser Thr Pro
130 135 140

Arg Ser Lys Arg Leu Leu Ser Asp Asp Arg Ser Asn Ile Leu Ile Tyr
145 150 155 160

Met Thr Gly His Gly Gly Asn Gly Phe Leu Lys Phe Gln Asp Ser Glu
165 170 175

Glu Ile Thr Asn Ile Glu Leu Ala Asp Ala Phe Glu Gln Met Trp Gln
180 185 190

Lys Arg Arg Tyr Asn Glu Leu Leu Phe Ile Ile Asp Thr Cys Gln Gly
195 200 205

Ala ser Met Tyr Glu Arg Phe Tyr Ser Pro Asn Ile Met Ala Leu Ala

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 210 215 220

Ser Ser Gln Val Gly Glu Asp Ser Leu Ser His Gln Pro Asp Pro Ala
 225 230 235 240

Ile Gly Val His Leu Met Asp Arg Tyr Thr Phe Tyr Val Leu Glu Phe
 245 250 255

Leu Glu Glu Ile Asn Pro Ala Ser Gln Thr Asn Met Asn Asp Leu Phe
 260 265 270

Gln Val Cys Pro Lys Ser Leu Cys Val Ser Thr Pro Gly His Arg Thr
 275 280 285

Asp Leu Phe Gln Arg Asp Pro Lys Asn Val Leu Ile Thr Asp Phe Phe
 290 295 300

Gly Ser Val Arg Lys Val Glu Ile Thr Thr Glu Thr Ile Lys Leu Gln
 305 310 315 320

Gln Asp Ser Glu Ile Met Glu Ser Ser Tyr Lys Glu Asp Gln Met Asp
 325 330 335

Glu Lys Leu Met Glu Pro Leu Lys Tyr Ala Glu Gln Leu Pro Val Ala
 340 345 350

Gln Ile Ile His Gln Lys Pro Lys Leu Lys Asp Trp His Pro Pro Gly
 355 360 365

Gly Phe Ile Leu Gly Leu Trp Ala Leu Ile Ile Met Val Phe Phe Lys
 370 375 380

Thr Tyr Gly Ile Lys His Met Lys Phe Ile Phe
 385 390 395

<210> 77
 <211> 217
 <212> PRT
 <213> Homo sapiens

<400> 77

Met Glu Ala Ile Ala Lys Tyr Asp Phe Lys Ala Thr Ala Asp Asp Glu
 1 5 10 15

Leu Ser Phe Lys Arg Gly Asp Ile Leu Lys Val Leu Asn Glu Glu Cys
 20 25 30

Asp Gln Asn Trp Tyr Lys Ala Glu Leu Asn Gly Lys Asp Gly Phe Ile
 35 40 45

Pro Lys Asn Tyr Ile Glu Met Lys Pro His Pro Trp Phe Phe Gly Lys
 50 55 60

Ile Pro Arg Ala Lys Ala Glu Glu Met Leu Ser Lys Gln Arg His Asp
 65 70 75 80

Gly Ala Phe Leu Ile Arg Glu Ser Glu Ser Ala Pro Gly Asp Phe Ser
 85 90 95

Leu Ser Val Lys Phe Gly Asn Asp Val Gln His Phe Lys Val Leu Arg
 100 105 110

Asp Gly Ala Gly Lys Tyr Phe Leu Trp Val Val Lys Phe Asn Ser Leu
 115 120 125

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Asn Glu Leu Val Asp Tyr His Arg Ser Thr Ser Val Ser Arg Asn Gln
 130 135 140

Gln Ile Phe Leu Arg Asp Ile Glu Gln Val Pro Gln Gln Pro Thr Tyr
 145 150 155 160

Val Gln Ala Leu Phe Asp Phe Asp Pro Gln Glu Asp Gly Glu Leu Gly
 165 170 175

Phe Arg Arg Gly Asp Phe Ile His Val Met Asp Asn Ser Asp Pro Asn
 180 185 190

Trp Trp Lys Gly Ala Cys His Gly Gln Thr Gly Met Phe Pro Arg Asn
 195 200 205

Tyr Val Thr Pro Val Asn Arg Asn Val
 210 215

<210> 78
 <211> 443
 <212> PRT
 <213> Homo sapiens

<400> 78

Met Glu Cys Leu Arg Ser Leu Pro Cys Leu Leu Pro Arg Ala Met Arg
 1 5 10 15

Leu Pro Arg Arg Thr Leu Cys Ala Leu Ala Leu Asp Val Thr Ser Val
 20 25 30

Gly Pro Pro Val Ala Ala Cys Gly Arg Arg Ala Asn Leu Ile Gly Arg
 35 40 45

Ser Arg Ala Ala Gln Leu Cys Gly Pro Asp Arg Leu Arg Val Ala Gly
 50 55 60

Glu Val His Arg Phe Arg Thr Ser Asp Val Ser Gln Ala Thr Leu Ala
 65 70 75 80

Ser Val Ala Pro Val Phe Thr Val Thr Lys Phe Asp Lys Gln Gly Asn
 85 90 95

Val Thr Ser Phe Glu Arg Lys Lys Thr Glu Leu Tyr Gln Glu Leu Gly
 100 105 110

Leu Gln Ala Arg Asp Leu Arg Phe Gln His Val Met Ser Ile Thr Val
 115 120 125

Arg Asn Asn Arg Ile Ile Met Arg Met Glu Tyr Leu Lys Ala Val Ile
 130 135 140

Thr Pro Glu Cys Leu Leu Ile Leu Asp Tyr Arg Asn Leu Asn Leu Glu
 145 150 155 160

Gln Trp Leu Phe Arg Glu Leu Pro Ser Gln Leu Ser Gly Glu Gly Gln
 165 170 175

Leu Val Thr Tyr Pro Leu Pro Phe Glu Phe Arg Ala Ile Glu Ala Leu
 180 185 190

Leu Gln Tyr Trp Ile Asn Thr Leu Gln Gly Lys Leu Ser Ile Leu Gln
 195 200 205

Pro Leu Ile Leu Glu Thr Leu Asp Ala Leu Val Asp Pro Lys His Ser
 210 215 220

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ser Val Asp Arg Ser Lys Leu His Ile Leu Leu Gln Asn Gly Lys Ser
225 230 235 240

Leu Ser Glu Leu Glu Thr Asp Ile Lys Ile Phe Lys Glu Ser Ile Leu
245 250 255

Glu Ile Leu Asp Glu Glu Glu Leu Leu Glu Glu Leu Cys Val Ser Lys
260 265 270

Trp Ser Asp Pro Gln Val Phe Glu Lys Ser Ser Ala Gly Ile Asp His
275 280 285

Ala Glu Glu Met Glu Leu Leu Leu Glu Asn Tyr Tyr Arg Leu Ala Asp
290 295 300

Asp Leu Ser Asn Ala Ala Arg Glu Leu Arg Val Leu Ile Asp Asp Ser
305 310 315 320

Gln Ser Ile Ile Phe Ile Asn Leu Asp Ser His Arg Asn Val Met Met
325 330 335

Arg Leu Asn Leu Gln Leu Thr Met Gly Thr Phe Ser Leu Ser Leu Phe
340 345 350

Gly Leu Met Gly Val Ala Phe Gly Met Asn Leu Glu Ser Ser Leu Glu
355 360 365

Glu Asp His Arg Ile Phe Trp Leu Ile Thr Gly Ile Met Phe Met Gly
370 375 380

Ser Gly Leu Ile Trp Arg Arg Leu Leu Ser Phe Leu Gly Arg Gln Leu
385 390 395 400

Glu Ala Pro Leu Pro Pro Met Met Ala Ser Leu Pro Lys Lys Thr Leu
405 410 415

Leu Ala Asp Arg Ser Met Glu Leu Lys Asn Ser Leu Arg Leu Asp Gly
420 425 430

Leu Gly Ser Gly Arg Ser Ile Leu Thr Asn Arg
435 440

<210> 79
<211> 1928
<212> PRT
<213> Homo sapiens

<400> 79

Gly Gln Val Arg Arg Arg Leu Gln Glu Leu Asp Gly Glu Leu Glu Ala
1 5 10 15

Ala Leu Gly Leu Leu Asp Ile Ile Leu Ala Lys Asn Pro Ser Gly Leu
20 25 30

Thr Gln Tyr Ile Pro Val Leu Val Asp Ser Phe Leu Pro Leu Leu Lys
35 40 45

Ser pro Leu Ala Ala Pro Arg Ile Lys Asn Pro Phe Leu Ser Leu Ala
50 55 60

Ala cys Val Met Pro Ser Arg Leu Lys Ala Leu Gly Thr Leu Val Ser
65 70 75 80

His val Thr Leu Arg Leu Leu Lys Pro Glu Cys Val Leu Asp Lys Ser
85 90 95

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Trp Cys Gln Glu Glu Leu Ser Val Ala Val Lys Arg Ala Val Met Leu
100 105 110

Leu His Thr His Thr Ile Thr Ser Arg Val Gly Lys Gly Glu Pro Gly
115 120 125

Ala Ala Pro Leu Ser Ala Pro Ala Phe Ser Leu Val Phe Pro Phe Leu
130 135 140

Lys Met Val Leu Thr Glu Met Pro His His Ser Glu Glu Glu Glu Glu
145 150 155 160

Trp Met Ala Gln Ile Leu Gln Ile Leu Thr Val Gln Ala Gln Leu Arg
165 170 175

Ala Ser Pro Asn Thr Pro Pro Gly Arg Val Asp Glu Asn Gly Pro Glu
180 185 190

Leu Leu Pro Arg Val Ala Met Leu Arg Leu Leu Thr Trp Val Ile Gly
195 200 205

Thr Gly Ser Pro Arg Leu Gln Val Leu Ala Ser Asp Thr Leu Thr Thr
210 215 220

Leu Cys Ala Ser Ser Ser Gly Asp Asp Gly Cys Ala Phe Ala Glu Gln
225 230 235 240

Glu Glu Val Asp Val Leu Leu Cys Ala Leu Gln Ser Pro Cys Ala Ser
245 250 255

Val Arg Glu Thr Val Leu Arg Gly Leu Met Glu Leu His Met Val Leu
260 265 270

Pro Ala Pro Asp Thr Asp Glu Lys Asn Gly Leu Asn Leu Leu Arg Arg
275 280 285

Leu Trp Val Val Lys Phe Asp Lys Glu Glu Glu Ile Arg Lys Leu Ala
290 295 300

Glu Arg Leu Trp Ser Met Met Gly Leu Asp Leu Gln Pro Asp Leu Cys
305 310 315 320

Ser Leu Leu Ile Asp Asp Val Ile Tyr His Glu Ala Ala Val Arg Gln
325 330 335

Ala Gly Ala Glu Ala Leu Ser Gln Ala Val Ala Arg Tyr Gln Arg Gln
340 345 350

Ala Ala Glu Val Met Gly Arg Leu Met Glu Ile Tyr Gln Glu Lys Leu
355 360 365

Tyr Arg Pro Pro Pro Val Leu Asp Ala Leu Gly Arg Val Ile Ser Glu
370 375 380

Ser Pro Pro Asp Gln Trp Glu Ala Arg Cys Gly Leu Ala Leu Ala Leu
385 390 395 400

Asn Lys Leu Ser Gln Tyr Leu Asp Ser Ser Gln Val Lys Pro Leu Phe
405 410 415

Gln Phe Phe Val Pro Asp Ala Leu Asn Asp Arg His Pro Asp Val Arg
420 425 430

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Lys Cys Met Leu Asp Ala Ala Leu Ala Thr Leu Asn Thr His Gly Lys
 435 440 445

Glu Asn Val Asn Ser Leu Leu Pro Val Phe Glu Glu Phe Leu Lys Asn
 450 455 460

Ala Pro Asn Asp Ala Ser Tyr Asp Ala Val Arg Gln Ser Val Val Val
 465 470 475 480

Leu Met Gly Ser Leu Ala Lys His Leu Asp Lys Ser Asp Pro Lys Val
 485 490 495

Lys Pro Ile Val Ala Lys Leu Ile Ala Ala Leu Ser Thr Pro Ser Gln
 500 505 510

Gln Val Gln Glu Ser Val Ala Ser Cys Leu Pro Pro Leu Val Pro Ala
 515 520 525

Ile Lys Glu Asp Ala Gly Gly Met Ile Gln Arg Leu Met Gln Gln Leu
 530 535 540

Leu Glu Ser Asp Lys Tyr Ala Glu Arg Lys Gly Ala Ala Tyr Gly Leu
 545 550 555 560

Ala Gly Leu Val Lys Gly Leu Gly Ile Leu Ser Leu Lys Gln Gln Glu
 565 570 575

Met Met Ala Ala Leu Thr Asp Ala Ile Gln Asp Lys Lys Asn Phe Arg
 580 585 590

Arg Arg Glu Gly Ala Leu Phe Ala Phe Glu Met Leu Cys Thr Met Leu
 595 600 605

Gly Lys Leu Phe Glu Pro Tyr Val Val His Val Leu Pro His Leu Leu
 610 615 620

Leu Cys Phe Gly Asp Gly Asn Gln Tyr Val Arg Glu Ala Ala Asp Asp
 625 630 635 640

Cys Ala Lys Ala Val Met Ser Asn Leu Ser Ala His Gly Val Lys Leu
 645 650 655

Val Leu Pro Ser Leu Leu Ala Ala Leu Glu Glu Glu Ser Trp Arg Thr
 660 665 670

Lys Ala Gly Ser Val Glu Leu Leu Gly Ala Met Ala Tyr Cys Ala Pro
 675 680 685

Lys Gln Leu Ser Ser Cys Leu Pro Asn Ile Val Pro Lys Leu Thr Glu
 690 695 700

Val Leu Thr Asp Ser His Val Lys Val Gln Lys Ala Gly Gln Gln Ala
 705 710 715 720

Leu Arg Gln Ile Gly Ser Val Ile Arg Asn Pro Glu Ile Leu Ala Ile
 725 730 735

Ala Pro Val Leu Leu Asp Val Leu Thr Asp Pro Ser Arg Lys Thr Gln
 740 745 750

Lys Cys Leu Gln Thr Leu Leu Asp Thr Lys Phe Val His Phe Ile Asp
 755 760 765

Ala Pro Ser Leu Ala Leu Ile Met Pro Ile Val Gln Arg Ala Phe Gln
 770 775 780

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Asp Arg Ser Thr Asp Thr Arg Lys Met Ala Ala Gln Ile Ile Gly Asn
 785 790 795 800
 Met Tyr Ser Leu Thr Asp Gln Lys Asp Leu Ala Pro Tyr Leu Pro Ser
 805 810 815
 Val Thr Pro Gly Leu Lys Ala Ser Leu Leu Asp Pro Val Pro Glu Val
 820 825 830
 Arg Thr Val Ser Ala Lys Ala Leu Gly Val Met Val Lys Gly Met Gly
 835 840 845
 Glu Ser Cys Phe Glu Asp Leu Leu Pro Trp Leu Met Glu Thr Leu Thr
 850 855 860
 Tyr Glu Gln Ser Ser Val Asp Arg Ser Gly Ala Ala Gln Gly Leu Ala
 865 870 875 880
 Glu Val Met Ala Gly Leu Gly Val Glu Lys Leu Glu Lys Leu Met Pro
 885 890 895
 Glu Ile Val Ala Thr Ala Ser Lys Val Asp Ile Ala Pro His Val Arg
 900 905 910
 Asp Gly Tyr Ile Met Met Phe Asn Tyr Leu Pro Ile Thr Phe Gly Asp
 915 920 925
 Lys Phe Thr Pro Tyr Val Gly Pro Ile Ile Pro Cys Ile Leu Lys Ala
 930 935 940
 Leu Ala Asp Glu Asn Glu Phe Val Arg Asp Thr Ala Leu Arg Ala Gly
 945 950 955 960
 Gln Arg Val Ile Ser Met Tyr Ala Glu Thr Ala Ile Ala Leu Leu Leu
 965 970 975
 Pro Gln Leu Glu Gln Gly Leu Phe Asp Asp Leu Trp Arg Ile Arg Phe
 980 985 990
 Ser Ser Val Gln Leu Leu Gly Asp Leu Leu Phe His Ile Ser Gly Val
 995 1000 1005
 Thr Gly Lys Met Thr Thr Glu Thr Ala Ser Glu Asp Asp Asn Phe
 1010 1015 1020
 Gly Thr Ala Gln Ser Asn Lys Ala Ile Ile Thr Ala Leu Gly Val
 1025 1030 1035
 Glu Arg Arg Asn Arg Val Leu Ala Gly Leu Tyr Met Gly Arg Ser
 1040 1045 1050
 Asp Thr Gln Leu Val Val Arg Gln Ala Ser Leu His Val Trp Lys
 1055 1060 1065
 Ile Val Val Ser Asn Thr Pro Arg Thr Leu Arg Glu Ile Leu Pro
 1070 1075 1080
 Thr Leu Phe Gly Leu Leu Leu Gly Phe Leu Ala Ser Thr Cys Ala
 1085 1090 1095
 Asp Lys Arg Thr Ile Ala Ala Arg Thr Leu Gly Asp Leu Val Arg
 1100 1105 1110

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Lys Leu Gly Glu Lys Ile Leu Pro Glu Ile Ile Pro Ile Leu Glu
 1115 1120 1125

 Glu Gly Leu Arg Ser Gln Lys Ser Asp Glu Arg Gln Gly Val Cys
 1130 1135 1140

 Ile Gly Leu Ser Glu Ile Met Lys Ser Thr Ser Arg Asp Ala Val
 1145 1150 1155

 Leu Tyr Phe Ser Glu Ser Leu Val Pro Thr Ala Arg Lys Ala Leu
 1160 1165 1170

 Cys Asp Pro Leu Glu Glu Val Arg Glu Ala Ala Ala Lys Thr Phe
 1175 1180 1185

 Glu Gln Leu His Ser Thr Ile Gly His Gln Ala Leu Glu Asp Ile
 1190 1195 1200

 Leu Pro Phe Leu Leu Lys Gln Leu Asp Asp Glu Glu Val Ser Glu
 1205 1210 1215

 Phe Ala Leu Asp Gly Leu Lys Gln Val Met Ala Ile Lys Ser Arg
 1220 1225 1230

 Val Val Leu Pro Tyr Leu Val Pro Lys Leu Thr Thr Pro Pro Val
 1235 1240 1245

 Asn Thr Arg Val Leu Ala Phe Leu Ser Ser Val Ala Gly Asp Ala
 1250 1255 1260

 Leu Thr Arg His Leu Gly Val Ile Leu Pro Ala Val Met Leu Ala
 1265 1270 1275

 Leu Lys Glu Lys Leu Gly Thr Pro Asp Glu Gln Leu Glu Met Ala
 1280 1285 1290

 Asn Cys Gln Ala Val Ile Leu Ser Val Glu Asp Asp Thr Gly His
 1295 1300 1305

 Arg Ile Ile Ile Glu Asp Leu Leu Glu Ala Thr Arg Ser Pro Glu
 1310 1315 1320

 Val Gly Met Arg Gln Ala Ala Ala Ile Ile Leu Asn Ile Tyr Cys
 1325 1330 1335

 Ser Arg Ser Lys Ala Asp Tyr Thr Ser His Leu Arg Ser Leu Val
 1340 1345 1350

 Ser Gly Leu Ile Arg Leu Phe Asn Asp Ser Ser Pro Val Val Leu
 1355 1360 1365

 Glu Glu Ser Trp Asp Ala Leu Asn Ala Ile Thr Lys Lys Leu Asp
 1370 1375 1380

 Ala Gly Asn Gln Leu Ala Leu Ile Glu Glu Leu His Lys Glu Ile
 1385 1390 1395

 Arg Leu Ile Gly Asn Glu Ser Lys Gly Glu His Val Pro Gly Phe
 1400 1405 1410

 Cys Leu Pro Lys Lys Gly Val Thr Ser Ile Leu Pro Val Leu Arg
 1415 1420 1425

 Glu Gly Val Leu Thr Gly Ser Pro Glu Gln Lys Glu Glu Ala Ala
 1430 1435 1440

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Lys Ala Leu Gly Leu Val Ile Arg Leu Thr Ser Ala Asp Val Leu
 1445 1450 1455
 Arg Pro Ser Val Val Ser Ile Thr Gly Pro Leu Ile Arg Ile Leu
 1460 1465 1470
 Gly Asp Arg Phe Ser Trp Asn Val Lys Ala Ala Leu Leu Glu Thr
 1475 1480 1485
 Leu Ser Leu Leu Leu Ala Lys Val Gly Ile Ala Leu Lys Pro Phe
 1490 1495 1500
 Leu Pro Gln Leu Gln Thr Thr Phe Thr Lys Ala Leu Gln Asp Ser
 1505 1510 1515
 Asn Arg Gly Val Arg Leu Lys Ala Ala Asp Ala Leu Gly Lys Leu
 1520 1525 1530
 Ile Ser Ile His Ile Lys Val Asp Pro Leu Phe Thr Glu Leu Leu
 1535 1540 1545
 Asn Gly Ile Arg Ala Met Glu Asp Pro Gly Val Arg Asp Thr Met
 1550 1555 1560
 Leu Gln Ala Leu Arg Phe Val Ile Gln Gly Ala Gly Ala Lys Val
 1565 1570 1575
 Asp Ala Val Ile Arg Lys Asn Ile Val Ser Leu Leu Leu Ser Met
 1580 1585 1590
 Leu Gly His Asp Glu Asp Asn Thr Arg Ile Ser Ser Ala Gly Cys
 1595 1600 1605
 Leu Gly Glu Leu Cys Ala Phe Leu Thr Glu Glu Glu Leu Ser Ala
 1610 1615 1620
 Val Leu Gln Gln Cys Leu Leu Ala Asp Val Ser Gly Ile Asp Trp
 1625 1630 1635
 Met Val Arg His Gly Arg Ser Leu Ala Leu Ser Val Ala Val Asn
 1640 1645 1650
 Val Ala Pro Gly Arg Leu Cys Ala Gly Arg Tyr Ser Ser Asp Val
 1655 1660 1665
 Gln Glu Met Ile Leu Ser Ser Ala Thr Ala Asp Arg Ile Pro Ile
 1670 1675 1680
 Ala Val Ser Gly Val Arg Gly Met Gly Phe Leu Met Arg His His
 1685 1690 1695
 Ile Glu Thr Gly Gly Gly Gln Leu Pro Arg Lys Leu Ser Ser Leu
 1700 1705 1710
 Phe Val Lys Cys Leu Gln Asn Pro Ser Ser Asp Ile Arg Leu Val
 1715 1720 1725
 Ala Glu Lys Met Ile Trp Trp Ala Asn Lys Asp Pro Leu Pro Pro
 1730 1735 1740
 Leu Asp Pro Gln Ala Ile Lys Pro Ile Leu Lys Ala Leu Leu Asp
 1745 1750 1755

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Asn Thr Lys Asp Lys Asn Thr Val Val Arg Ala Tyr Ser Asp Gln
 1760 1765 1770

Ala Ile Val Asn Leu Leu Lys Met Arg Gln Gly Glu Glu Val Phe
 1775 1780 1785

Gln Ser Leu Ser Lys Ile Leu Asp Val Ala Ser Leu Glu Val Leu
 1790 1795 1800

Asn Glu Val Asn Arg Arg Ser Leu Lys Lys Leu Ala Lys Pro Gly
 1805 1810 1815

Arg Leu His Gly Ala Gly Gly Arg His His Pro Asp Met Arg Gly
 1820 1825 1830

Leu Gly Ser Ser Ser Ile Ala Ala Pro His Leu Cys Ser Met Phe
 1835 1840 1845

Ser Phe Leu Lys Ile His Leu Phe Gln Trp Gly Ala Trp Lys Met
 1850 1855 1860

Ala Phe Pro Glu Ser Ile Leu Ile Ser Ile Asp His Ser Gln Ser
 1865 1870 1875

Leu Lys Ser Asn Pro His Thr Thr Glu Asn Cys Leu Leu His Leu
 1880 1885 1890

Ser Pro Phe Pro Val Glu Lys Arg Arg Lys Ser Thr Arg Met Arg
 1895 1900 1905

Leu Ser Lys Trp Gln Pro Arg Ser Cys Leu Ser Ser Leu Ala Trp
 1910 1915 1920

Leu Gly Leu Glu Leu
 1925

<210> 80
 <211> 325
 <212> PRT
 <213> Homo sapiens

<400> 80

Met Ala Leu Ala Asp Ser Thr Arg Gly Leu Pro Asn Gly Gly Gly Gly
 1 5 10 15

Gly Gly Gly Ser Gly Ser Ser Ser Ser Ala Glu Pro Pro Leu Phe
 20 25 30

Pro Asp Ile Val Glu Leu Asn Val Gly Gly Gln Val Tyr Val Thr Arg
 35 40 45

Arg Cys Thr Val Val Ser Val Pro Asp Ser Leu Leu Trp Arg Met Phe
 50 55 60

Thr Gln Gln Gln Pro Gln Glu Leu Ala Arg Asp Ser Lys Gly Arg Phe
 65 70 75 80

Phe Leu Asp Arg Asp Gly Phe Leu Phe Arg Tyr Ile Leu Asp Tyr Leu
 85 90 95

Arg Asp Leu Gln Leu Val Leu Pro Asp Tyr Phe Pro Glu Arg Ser Arg
 100 105 110

Leu Gln Arg Glu Ala Glu Tyr Phe Glu Leu Pro Glu Leu Val Arg Arg
 115 120 125

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Leu Gly Ala Pro Gln Gln Pro Gly Pro Gly Pro Pro Ser Arg Arg
130 135 140

Gly Val His Lys Glu Gly Ser Leu Gly Asp Glu Leu Leu Pro Leu Gly
145 150 155 160

Tyr Ser Glu Pro Glu Gln Gln Glu Gly Ala Ser Ala Gly Ala Pro Ser
165 170 175

Pro Thr Leu Glu Leu Ala Ser Arg Ser Pro Ser Gly Gly Ala Ala Gly
180 185 190

Pro Leu Leu Thr Pro Ser Gln Ser Leu Asp Gly Ser Arg Arg Ser Gly
195 200 205

Tyr Ile Thr Ile Gly Tyr Arg Gly Ser Tyr Thr Ile Gly Arg Asp Ala
210 215 220

Gln Ala Asp Ala Lys Phe Arg Arg Val Ala Arg Ile Thr Val Cys Gly
225 230 235 240

Lys Thr Ser Leu Ala Lys Glu Val Phe Gly Asp Thr Leu Asn Glu Ser
245 250 255

Arg Asp Pro Asp Arg Pro Pro Glu Arg Tyr Thr Ser Arg Tyr Tyr Leu
260 265 270

Lys Phe Asn Phe Leu Glu Gln Ala Phe Asp Lys Leu Ser Glu Ser Gly
275 280 285

Phe His Met Val Ala Cys Ser Ser Thr Gly Thr Cys Ala Phe Ala Ser
290 295 300

Ser Thr Asp Gln Ser Glu Asp Lys Ile Trp Thr Ser Tyr Thr Glu Tyr
305 310 315 320

Val Phe Cys Arg Glu
325

<210> 81
<211> 618
<212> PRT
<213> Homo sapiens

<400> 81

Met Arg Arg Asp Val Arg Ile Leu Leu Leu Gly Glu Ala Gln Val Gly
1 5 10 15

Lys Thr Ser Leu Ile Leu Ser Leu Val Gly Glu Glu Phe Pro Glu Glu
20 25 30

Val Pro Pro Arg Ala Glu Glu Ile Thr Ile Pro Ala Asp Val Thr Pro
35 40 45

Glu Lys Val Pro Thr His Ile Val Asp Tyr Ser Glu Ala Glu Gln Thr
50 55 60

Asp Glu Glu Leu Arg Glu Glu Ile His Lys Ala Asn Val Val Cys Val
65 70 75 80

Val Tyr Asp Val Ser Glu Glu Ala Thr Ile Glu Lys Ile Arg Thr Lys
85 90 95

Trp Ile Pro Leu Val Asn Gly Gly Thr Thr Gln Gly Pro Arg Val Pro
100 105 110

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ile Ile Leu Val Gly Asn Lys Ser Asp Leu Arg Ser Gly Ser Ser Met
 115 120 125

Glu Ala Val Leu Pro Ile Met Ser Gln Phe Pro Glu Ile Glu Thr Cys
 130 135 140

Val Glu Cys Ser Ala Lys Asn Leu Arg Asn Ile Ser Glu Leu Phe Tyr
 145 150 155 160

Tyr Ala Gln Lys Ala Val Leu His Pro Thr Ala Pro Leu Tyr Asp Pro
 165 170 175

Glu Ala Lys Gln Leu Arg Pro Ala Cys Ala Gln Ala Leu Thr Arg Ile
 180 185 190

Phe Arg Leu Ser Asp Gln Asp Leu Asp Gln Ala Leu Ser Asp Glu Glu
 195 200 205

Leu Asn Ala Phe Gln Lys Ser Cys Phe Gly His Pro Leu Ala Pro Gln
 210 215 220

Ala Leu Glu Asp Val Lys Thr Val Val Cys Arg Asn Val Ala Gly Gly
 225 230 235 240

Val Arg Glu Asp Arg Leu Thr Leu Asp Gly Phe Leu Phe Leu Asn Thr
 245 250 255

Leu Phe Ile Gln Arg Gly Arg His Glu Thr Thr Trp Thr Ile Leu Arg
 260 265 270

Arg Phe Gly Tyr Ser Asp Ala Leu Glu Leu Thr Ala Asp Tyr Leu Ser
 275 280 285

Pro Leu Ile His Val Pro Pro Gly Cys Ser Thr Glu Leu Asn His Leu
 290 295 300

Gly Tyr Gln Phe Val Gln Arg Val Phe Glu Lys His Asp Gln Asp Arg
 305 310 315 320

Asp Gly Ala Leu Ser Pro Val Glu Leu Gln Ser Leu Phe Ser Val Phe
 325 330 335

Pro Ala Ala Pro Trp Gly Pro Glu Leu Pro Arg Thr Val Arg Thr Glu
 340 345 350

Ala Gly Arg Leu Pro Leu His Gly Tyr Leu Cys Gln Trp Thr Leu Val
 355 360 365

Thr Tyr Leu Asp Val Arg Ser Cys Leu Gly His Leu Gly Tyr Leu Gly
 370 375 380

Tyr Pro Thr Leu Cys Glu Gln Asp Gln Ala His Ala Ile Thr Val Thr
 385 390 395 400

Arg Glu Lys Arg Leu Asp Gln Glu Lys Gly Gln Thr Gln Arg Ser Val
 405 410 415

Leu Leu Cys Lys Val Val Gly Ala Arg Gly Val Gly Lys Ser Ala Phe
 420 425 430

Leu Gln Ala Phe Leu Gly Arg Gly Leu Gly His Gln Asp Thr Arg Glu
 435 440 445

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 Gln Pro Pro Gly Tyr Ala Ile Asp Thr Val Gln Val Asn Gly Gln Glu
 450 455 460

Lys Tyr Leu Ile Leu Cys Glu Val Gly Thr Asp Gly Leu Leu Ala Thr
 465 470 475 480

Ser Leu Asp Ala Thr Cys Asp Val Ala Cys Leu Met Phe Asp Gly Ser
 485 490 495

Asp Pro Lys Ser Phe Ala His Cys Ala Ser Val Tyr Lys His His Tyr
 500 505 510

Met Asp Gly Gln Thr Pro Cys Leu Phe Val Ser Ser Lys Ala Asp Leu
 515 520 525

Pro Glu Gly Val Ala Val Ser Gly Pro Ser Pro Ala Glu Phe Cys Arg
 530 535 540

Lys His Arg Leu Pro Ala Pro Val Pro Phe Ser Cys Ala Gly Pro Ala
 545 550 555 560

Glu Pro Ser Thr Thr Ile Phe Thr Gln Leu Ala Thr Met Ala Ala Phe
 565 570 575

Pro His Leu Val His Ala Glu Leu His Pro Ser Ser Phe Trp Leu Arg
 580 585 590

Gly Leu Leu Gly Val Val Gly Ala Ala Val Ala Ala Val Leu Ser Phe
 595 600 605

Ser Leu Tyr Arg Val Leu Val Lys Ser Gln
 610 615

<210> 82
 <211> 69
 <212> PRT
 <213> Homo sapiens

<400> 82

Val Met Leu Ala Ala Ser Tyr Trp Ser Leu Leu Ala Pro Ala Val Glu
 1 5 10 15

Met Ala Thr Ser Ser Gly Gly Phe Gly Ala Phe Ala Phe Phe Pro Val
 20 25 30

Ala Val Gly Phe Thr Leu Gly Ala Ala Phe Val Tyr Leu Ala Asp Leu
 35 40 45

Leu Met Pro His Leu Lys Asn Cys Pro Leu Asp Gln Thr Ala Glu Cys
 50 55 60

Asp Val Gly Arg Leu
 65

<210> 83
 <211> 731
 <212> PRT
 <213> Homo sapiens

<400> 83

Pro Glu Glu Thr Gln Thr Gln Asp Gln Pro Met Glu Glu Glu Glu Val
 1 5 10 15

Glu Thr Phe Ala Phe Gln Ala Glu Ile Ala Gln Leu Met Ser Leu Ile
 20 25 30

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ile Asn Thr Phe Tyr Ser Asn Lys Glu Ile Phe Leu Arg Glu Leu Ile
35 40 45

Ser Asn Ser Ser Asp Ala Leu Asp Lys Ile Arg Tyr Glu Thr Leu Thr
50 55 60

Asp Pro Ser Lys Leu Asp Ser Gly Lys Glu Leu His Ile Asn Leu Ile
65 70 75 80

Pro Asn Lys Gln Asp Arg Thr Leu Thr Ile Val Asp Thr Gly Ile Gly
85 90 95

Met Thr Lys Ala Asp Leu Ile Asn Asn Leu Gly Thr Ile Ala Lys Ser
100 105 110

Gly Thr Lys Ala Phe Met Glu Ala Leu Gln Ala Gly Ala Asp Ile Ser
115 120 125

Met Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Tyr Leu Val Ala
130 135 140

Glu Lys Val Thr Val Ile Thr Lys His Asn Asp Asp Glu Gln Tyr Ala
145 150 155 160

Trp Glu Ser Ser Ala Gly Gly Ser Phe Thr Val Arg Thr Asp Thr Gly
165 170 175

Glu Pro Met Gly Arg Gly Thr Lys Val Ile Leu His Leu Lys Glu Asp
180 185 190

Gln Thr Glu Tyr Leu Glu Glu Arg Arg Ile Lys Glu Ile Val Lys Lys
195 200 205

His Ser Gln Phe Ile Gly Tyr Pro Ile Thr Leu Phe Val Glu Lys Glu
210 215 220

Arg Asp Lys Glu Val Ser Asp Asp Glu Ala Glu Glu Lys Glu Asp Lys
225 230 235 240

Glu Glu Glu Lys Glu Lys Glu Glu Lys Glu Ser Glu Asp Lys Pro Glu
245 250 255

Ile Glu Asp Val Gly Ser Asp Glu Glu Glu Glu Lys Lys Asp Gly Asp
260 265 270

Lys Lys Lys Lys Lys Lys Ile Lys Glu Lys Tyr Ile Asp Gln Glu Glu
275 280 285

Leu Asn Lys Thr Lys Pro Ile Trp Thr Arg Asn Pro Asp Asp Ile Thr
290 295 300

Asn Glu Glu Tyr Gly Glu Phe Tyr Lys Ser Leu Thr Asn Asp Trp Glu
305 310 315 320

Asp His Leu Ala Val Lys His Phe Ser Val Glu Gly Gln Leu Glu Phe
325 330 335

Arg Ala Leu Leu Phe Val Pro Arg Arg Ala Pro Phe Asp Leu Phe Glu
340 345 350

Asn Arg Lys Lys Lys Asn Asn Ile Lys Leu Tyr Val Arg Arg Val Phe
355 360 365

Ile Met Asp Asn Cys Glu Glu Leu Ile Pro Glu Tyr Leu Asn Phe Ile
370 375 380

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Arg Gly Val Val Asp Ser Glu Asp Leu Pro Leu Asn Ile Ser Arg Glu
 385 390 395 400
 Met Leu Gln Gln Ser Lys Ile Leu Lys Val Ile Arg Lys Asn Leu Val
 405 410 415
 Lys Lys Cys Leu Glu Leu Phe Thr Glu Leu Ala Glu Asp Lys Glu Asn
 420 425 430
 Tyr Lys Lys Phe Tyr Glu Gln Phe Ser Lys Asn Ile Lys Leu Gly Ile
 435 440 445
 His Glu Asp Ser Gln Asn Arg Lys Lys Leu Ser Glu Leu Leu Arg Tyr
 450 455 460
 Tyr Thr Ser Ala Ser Gly Asp Glu Met Val Ser Leu Lys Asp Tyr Cys
 465 470 475 480
 Thr Arg Met Lys Glu Asn Gln Lys His Ile Tyr Tyr Ile Thr Gly Glu
 485 490 495
 Thr Lys Asp Gln Val Ala Asn Ser Ala Phe Val Glu Arg Leu Arg Lys
 500 505 510
 His Gly Leu Glu Val Ile Tyr Met Ile Glu Pro Ile Asp Glu Tyr Cys
 515 520 525
 Val Gln Gln Leu Lys Glu Phe Glu Gly Lys Thr Leu Val Ser Val Thr
 530 535 540
 Lys Glu Gly Leu Glu Leu Pro Glu Asp Glu Glu Glu Lys Lys Lys Gln
 545 550 555 560
 Glu Glu Lys Lys Thr Lys Phe Glu Asn Leu Cys Lys Ile Met Lys Asp
 565 570 575
 Ile Leu Glu Lys Lys Val Glu Lys Val Val Val Ser Asn Arg Leu Val
 580 585 590
 Thr Ser Pro Cys Cys Ile Val Thr Ser Thr Tyr Gly Trp Thr Ala Asn
 595 600 605
 Met Glu Arg Ile Met Lys Ala Gln Ala Leu Arg Asp Asn Ser Thr Met
 610 615 620
 Gly Tyr Met Ala Ala Lys Lys His Leu Glu Ile Asn Pro Asp His Ser
 625 630 635 640
 Ile Ile Glu Thr Leu Arg Gln Lys Ala Glu Ala Asp Lys Asn Asp Lys
 645 650 655
 Ser Val Lys Asp Leu Val Ile Leu Leu Tyr Glu Thr Ala Leu Leu Ser
 660 665 670
 Ser Gly Phe Ser Leu Glu Asp Pro Gln Thr His Ala Asn Arg Ile Tyr
 675 680 685
 Arg Met Ile Lys Leu Gly Leu Gly Ile Asp Glu Asp Asp Pro Thr Ala
 690 695 700
 Asp Asp Thr Ser Ala Ala Val Thr Glu Glu Met Pro Pro Leu Glu Gly
 705 710 715 720

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 Asp Asp Asp Thr Ser Arg Met Glu Glu Val Asp
 725 730

<210> 84
 <211> 1255
 <212> PRT
 <213> Homo sapiens

<400> 84

Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
 1 5 10 15

Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys
 20 25 30

Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
 35 40 45

Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
 50 55 60

Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
 65 70 75 80

Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
 85 90 95

Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
 100 105 110

Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
 115 120 125

Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
 130 135 140

Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
 145 150 155 160

Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
 165 170 175

Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
 180 185 190

His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
 195 200 205

Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
 210 215 220

Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
 225 230 235 240

Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
 245 250 255

His phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
 260 265 270

Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
 275 280 285

Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
 290 295 300

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
305 310 315 320

Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
325 330 335

Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu
340 345 350

Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys
355 360 365

Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp
370 375 380

Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe
385 390 395 400

Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro
405 410 415

Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg
420 425 430

Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu
435 440 445

Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly
450 455 460

Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val
465 470 475 480

Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr
485 490 495

Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His
500 505 510

Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
515 520 525

Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys
530 535 540

Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys
545 550 555 560

Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys
565 570 575

Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp
580 585 590

Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu
595 600 605

Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln
610 615 620

Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys
625 630 635 640

Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Ile Ser

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 645 650 655

Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly
 660 665 670

Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg
 675 680 685

Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly
 690 695 700

Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu
 705 710 715 720

Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys
 725 730 735

Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile
 740 745 750

Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu
 755 760 765

Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg
 770 775 780

Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu
 785 790 795 800

Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg
 805 810 815

Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly
 820 825 830

Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala
 835 840 845

Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe
 850 855 860

Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp
 865 870 875 880

Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg
 885 890 895

Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val
 900 905 910

Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala
 915 920 925

Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro
 930 935 940

Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met
 945 950 955 960

Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe
 965 970 975

Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu
 980 985 990

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu
995 1000 1005

Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr
1010 1015 1020

Leu Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly
1025 1030 1035

Ala Gly Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg
1040 1045 1050

Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu
1055 1060 1065

Glu Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser
1070 1075 1080

Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly Leu
1085 1090 1095

Gln Ser Leu Pro Thr His Asp Pro Ser Pro Leu Gln Arg Tyr Ser
1100 1105 1110

Glu Asp Pro Thr Val Pro Leu Pro Ser Glu Thr Asp Gly Tyr Val
1115 1120 1125

Ala Pro Leu Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro
1130 1135 1140

Asp Val Arg Pro Gln Pro Pro Ser Pro Arg Glu Gly Pro Leu Pro
1145 1150 1155

Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu Arg Pro Lys Thr Leu
1160 1165 1170

Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val Phe Ala Phe Gly
1175 1180 1185

Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln Gly Gly Ala
1190 1195 1200

Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala Phe Asp
1205 1210 1215

Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala Pro
1220 1225 1230

Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr
1235 1240 1245

Leu Gly Leu Asp Val Pro Val
1250 1255

<210> 85
<211> 296
<212> PRT
<213> Homo sapiens

<400> 85

Ala Glu Gly Met Val Cys Asn His Leu Cys Ser Ser Asp Gly Cys Trp
1 5 10 15

Gly Pro Gly Pro Asp Gln Cys Leu Ser Cys Arg Arg Phe Ser Arg Gly
20 25 30

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Arg Ile Cys Ile Glu Ser Cys Asn Leu Tyr Asp Gly Gly Asn Asp Thr
35 40 45

Thr Phe Leu Phe Ser Phe Phe Phe Val Phe Thr Phe Gln Gly Pro Asp
50 55 60

Asn Cys Thr Lys Cys Ser His Phe Lys Asp Gly Pro Asn Cys Val Glu
65 70 75 80

Lys Cys Pro Asp Gly Leu Gln Gly Ala Asn Ser Phe Ile Phe Lys Tyr
85 90 95

Ala Asp Pro Asp Arg Glu Cys His Pro Cys His Pro Asn Cys Thr Gln
100 105 110

Gly Thr Pro Leu Ile Ala Ala Gly Val Ile Gly Gly Leu Phe Ile Leu
115 120 125

Val Ile Val Gly Leu Thr Phe Ala Val Tyr Val Arg Arg Lys Ser Ile
130 135 140

Lys Lys Lys Arg Ala Leu Arg Arg Phe Leu Glu Thr Glu Leu Val Glu
145 150 155 160

Pro Leu Thr Pro Ser Gly Thr Ala Pro Asn Gln Ala Gln Leu Arg Ile
165 170 175

Leu Lys Glu Thr Glu Leu Lys Arg Val Lys Val Leu Gly Ser Gly Ala
180 185 190

Phe Gly Thr Val Tyr Lys Gly Ile Trp Val Pro Glu Gly Glu Thr Val
195 200 205

Lys Ile Pro Val Ala Ile Lys Ile Leu Asn Glu Thr Thr Gly Pro Lys
210 215 220

Ala Asn Val Glu Phe Met Asp Glu Ala Leu Ile Met Ala Ser Met Asp
225 230 235 240

His Pro His Leu Val Arg Leu Leu Gly Val Cys Leu Ser Pro Thr Ile
245 250 255

Gln Leu Val Thr Gln Leu Met Pro His Gly Cys Leu Leu Glu Tyr Val
260 265 270

His Glu His Lys Asp Asn Ile Gly Ser Gln Leu Leu Leu Asn Trp Cys
275 280 285

Val Gln Ile Ala Lys Val Ser Ala
290 295

<210> 86
<211> 1257
<212> PRT
<213> Homo sapiens

<400> 86

Met Ala Ser Cys Ser Phe Thr Arg Asp Gln Ala Thr Arg Arg Leu Arg
1 5 10 15

Gly Ala Ala Ala Ala Ala Ala Ala Ala Leu Ala Ala Val Val Thr Thr
20 25 30

Pro Leu Leu Ser Ser Gly Thr Pro Thr Ala Leu Ile Gly Thr Gly Ser

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 35 40 45

Ser Cys Pro Gly Ala Met Trp Leu Ser Thr Ala Thr Gly Ser Arg Ser
 50 55 60

Asp Ser Glu Ser Glu Glu Glu Asp Leu Pro Val Gly Glu Glu Val Cys
 65 70 75 80

Lys Arg Gly Tyr Leu Arg Lys Gln Lys His Gly His Arg Arg Tyr Phe
 85 90 95

Val Leu Lys Leu Glu Thr Ala Asp Ala Pro Ala Arg Leu Glu Tyr Tyr
 100 105 110

Glu Asn Ala Arg Lys Phe Arg His Ser Val Arg Ala Ala Ala Ala
 115 120 125

Ala Ala Ala Ala Ala Ser Gly Ala Ala Ile Pro Pro Leu Ile Pro Pro
 130 135 140

Arg Arg Val Ile Thr Leu Tyr Gln Cys Phe Ser Val Ser Gln Arg Ala
 145 150 155 160

Asp Ala Arg Tyr Arg His Leu Ile Ala Leu Phe Thr Gln Asp Glu Tyr
 165 170 175

Phe Ala Met Val Ala Glu Asn Glu Ser Glu Gln Glu Ser Trp Tyr Leu
 180 185 190

Leu Leu Ser Arg Leu Ile Leu Glu Ser Lys Arg Arg Arg Cys Gly Thr
 195 200 205

Leu Gly Ala Gln Pro Asp Gly Glu Pro Ala Ala Leu Ala Ala Ala Ala
 210 215 220

Ala Ala Glu Pro Pro Phe Tyr Lys Asp Val Trp Gln Val Ile Val Lys
 225 230 235 240

Pro Arg Gly Leu Gly His Arg Lys Glu Leu Ser Gly Val Phe Arg Leu
 245 250 255

Cys Leu Thr Asp Glu Glu Val Val Phe Val Arg Leu Asn Thr Glu Val
 260 265 270

Ala Ser Val Val Val Gln Leu Leu Ser Ile Arg Arg Cys Gly His Ser
 275 280 285

Glu Gln Tyr Phe Phe Leu Glu Val Gly Arg Ser Thr Val Ile Gly Pro
 290 295 300

Gly Glu Leu Trp Met Gln Val Asp Asp Cys Val Val Ala Gln Asn Met
 305 310 315 320

His Glu Leu Phe Leu Glu Lys Met Arg Ala Leu Cys Ala Asp Glu Tyr
 325 330 335

Arg Ala Arg Cys Arg Ser Tyr Ser Ile Ser Ile Gly Ala His Leu Leu
 340 345 350

Thr Leu Leu Ser Ala Arg Arg His Leu Gly Leu Val Pro Leu Glu Pro
 355 360 365

Gly Gly Trp Leu Arg Arg Ser Arg Phe Glu Gln Phe Cys His Leu Arg
 370 375 380

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ala Ile Gly Asp Gly Glu Asp Glu Met Leu Phe Thr Arg Arg Phe Val
385 390 395 400

Thr Pro Ser Glu Pro Val Ala His Ser Arg Arg Gly Arg Leu His Leu
405 410 415

Pro Arg Gly Arg Arg Ser Arg Arg Ala Val Ser Val Pro Ala Ser Phe
420 425 430

Phe Arg Arg Leu Ala Pro Ser Pro Ala Arg Pro Arg His Pro Ala Glu
435 440 445

Ala Pro Asn Asn Gly Ala Arg Leu Ser Ser Glu Val Ser Gly Ser Gly
450 455 460

Ser Gly Asn Phe Gly Glu Glu Gly Asn Pro Gln Gly Lys Glu Asp Gln
465 470 475 480

Glu Gly Ser Gly Gly Asp Tyr Met Pro Met Asn Asn Trp Gly Ser Gly
485 490 495

Asn Gly Arg Gly Ser Gly Gly Gly Gln Gly Ser Asn Gly Gln Gly Ser
500 505 510

Ser Ser His Ser Ser Gly Gly Asn Gln Cys Ser Gly Glu Gly Gln Gly
515 520 525

Ser Arg Gly Gly Gln Gly Ser Asn Gly Gln Gly Ser Gly Gly Asn Gln
530 535 540

Cys Ser Arg Asp Gly Gln Gly Thr Ala Gly Gly His Gly Ser Gly Gly
545 550 555 560

Gly Gln Arg Pro Gly Gly Gly His Gly Ser Gly Gly Gly Gln Gly Pro
565 570 575

Gly Asp Gly His Gly Ser Gly Gly Gly Lys Asn Ser Gly Gly Gly Lys
580 585 590

Gly Ser Gly Ser Gly Lys Gly Ser Asp Gly Asp Gly Glu Arg Gly Lys
595 600 605

Ser Leu Lys Lys Arg Ser Tyr Phe Gly Lys Leu Thr Gln Ser Lys Gln
610 615 620

Gln Gln Met Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Ala
625 630 635 640

Gly Gly Thr Gly Gly Lys Gly Lys Ser Gly Gly Arg Phe Arg Leu Tyr
645 650 655

Phe Cys Val Asp Arg Gly Ala Thr Lys Glu Cys Lys Glu Ala Lys Glu
660 665 670

Val Lys Asp Ala Glu Ile Pro Glu Gly Ala Ala Arg Gly Pro His Arg
675 680 685

Ala Arg Ala Phe Asp Glu Asp Glu Asp Asp Pro Tyr Val Pro Met Arg
690 695 700

Pro Gly Val Ala Thr Pro Leu Val Ser Ser Ser Asp Tyr Met Pro Met
705 710 715 720

Ala pro Gln Asn Val Ser Ala Ser Lys Lys Arg His Ser Arg Ser Pro

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Phe Glu Asp Ser Arg Gly Tyr Met Met Met Phe Pro Arg Val Ser Pro
725 730 735
740 745 750

Pro Pro Ala Pro Ser Pro Pro Lys Ala Pro Asp Thr Asn Lys Glu Asp
755 760 765

Asp Ser Lys Asp Asn Asp Ser Glu Ser Asp Tyr Met Phe Met Ala Pro
770 775 780

Gly Ala Gly Ala Ile Pro Lys Asn Pro Arg Asn Pro Gln Gly Gly Ser
785 790 795 800

Ser Ser Lys Ser Trp Ser Ser Tyr Phe Ser Leu Pro Asn Pro Phe Arg
805 810 815

Ser Ser Pro Leu Gly Gln Asn Asp Asn Ser Glu Tyr Val Pro Met Leu
820 825 830

Pro Gly Lys Phe Leu Gly Arg Gly Leu Asp Lys Glu Val Ser Tyr Asn
835 840 845

Trp Asp Pro Lys Asp Ala Ala Ser Lys Pro Ser Gly Glu Gly Ser Phe
850 855 860

Ser Lys Pro Gly Asp Gly Gly Ser Pro Ser Lys Pro Ser Asp His Glu
865 870 875 880

Pro Pro Lys Asn Lys Ala Lys Arg Pro Asn Arg Leu Ser Phe Ile Thr
885 890 895

Lys Gly Tyr Lys Ile Lys Pro Lys Pro Gln Lys Pro Thr His Glu Gln
900 905 910

Arg Glu Ala Asp Ser Ser Ser Asp Tyr Val Asn Met Asp Phe Thr Lys
915 920 925

Arg Glu Ser Asn Thr Pro Ala Pro Ser Thr Gln Gly Leu Pro Asp Ser
930 935 940

Trp Gly Ile Ile Ala Glu Pro Arg Gln Ser Ala Phe Ser Asn Tyr Val
945 950 955 960

Asn Val Glu Phe Gly Val Pro Phe Pro Asn Pro Ala Asn Asp Leu Ser
965 970 975

Asp Leu Leu Arg Ala Ile Pro Arg Ala Asn Pro Leu Ser Leu Asp Ser
980 985 990

Ala Arg Trp Pro Leu Pro Pro Leu Pro Leu Ser Ala Thr Gly Ser Asn
995 1000 1005

Ala Ile Glu Glu Glu Gly Asp Tyr Ile Glu Val Ile Phe Asn Ser
1010 1015 1020

Ala Met Thr Pro Ala Met Ala Leu Ala Asp Ser Ala Ile Arg Tyr
1025 1030 1035

Asp Ala Glu Thr Gly Arg Ile Tyr Val Val Asp Pro Phe Ser Glu
1040 1045 1050

Cys Cys Met Asp Ile Ser Leu Ser Pro Ser Arg Cys Ser Glu Pro
1055 1060 1065

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Pro Val Ala Arg Leu Leu Gln Glu Glu Glu Gln Glu Arg Arg
1070 1075 1080

Arg Pro Gln Ser Arg Ser Gln Ser Phe Phe Ala Ala Ala Arg Ala
1085 1090 1095

Ala Val Ser Ala Phe Pro Thr Asp Ser Leu Glu Arg Asp Leu Ser
1100 1105 1110

Pro Ser Ser Ala Pro Ala Val Ala Ser Ala Ala Glu Pro Thr Leu
1115 1120 1125

Ala Leu Ser Gln Val Val Ala Ala Ala Ser Ala Leu Ala Ala Ala
1130 1135 1140

Pro Gly Ile Gly Ala Ala Ala Ala Ala Ala Gly Phe Asp Ser Ala
1145 1150 1155

Ser Ala Arg Trp Phe Gln Pro Val Ala Asn Ala Ala Asp Ala Glu
1160 1165 1170

Ala Val Arg Gly Ala Gln Asp Val Ala Gly Gly Ser Asn Pro Gly
1175 1180 1185

Ala His Asn Pro Ser Ala Asn Leu Ala Arg Gly Asp Asn Gln Ala
1190 1195 1200

Gly Gly Ala Ala Ala Ala Ala Ala Ala Pro Glu Pro Pro Pro Arg
1205 1210 1215

Ser Arg Arg Val Pro Arg Pro Pro Glu Arg Glu Asp Ser Asp Asn
1220 1225 1230

Asp Asp Asp Thr His Val Arg Met Asp Phe Ala Arg Arg Asp Asn
1235 1240 1245

Gln Phe Asp Ser Pro Lys Arg Gly Arg
1250 1255

<210> 87
<211> 1111
<212> PRT
<213> Homo sapiens

<400> 87

Ser Ser Leu Leu Glu Lys Met Thr Ser Ser Asp Lys Asp Phe Arg Phe
1 5 10 15

Met Ala Thr Ser Asp Leu Met Ser Glu Leu Gln Lys Asp Ser Ile Gln
20 25 30

Leu Asp Glu Asp Ser Glu Arg Lys Val Val Lys Met Leu Leu Arg Leu
35 40 45

Leu Glu Asp Lys Asn Gly Glu Val Gln Asn Leu Ala Val Lys Trp Leu
50 55 60

Gly Val Pro Leu Gly Ala Phe His Ala Ser Leu Leu His Cys Leu Leu
65 70 75 80

Pro Gln Leu Ser Ser Pro Arg Leu Ala Val Arg Lys Arg Ala Val Gly
85 90 95

Ala Leu Gly His Leu Ala Thr Ala Cys Ser Thr Asp Leu Phe Val Glu
100 105 110

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Leu Ala Asp His Leu Leu Asp Arg Leu Pro Gly Pro Arg Val Pro Thr
115 120 125

Ser Pro Thr Ala Ile Arg Thr Leu Ile Gln Cys Leu Gly Ser Val Gly
130 135 140

Arg Gln Ala Gly His Arg Leu Gly Ala His Leu Asp Arg Leu Val Pro
145 150 155 160

Leu Val Glu Asp Phe Cys Asn Leu Asp Asp Asp Glu Leu Arg Glu Ser
165 170 175

Cys Leu Gln Ala Phe Glu Ala Phe Leu Arg Lys Cys Pro Lys Glu Met
180 185 190

Gly Pro His Val Pro Asn Val Thr Ser Leu Cys Leu Gln Tyr Ile Lys
195 200 205

His Asp Pro Asn Tyr Asn Tyr Asp Ser Asp Glu Asp Glu Glu Gln Met
210 215 220

Glu Thr Glu Asp Ser Glu Phe Ser Glu Gln Glu Ser Glu Asp Glu Tyr
225 230 235 240

Ser Asp Asp Asp Asp Met Ser Trp Lys Val Arg Arg Ala Ala Ala Lys
245 250 255

Cys Ile Ala Ala Leu Ile Ser Ser Arg Pro Asp Leu Leu Pro Asp Phe
260 265 270

His Cys Thr Leu Ala Pro Val Leu Ile Arg Arg Phe Lys Glu Arg Glu
275 280 285

Glu Asn Val Lys Ala Asp Val Phe Thr Ala Tyr Ile Val Leu Leu Arg
290 295 300

Gln Thr Arg Pro Pro Lys Gly Trp Leu Glu Ala Met Glu Glu Pro Thr
305 310 315 320

Gln Thr Gly Ser Asn Leu His Met Leu Arg Gly Gln Val Pro Leu Val
325 330 335

Val Lys Ala Leu Gln Arg Gln Leu Lys Asp Arg Ser Val Arg Ala Arg
340 345 350

Gln Gly Cys Phe Ser Leu Leu Thr Glu Leu Ala Gly Val Leu Pro Gly
355 360 365

Ser Leu Ala Glu His Met Pro Val Leu Val Ser Gly Ile Ile Phe Ser
370 375 380

Leu Ala Asp Arg Ser Ser Ser Ser Thr Ile Arg Met Asp Ala Leu Ala
385 390 395 400

Phe Leu Gln Gly Leu Leu Gly Thr Glu Pro Ala Glu Ala Phe His Pro
405 410 415

His Leu Pro Ile Leu Leu Pro Pro Val Met Ala Cys Val Ala Asp Ser
420 425 430

Phe Tyr Lys Ile Ala Ala Glu Ala Leu Val Val Leu Gln Glu Leu Val
435 440 445

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Arg Ala Leu Trp Pro Leu His Arg Pro Arg Met Leu Asp Pro Glu Pro
450 455 460

Tyr Val Gly Glu Met Ser Ala Val Thr Leu Ala Arg Leu Arg Ala Thr
465 470 475 480

Asp Leu Asp Gln Glu Val Lys Glu Arg Ala Ile Ser Cys Met Gly His
485 490 495

Leu Val Gly His Leu Gly Asp Arg Leu Gly Asp Asp Leu Glu Pro Thr
500 505 510

Leu Leu Leu Leu Leu Asp Arg Leu Arg Asn Glu Ile Thr Arg Leu Pro
515 520 525

Ala Ile Lys Ala Leu Thr Leu Val Ala Val Ser Pro Leu Gln Leu Asp
530 535 540

Leu Gln Pro Ile Leu Ala Glu Ala Leu His Ile Leu Ala Ser Phe Leu
545 550 555 560

Arg Lys Asn Gln Arg Ala Leu Arg Leu Ala Thr Leu Ala Ala Leu Asp
565 570 575

Ala Leu Ala Gln Ser Gln Gly Leu Ser Leu Pro Pro Ser Ala Val Gln
580 585 590

Ala Val Leu Ala Glu Leu Pro Ala Leu Val Asn Glu Ser Asp Met His
595 600 605

Val Ala Gln Leu Ala Val Asp Phe Leu Ala Thr Val Thr Gln Ala Gln
610 615 620

Pro Ala Ser Leu Val Glu Val Ser Gly Pro Val Leu Ser Glu Leu Leu
625 630 635 640

Arg Leu Leu Arg Ser Pro Leu Leu Pro Ala Gly Val Leu Ala Ala Ala
645 650 655

Glu Gly Phe Leu Gln Ala Leu Val Gly Thr Arg Pro Pro Cys Val Asp
660 665 670

Tyr Ala Lys Leu Ile Ser Leu Leu Thr Ala Pro Val Tyr Glu Gln Ala
675 680 685

Val Asp Gly Gly Pro Gly Leu His Lys Gln Val Phe His Ser Leu Ala
690 695 700

Arg Cys Val Ala Ala Leu Ser Ala Ala Cys Pro Gln Glu Ala Ala Ser
705 710 715 720

Thr Ala Ser Arg Leu Val Cys Asp Ala Arg Ser Pro His Ser Ser Thr
725 730 735

Gly Val Lys Val Leu Ala Phe Leu Ser Leu Ala Glu Val Gly Gln Val
740 745 750

Ala Gly Pro Gly Pro Gln Arg Glu Leu Lys Ala Val Leu Leu Glu Ala
755 760 765

Leu Gly Ser Pro Ser Glu Asp Val Arg Ala Ala Ala Ser Tyr Ala Leu
770 775 780

Gly Arg Val Gly Ala Gly Ser Leu Pro Asp Phe Leu Pro Phe Leu Leu
785 790 795 800

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Glu Gln Ile Glu Ala Glu Pro Arg Arg Gln Tyr Leu Leu Leu His Ser
805 810 815

Leu Arg Glu Ala Leu Gly Ala Ala Gln Pro Asp Ser Leu Lys Pro Tyr
820 825 830

Ala Glu Asp Ile Trp Ala Leu Leu Phe Gln Arg Cys Glu Gly Ala Glu
835 840 845

Glu Gly Thr Arg Gly Val Val Ala Glu Cys Ile Gly Lys Leu Val Leu
850 855 860

Val Asn Pro Ser Phe Leu Leu Pro Arg Leu Arg Lys Gln Leu Ala Ala
865 870 875 880

Gly Arg Pro His Thr Arg Ser Thr Val Ile Thr Ala Val Lys Phe Leu
885 890 895

Ile Ser Asp Gln Pro His Pro Ile Asp Pro Leu Leu Lys Ser Phe Ile
900 905 910

Ala Val His Asn Lys Pro Ser Leu Val Arg Asp Leu Leu Asp Asp Ile
915 920 925

Leu Pro Leu Leu Tyr Gln Glu Thr Lys Ile Arg Arg Asp Leu Ile Arg
930 935 940

Glu Val Glu Met Gly Pro Phe Lys His Thr Val Asp Asp Gly Leu Asp
945 950 955 960

Val Arg Lys Ala Ala Phe Glu Cys Met Tyr Ser Leu Leu Glu Ser Cys
965 970 975

Leu Gly Gln Leu Asp Ile Cys Glu Phe Leu Asn His Val Glu Asp Gly
980 985 990

Leu Lys Asp His Tyr Asp Ile Arg Met Leu Thr Phe Ile Met Val Ala
995 1000 1005

Arg Leu Ala Thr Leu Cys Pro Ala Pro Val Leu Gln Arg Val Asp
1010 1015 1020

Arg Leu Ile Glu Pro Leu Arg Ala Thr Cys Thr Ala Lys Val Lys
1025 1030 1035

Ala Gly Ser Val Lys Gln Glu Phe Glu Lys Gln Asp Glu Leu Lys
1040 1045 1050

Arg Ser Ala Met Arg Ala Val Ala Ala Leu Leu Thr Ile Pro Glu
1055 1060 1065

Val Gly Lys Ser Pro Ile Met Ala Asp Phe Ser Ser Gln Ile Arg
1070 1075 1080

Ser Asn Pro Glu Leu Ala Ala Leu Phe Glu Ser Ile Gln Lys Asp
1085 1090 1095

Ser Ala Ser Ala Pro Ser Thr Asp Ser Met Glu Leu Ser
1100 1105 1110

<210> 88
<211> 443
<212> PRT
<213> Homo sapiens

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

<400> 88

Ala Pro Glu Glu Arg Asp Leu Thr Gln Glu Gln Thr Glu Lys Leu Leu
 1 5 10 15

Gln Phe Gln Asp Leu Thr Gly Ile Glu Ser Met Asp Gln Cys Arg His
 20 25 30

Thr Leu Glu Gln His Asn Trp Asn Ile Glu Ala Ala Val Gln Asp Arg
 35 40 45

Leu Asn Glu Gln Glu Gly Val Pro Ser Val Phe Asn Pro Pro Pro Ser
 50 55 60

Arg Pro Leu Gln Val Asn Thr Ala Asp His Arg Ile Tyr Ser Tyr Val
 65 70 75 80

Val Ser Arg Pro Gln Pro Arg Gly Leu Leu Gly Trp Gly Tyr Tyr Leu
 85 90 95

Ile Met Leu Pro Phe Arg Phe Thr Tyr Tyr Thr Ile Leu Asp Ile Phe
 100 105 110

Arg Phe Ala Leu Arg Phe Ile Arg Pro Asp Pro Arg Ser Arg Val Thr
 115 120 125

Asp Pro Val Gly Asp Ile Val Ser Phe Met His Ser Phe Glu Glu Lys
 130 135 140

Tyr Gly Arg Ala His Pro Val Phe Tyr Gln Gly Thr Tyr Ser Gln Ala
 145 150 155 160

Leu Asn Asp Ala Lys Arg Glu Leu Arg Phe Leu Leu Val Tyr Leu His
 165 170 175

Gly Asp Asp His Gln Asp Ser Asp Glu Phe Cys Arg Asn Thr Leu Cys
 180 185 190

Ala Pro Glu Val Ile Ser Leu Ile Asn Thr Arg Met Leu Phe Trp Ala
 195 200 205

Cys Ser Thr Asn Lys Pro Glu Gly Tyr Arg Val Ser Gln Ala Leu Arg
 210 215 220

Glu Asn Thr Tyr Pro Phe Leu Ala Met Ile Met Leu Lys Asp Arg Arg
 225 230 235 240

Met Thr Val Val Gly Arg Leu Glu Gly Leu Ile Gln Pro Asp Asp Leu
 245 250 255

Ile Asn Gln Leu Thr Phe Ile Met Asp Ala Asn Gln Thr Tyr Leu Val
 260 265 270

Ser Glu Arg Leu Glu Arg Glu Glu Arg Asn Gln Thr Gln Val Leu Arg
 275 280 285

Gln Gln Gln Asp Glu Ala Tyr Leu Ala Ser Leu Arg Ala Asp Gln Glu
 290 295 300

Lys Glu Arg Lys Lys Arg Glu Glu Arg Glu Arg Lys Arg Arg Lys Glu
 305 310 315 320

Glu Glu Val Gln Gln Gln Lys Leu Ala Glu Glu Arg Arg Arg Gln Asn
 325 330 335

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Leu Gln Glu Glu Lys Glu Arg Lys Leu Glu Cys Leu Pro Pro Glu Pro
340 345 350

Ser Pro Asp Asp Pro Glu Ser Val Lys Ile Ile Phe Lys Leu Pro Asn
355 360 365

Asp Ser Arg Val Glu Arg Arg Phe His Phe Ser Gln Ser Leu Thr Val
370 375 380

Ile His Asp Phe Leu Phe Ser Leu Lys Glu Ser Pro Glu Lys Phe Gln
385 390 395 400

Ile Glu Ala Asn Phe Pro Arg Arg Val Leu Pro Cys Ile Pro Ser Glu
405 410 415

Glu Trp Pro Asn Pro Pro Thr Leu Gln Glu Ala Gly Leu Ser His Thr
420 425 430

Glu Val Leu Phe Val Gln Asp Leu Thr Asp Glu
435 440

<210> 89
<211> 306
<212> PRT
<213> Homo sapiens.

<400> 89

Met Ala Ser Pro Gly Cys Leu Trp Leu Leu Ala Val Ala Leu Leu Pro
1 5 10 15

Trp Thr Cys Ala Ser Arg Ala Leu Gln His Leu Asp Pro Pro Ala Pro
20 25 30

Leu Pro Leu Val Ile Trp His Gly Met Gly Asp Ser Cys Cys Asn Pro
35 40 45

Leu Ser Met Gly Ala Ile Lys Lys Met Val Glu Lys Lys Ile Pro Gly
50 55 60

Ile Tyr Val Leu Ser Leu Glu Ile Gly Lys Thr Leu Met Glu Asp Val
65 70 75 80

Glu Asn Ser Phe Phe Leu Asn Val Asn Ser Gln Val Thr Thr Val Cys
85 90 95

Gln Ala Leu Ala Lys Asp Pro Lys Leu Gln Gln Gly Tyr Asn Ala Met
100 105 110

Gly Phe Ser Gln Gly Gly Gln Phe Leu Arg Ala Val Ala Gln Arg Cys
115 120 125

Pro Ser Pro Pro Met Ile Asn Leu Ile Ser Val Gly Gly Gln His Gln
130 135 140

Gly Val Phe Gly Leu Pro Arg Cys Pro Gly Glu Ser Ser His Ile Cys
145 150 155 160

Asp Phe Ile Arg Lys Thr Leu Asn Ala Gly Ala Tyr Ser Lys Val Val
165 170 175

Gln Glu Arg Leu Val Gln Ala Glu Tyr Trp His Asp Pro Ile Lys Glu
180 185 190

Asp Val Tyr Arg Asn His Ser Ile Phe Leu Ala Asp Ile Asn Gln Glu
195 200 205

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Arg Gly Ile Asn Glu Ser Tyr Lys Lys Asn Leu Met Ala Leu Lys Lys
 210 215 220

Phe Val Met Val Lys Phe Leu Asn Asp Ser Ile Val Asp Pro Val Asp
 225 230 235 240

Ser Glu Trp Phe Gly Phe Tyr Arg Ser Gly Gln Ala Lys Glu Thr Ile
 245 250 255

Pro Leu Gln Glu Thr Ser Leu Tyr Thr Gln Asp Arg Leu Gly Leu Lys
 260 265 270

Glu Met Asp Asn Ala Gly Gln Leu Val Phe Leu Ala Thr Glu Gly Asp
 275 280 285

His Leu Gln Leu Ser Glu Glu Trp Phe Tyr Ala His Ile Ile Pro Phe
 290 295 300

Leu Gly
 305

<210> 90
 <211> 461
 <212> PRT
 <213> Homo sapiens

<400> 90

Met Tyr Asn Thr Val Trp Ser Met Asp Arg Asp Asp Ala Asp Trp Arg
 1 5 10 15

Glu Val Met Met Pro Tyr Ser Thr Glu Leu Ile Phe Tyr Ile Glu Met
 20 25 30

Asp Pro Pro Ala Leu Pro Pro Lys Pro Pro Lys Pro Met Thr Ser Ala
 35 40 45

Val Pro Asn Gly Met Lys Asp Ser Ser Val Ser Leu Gln Asp Ala Glu
 50 55 60

Trp Tyr Trp Gly Asp Ile Ser Arg Glu Glu Val Asn Asp Lys Leu Arg
 65 70 75 80

Asp Met Pro Asp Gly Thr Phe Leu Val Arg Asp Ala Ser Thr Lys Met
 85 90 95

Gln Gly Asp Tyr Thr Leu Thr Leu Arg Lys Gly Gly Asn Asn Lys Leu
 100 105 110

Ile Lys Ile Tyr His Arg Asp Gly Lys Tyr Gly Phe Ser Asp Pro Leu
 115 120 125

Thr Phe Asn Ser Val Val Glu Leu Ile Asn His Tyr His His Glu Ser
 130 135 140

Leu Ala Gln Tyr Asn Pro Lys Leu Asp Val Lys Leu Met Tyr Pro Val
 145 150 155 160

Ser Arg Tyr Gln Gln Asp Gln Leu Val Lys Glu Asp Asn Ile Asp Ala
 165 170 175

Val Gly Lys Lys Leu Gln Glu Tyr His Ser Gln Tyr Gln Glu Lys Ser
 180 185 190

Lys Glu Tyr Asp Arg Leu Tyr Glu Glu Tyr Thr Arg Thr Ser Gln Glu

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 195 200 205

Ile Gln Met Lys Arg Thr Ala Ile Glu Ala Phe Asn Glu Thr Ile Lys
 210 215 220

Ile Phe Glu Glu Gln Cys His Thr Gln Glu Gln His Ser Lys Glu Tyr
 225 230 235 240

Ile Glu Arg Phe Arg Arg Glu Gly Asn Glu Lys Glu Ile Glu Arg Ile
 245 250 255

Met Met Asn Tyr Asp Lys Leu Lys Ser Arg Leu Gly Glu Ile His Asp
 260 265 270

Ser Lys Met Arg Leu Glu Gln Asp Leu Lys Lys Gln Ala Leu Asp Asn
 275 280 285

Arg Glu Ile Asp Lys Lys Met Asn Ser Ile Lys Pro Asp Leu Ile Gln
 290 295 300

Leu Arg Lys Ile Arg Asp Gln His Leu Val Trp Leu Asn His Lys Gly
 305 310 315 320

Val Arg Gln Lys Arg Leu Asn Val Trp Leu Gly Ile Lys Asn Glu Asp
 325 330 335

Ala Asp Glu Asn Tyr Phe Ile Asn Glu Glu Asp Glu Asn Leu Pro His
 340 345 350

Tyr Asp Glu Lys Thr Trp Phe Val Glu Asp Ile Asn Arg Val Gln Ala
 355 360 365

Glu Asp Leu Leu Tyr Gly Lys Pro Asp Gly Ala Phe Leu Ile Arg Glu
 370 375 380

Ser Ser Lys Lys Gly Cys Tyr Ala Cys Ser Val Val Ala Asp Gly Glu
 385 390 395 400

Val Lys His Cys Val Ile Tyr Ser Thr Ala Arg Gly Tyr Gly Phe Ala
 405 410 415

Glu Pro Tyr Asn Leu Tyr Ser Ser Leu Lys Glu Leu Val Leu His Tyr
 420 425 430

Gln Gln Thr Ser Leu Val Gln His Asn Asp Ser Leu Asn Val Arg Leu
 435 440 445

Ala Tyr Pro Val His Ala Gln Met Pro Ser Leu Cys Arg
 450 455 460

<210> 91
 <211> 724
 <212> PRT
 <213> Homo sapiens

<400> 91

Met Ser Ala Glu Gly Tyr Gln Tyr Arg Ala Leu Tyr Asp Tyr Lys Lys
 1 5 10 15

Glu Arg Glu Glu Asp Ile Asp Leu His Leu Gly Asp Ile Leu Thr Val
 20 25 30

Asn Lys Gly Ser Leu Val Ala Leu Gly Phe Ser Asp Gly Gln Glu Ala
 35 40 45

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Arg Pro Glu Glu Ile Gly Trp Leu Asn Gly Tyr Asn Glu Thr Thr Gly
50 55 60

Glu Arg Gly Asp Phe Pro Gly Thr Tyr Val Glu Tyr Ile Gly Arg Lys
65 70 75 80

Lys Ile Ser Pro Pro Thr Pro Lys Pro Arg Pro Pro Arg Pro Leu Pro
85 90 95

Val Ala Pro Gly Ser Ser Lys Thr Glu Ala Asp Val Glu Gln Gln Ala
100 105 110

Leu Thr Leu Pro Asp Leu Ala Glu Gln Phe Ala Pro Pro Asp Ile Ala
115 120 125

Pro Pro Leu Leu Ile Lys Leu Val Glu Ala Ile Glu Lys Lys Gly Leu
130 135 140

Glu Cys Ser Thr Leu Tyr Arg Thr Gln Ser Ser Ser Asn Leu Ala Glu
145 150 155 160

Leu Arg Gln Leu Leu Asp Cys Asp Thr Pro Ser Val Asp Leu Glu Met
165 170 175

Ile Asp Val His Val Leu Ala Asp Ala Phe Lys Arg Tyr Leu Leu Asp
180 185 190

Leu Pro Asn Pro Val Ile Pro Ala Ala Val Tyr Ser Glu Met Ile Ser
195 200 205

Leu Ala Pro Glu Val Gln Ser Ser Glu Glu Tyr Ile Gln Leu Leu Lys
210 215 220

Lys Leu Ile Arg Ser Pro Ser Ile Pro His Gln Tyr Trp Leu Thr Leu
225 230 235 240

Gln Tyr Leu Leu Lys His Phe Phe Lys Leu Ser Gln Thr Ser Ser Lys
245 250 255

Asn Leu Leu Asn Ala Arg Val Leu Ser Glu Ile Phe Ser Pro Met Leu
260 265 270

Phe Arg Phe Ser Ala Ala Ser Ser Asp Asn Thr Glu Asn Leu Ile Lys
275 280 285

Val Ile Glu Ile Leu Ile Ser Thr Glu Trp Asn Glu Arg Gln Pro Ala
290 295 300

Pro Ala Leu Pro Pro Lys Pro Pro Lys Pro Thr Thr Val Ala Asn Asn
305 310 315 320

Gly Met Asn Asn Asn Met Ser Leu Gln Asn Ala Glu Trp Tyr Trp Gly
325 330 335

Asp Ile Ser Arg Glu Glu Val Asn Glu Lys Leu Arg Asp Thr Ala Asp
340 345 350

Gly Thr Phe Leu Val Arg Asp Ala Ser Thr Lys Met His Gly Asp Tyr
355 360 365

Thr Leu Thr Leu Arg Lys Gly Gly Asn Asn Lys Leu Ile Lys Ile Phe
370 375 380

His Arg Asp Gly Lys Tyr Gly Phe Ser Asp Pro Leu Thr Phe Ser Ser
385 390 395 400

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Val Val Glu Leu Ile Asn His Tyr Arg Asn Glu Ser Leu Ala Gln Tyr
405 410 415

Asn Pro Lys Leu Asp Val Lys Leu Leu Tyr Pro Val Ser Lys Tyr Gln
420 425 430

Gln Asp Gln Val Val Lys Glu Asp Asn Ile Glu Ala Val Gly Lys Lys
435 440 445

Leu His Glu Tyr Asn Thr Gln Phe Gln Glu Lys Ser Arg Glu Tyr Asp
450 455 460

Arg Leu Tyr Glu Glu Tyr Thr Arg Thr Ser Gln Glu Ile Gln Met Lys
465 470 475 480

Arg Thr Ala Ile Glu Ala Phe Asn Glu Thr Ile Lys Ile Phe Glu Glu
485 490 495

Gln Cys Gln Thr Gln Glu Arg Tyr Ser Lys Glu Tyr Ile Glu Lys Phe
500 505 510

Lys Arg Glu Gly Asn Glu Lys Glu Ile Gln Arg Ile Met His Asn Tyr
515 520 525

Asp Lys Leu Lys Ser Arg Ile Ser Glu Ile Ile Asp Ser Arg Arg Arg
530 535 540

Leu Glu Glu Asp Leu Lys Lys Gln Ala Ala Glu Tyr Arg Glu Ile Asp
545 550 555 560

Lys Arg Met Asn Ser Ile Lys Pro Asp Leu Ile Gln Leu Arg Lys Thr
565 570 575

Arg Asp Gln Tyr Leu Met Trp Leu Thr Gln Lys Gly Val Arg Gln Lys
580 585 590

Lys Leu Asn Glu Trp Leu Gly Asn Glu Asn Thr Glu Asp Gln Tyr Ser
595 600 605

Leu Val Glu Asp Asp Glu Asp Leu Pro His His Asp Glu Lys Thr Trp
610 615 620

Asn Val Gly Ser Ser Asn Arg Asn Lys Ala Glu Asn Leu Leu Arg Gly
625 630 635 640

Lys Arg Asp Gly Thr Phe Leu Val Arg Glu Ser Ser Lys Gln Gly Cys
645 650 655

Tyr Ala Cys Ser Val Val Val Asp Gly Glu Val Lys His Cys Val Ile
660 665 670

Asn Lys Thr Ala Thr Gly Tyr Gly Phe Ala Glu Pro Tyr Asn Leu Tyr
675 680 685

Ser Ser Leu Lys Glu Leu Val Leu His Tyr Gln His Thr Ser Leu Val
690 695 700

Gln His Asn Asp Ser Leu Asn Val Thr Leu Ala Tyr Pro Val Tyr Ala
705 710 715 720

Gln Gln Arg Arg

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

<210> 92
 <211> 728
 <212> PRT
 <213> Homo sapiens

<400> 92

Met Ala Gly Pro Glu Gly Phe Gln Tyr Arg Ala Leu Tyr Pro Phe Arg
 1 5 10 15

Arg Glu Arg Pro Glu Asp Leu Glu Leu Leu Pro Gly Asp Val Leu Val
 20 25 30

Val Ser Arg Ala Ala Leu Gln Ala Leu Gly Val Ala Glu Gly Gly Glu
 35 40 45

Arg Cys Pro Gln Ser Val Gly Trp Met Pro Gly Leu Asn Glu Arg Thr
 50 55 60

Arg Gln Arg Gly Asp Phe Pro Gly Thr Tyr Val Glu Phe Leu Gly Pro
 65 70 75 80

Val Ala Leu Ala Arg Pro Gly Pro Arg Pro Arg Gly Pro Arg Pro Leu
 85 90 95

Pro Ala Arg Pro Arg Asp Gly Ala Pro Glu Pro Gly Leu Thr Leu Pro
 100 105 110

Asp Leu Pro Glu Gln Phe Ser Pro Pro Asp Val Ala Pro Pro Leu Leu
 115 120 125

Val Lys Leu Val Glu Ala Ile Glu Arg Thr Gly Leu Asp Ser Glu Ser
 130 135 140

His Tyr Arg Pro Glu Leu Pro Ala Pro Arg Thr Asp Trp Ser Leu Ser
 145 150 155 160

Asp Val Asp Gln Trp Asp Thr Ala Ala Leu Ala Asp Gly Ile Lys Ser
 165 170 175

Phe Leu Leu Ala Leu Pro Ala Pro Leu Val Thr Pro Glu Ala Ser Ala
 180 185 190

Glu Ala Arg Arg Ala Leu Arg Glu Ala Ala Gly Pro Val Gly Pro Ala
 195 200 205

Leu Glu Pro Pro Thr Leu Pro Leu His Arg Ala Leu Thr Leu Arg Phe
 210 215 220

Leu Leu Gln His Leu Gly Arg Val Ala Arg Arg Ala Pro Ala Leu Gly
 225 230 235 240

Pro Ala Val Arg Ala Leu Gly Ala Thr Phe Gly Pro Leu Leu Leu Arg
 245 250 255

Ala Pro Pro Pro Pro Ser Ser Pro Pro Gly Gly Ala Pro Asp Gly
 260 265 270

Ser Glu Pro Ser Pro Asp Phe Pro Ala Leu Leu Val Glu Lys Leu Leu
 275 280 285

Gln Glu His Leu Glu Glu Gln Glu Val Ala Pro Pro Ala Leu Pro Pro
 290 295 300

Lys pro Pro Lys Ala Lys Pro Ala Pro Thr Val Leu Ala Asn Gly Gly
 305 310 315 320

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ser Pro Pro Ser Leu Gln Asp Ala Glu Trp Tyr Trp Gly Asp Ile Ser
325 330 335

Arg Glu Glu Val Asn Glu Lys Leu Arg Asp Thr Pro Asp Gly Thr Phe
340 345 350

Leu Val Arg Asp Ala Ser Ser Lys Ile Gln Gly Glu Tyr Thr Leu Thr
355 360 365

Leu Arg Lys Gly Gly Asn Asn Lys Leu Ile Lys Val Phe His Arg Asp
370 375 380

Gly His Tyr Gly Phe Ser Glu Pro Leu Thr Phe Cys Ser Val Val Asp
385 390 395 400

Leu Ile Asn His Tyr Arg His Glu Ser Leu Ala Gln Tyr Asn Ala Lys
405 410 415

Leu Asp Thr Arg Leu Leu Tyr Pro Val Ser Lys Tyr Gln Gln Asp Gln
420 425 430

Ile Val Lys Glu Asp Ser Val Glu Ala Val Gly Ala Gln Leu Lys Val
435 440 445

Tyr His Gln Gln Tyr Gln Asp Lys Ser Arg Glu Tyr Asp Gln Leu Tyr
450 455 460

Glu Glu Tyr Thr Arg Thr Ser Gln Glu Leu Gln Met Lys Arg Thr Ala
465 470 475 480

Ile Glu Ala Phe Asn Glu Thr Ile Lys Ile Phe Glu Glu Gln Gly Gln
485 490 495

Thr Gln Glu Lys Cys Ser Lys Glu Tyr Leu Glu Arg Phe Arg Arg Glu
500 505 510

Gly Asn Glu Lys Glu Met Gln Arg Ile Leu Leu Asn Ser Glu Arg Leu
515 520 525

Lys Ser Arg Ile Ala Glu Ile His Glu Ser Arg Thr Lys Leu Glu Gln
530 535 540

Gln Leu Arg Ala Gln Ala Ser Asp Asn Arg Glu Ile Asp Lys Arg Met
545 550 555 560

Asn Ser Leu Lys Pro Asp Leu Met Gln Leu Arg Lys Ile Arg Asp Gln
565 570 575

Tyr Leu Val Trp Leu Thr Gln Lys Gly Ala Arg Gln Lys Lys Ile Asn
580 585 590

Glu Trp Leu Gly Ile Lys Asn Glu Thr Glu Asp Gln Tyr Ala Leu Met
595 600 605

Glu Asp Glu Asp Asp Leu Pro His His Glu Glu Arg Thr Trp Tyr Val
610 615 620

Gly Lys Ile Asn Arg Thr Gln Ala Glu Glu Met Leu Ser Gly Lys Arg
625 630 635 640

Asp Gly Thr Phe Leu Ile Arg Glu Ser Ser Gln Arg Gly Cys Tyr Ala
645 650 655

Cys ser Val Val Val Asp Gly Asp Thr Lys His Cys Val Ile Tyr Arg

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 660 665 670

Thr Ala Thr Gly Phe Gly Phe Ala Glu Pro Tyr Asn Leu Tyr Gly Ser
 675 680 685

Leu Lys Glu Leu Val Leu His Tyr Gln His Ala Ser Leu Val Gln His
 690 695 700

Asn Asp Ala Leu Thr Val Thr Leu Ala His Pro Val Arg Ala Pro Gly
 705 710 715 720

Pro Gly Pro Pro Pro Ala Ala Arg
 725

<210> 93
 <211> 534
 <212> PRT
 <213> Homo sapiens

<400> 93

Met Ile Trp Tyr Ile Leu Ile Ile Gly Ile Leu Leu Pro Gln Ser Leu
 1 5 10 15

Ala His Pro Gly Phe Phe Thr Ser Ile Gly Gln Met Thr Asp Leu Ile
 20 25 30

His Thr Glu Lys Asp Leu Val Thr Ser Leu Lys Asp Tyr Ile Lys Ala
 35 40 45

Glu Glu Asp Lys Leu Glu Gln Ile Lys Lys Trp Ala Glu Lys Leu Asp
 50 55 60

Arg Leu Thr Ser Thr Ala Thr Lys Asp Pro Glu Gly Phe Val Gly His
 65 70 75 80

Pro Val Asn Ala Phe Lys Leu Met Lys Arg Leu Asn Thr Glu Trp Ser
 85 90 95

Glu Leu Glu Asn Leu Val Leu Lys Asp Met Ser Asp Gly Phe Ile Ser
 100 105 110

Asn Leu Thr Ile Gln Arg Pro Val Leu Ser Asn Asp Glu Asp Gln Val
 115 120 125

Gly Ala Ala Lys Ala Leu Leu Arg Leu Gln Asp Thr Tyr Asn Leu Asp
 130 135 140

Thr Asp Thr Ile Ser Lys Gly Asn Leu Pro Gly Val Lys His Lys Ser
 145 150 155 160

Phe Leu Thr Ala Glu Asp Cys Phe Glu Leu Gly Lys Val Ala Tyr Thr
 165 170 175

Glu Ala Asp Tyr Tyr His Thr Glu Leu Trp Met Glu Gln Ala Leu Arg
 180 185 190

Gln Leu Asp Glu Gly Glu Ile Ser Thr Ile Asp Lys Val Ser Val Leu
 195 200 205

Asp Tyr Leu Ser Tyr Ala Val Tyr Gln Gln Gly Asp Leu Asp Lys Ala
 210 215 220

Leu Leu Leu Thr Lys Lys Leu Leu Glu Leu Asp Pro Glu His Gln Arg
 225 230 235 240

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ala Asn Gly Asn Leu Lys Tyr Phe Glu Tyr Ile Met Ala Lys Glu Lys
 245 250 255

Asp Val Asn Lys Ser Ala Ser Asp Asp Gln Ser Asp Gln Lys Thr Thr
 260 265 270

Pro Lys Lys Lys Gly Val Ala Val Asp Tyr Leu Pro Glu Arg Gln Lys
 275 280 285

Tyr Glu Met Leu Cys Arg Gly Glu Gly Ile Lys Met Thr Pro Arg Arg
 290 295 300

Gln Lys Lys Leu Phe Cys Arg Tyr His Asp Gly Asn Arg Asn Pro Lys
 305 310 315 320

Phe Ile Leu Ala Pro Ala Lys Gln Glu Asp Glu Trp Asp Lys Pro Arg
 325 330 335

Ile Ile Arg Phe His Asp Ile Ile Ser Asp Ala Glu Ile Glu Ile Val
 340 345 350

Lys Asp Leu Ala Lys Pro Arg Leu Ser Arg Ala Thr Val His Asp Pro
 355 360 365

Glu Thr Gly Lys Leu Thr Thr Ala Gln Tyr Arg Val Ser Lys Ser Ala
 370 375 380

Trp Leu Ser Gly Tyr Glu Asn Pro Val Val Ser Arg Ile Asn Met Arg
 385 390 395 400

Ile Gln Asp Leu Thr Gly Leu Asp Val Ser Thr Ala Glu Glu Leu Gln
 405 410 415

Val Ala Asn Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe
 420 425 430

Ala Arg Lys Asp Glu Pro Asp Ala Phe Lys Glu Leu Gly Thr Gly Asn
 435 440 445

Arg Ile Ala Thr Trp Leu Phe Tyr Met Ser Asp Val Ser Ala Gly Gly
 450 455 460

Ala Thr Val Phe Pro Glu Val Gly Ala Ser Val Trp Pro Lys Lys Gly
 465 470 475 480

Thr Ala Val Phe Trp Tyr Asn Leu Phe Ala Ser Gly Glu Gly Asp Tyr
 485 490 495

Ser Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Asn Lys Trp Val
 500 505 510

Ser Asn Lys Trp Leu His Glu Arg Gly Gln Glu Phe Arg Arg Pro Cys
 515 520 525

Thr Leu Ser Glu Leu Glu
 530

<210> 94
 <211> 389
 <212> PRT
 <213> Homo sapiens

<400> 94

Met Leu Ser Leu Arg Val Pro Leu Ala Pro Ile Thr Asp Pro Gln Gln
 1 5 10 15

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Leu Gln Leu Ser Pro Leu Lys Gly Leu Ser Leu Val Asp Lys Glu Asn
20 25 30

Thr Pro Pro Ala Leu Ser Gly Thr Arg Val Leu Ala Ser Lys Thr Ala
35 40 45

Arg Arg Ile Phe Gln Glu Pro Thr Glu Pro Lys Thr Lys Ala Ala Ala
50 55 60

Pro Gly Val Glu Asp Glu Pro Leu Leu Arg Glu Asn Pro Arg Arg Phe
65 70 75 80

Val Ile Phe Pro Ile Glu Tyr His Asp Ile Trp Gln Met Tyr Lys Lys
85 90 95

Ala Glu Ala Ser Phe Trp Thr Ala Glu Glu Val Asp Leu Ser Lys Asp
100 105 110

Ile Gln His Trp Glu Ser Leu Lys Pro Glu Glu Arg Tyr Phe Ile Ser
115 120 125

His Val Leu Ala Phe Phe Ala Ala Ser Asp Gly Ile Val Asn Glu Asn
130 135 140

Leu Val Glu Arg Phe Ser Gln Glu Val Gln Ile Thr Glu Ala Arg Cys
145 150 155 160

Phe Tyr Gly Phe Gln Ile Ala Met Glu Asn Ile His Ser Glu Met Tyr
165 170 175

Ser Leu Leu Ile Asp Thr Tyr Ile Lys Asp Pro Lys Glu Arg Glu Phe
180 185 190

Leu Phe Asn Ala Ile Glu Thr Met Pro Cys Val Lys Lys Lys Ala Asp
195 200 205

Trp Ala Leu Arg Trp Ile Gly Asp Lys Glu Ala Thr Tyr Gly Glu Arg
210 215 220

Val Val Ala Phe Ala Ala Val Glu Gly Ile Phe Phe Ser Gly Ser Phe
225 230 235 240

Ala Ser Ile Phe Trp Leu Lys Lys Arg Gly Leu Met Pro Gly Leu Thr
245 250 255

Phe Ser Asn Glu Leu Ile Ser Arg Asp Glu Gly Leu His Cys Asp Phe
260 265 270

Ala Cys Leu Met Phe Lys His Leu Val His Lys Pro Ser Glu Glu Arg
275 280 285

Val Arg Glu Ile Ile Ile Asn Ala Val Arg Ile Glu Gln Glu Phe Leu
290 295 300

Thr Glu Ala Leu Pro Val Lys Leu Ile Gly Met Asn Cys Thr Leu Met
305 310 315 320

Lys Gln Tyr Ile Glu Phe Val Ala Asp Arg Leu Met Leu Glu Leu Gly
325 330 335

Phe Ser Lys Val Phe Arg Val Glu Asn Pro Phe Asp Phe Met Glu Asn
340 345 350

Ile ser Leu Glu Gly Lys Thr Asn Phe Phe Glu Lys Arg Val Gly Glu

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 355 360 365

Tyr Gln Arg Met Gly Val Met Ser Ser Pro Thr Glu Asn Ser Phe Thr
 370 375 380

Leu Asp Ala Asp Phe
 385

<210> 95
 <211> 794
 <212> PRT
 <213> Homo sapiens

<400> 95

Met Arg Val Arg Ile Gly Leu Thr Leu Leu Cys Ala Val Leu Leu
 1 5 10 15

Ser Leu Ala Ser Ala Ser Ser Asp Glu Glu Gly Ser Gln Asp Glu Ser
 20 25 30

Leu Asp Ser Lys Thr Thr Leu Thr Ser Asp Glu Ser Val Lys Asp His
 35 40 45

Thr Thr Ala Gly Arg Val Val Ala Gly Gln Ile Phe Leu Asp Ser Glu
 50 55 60

Glu Ser Glu Leu Glu Ser Ser Ile Gln Glu Glu Glu Asp Ser Leu Lys
 65 70 75 80

Ser Gln Glu Gly Glu Ser Val Thr Glu Asp Ile Ser Phe Leu Glu Ser
 85 90 95

Pro Asn Pro Glu Asn Lys Asp Tyr Glu Glu Pro Lys Lys Val Arg Lys
 100 105 110

Pro Ala Leu Thr Ala Ile Glu Gly Thr Ala His Gly Glu Pro Cys His
 115 120 125

Phe Pro Phe Leu Phe Leu Asp Lys Glu Tyr Asp Glu Cys Thr Ser Asp
 130 135 140

Gly Arg Glu Asp Gly Arg Leu Trp Cys Ala Thr Thr Tyr Asp Tyr Lys
 145 150 155 160

Ala Asp Glu Lys Trp Gly Phe Cys Glu Thr Glu Glu Glu Ala Ala Lys
 165 170 175

Arg Arg Gln Met Gln Glu Ala Glu Met Met Tyr Gln Thr Gly Met Lys
 180 185 190

Ile Leu Asn Gly Ser Asn Lys Lys Ser Gln Lys Arg Glu Ala Tyr Arg
 195 200 205

Tyr Leu Gln Lys Ala Ala Ser Met Asn His Thr Lys Ala Leu Glu Arg
 210 215 220

Val Ser Tyr Ala Leu Leu Phe Gly Asp Tyr Leu Pro Gln Asn Ile Gln
 225 230 235 240

Ala Ala Arg Glu Met Phe Glu Lys Leu Thr Glu Glu Gly Ser Pro Lys
 245 250 255

Gly Gln Thr Ala Leu Gly Phe Leu Tyr Ala Ser Gly Leu Gly Val Asn
 260 265 270

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 Ser Ser Gln Ala Lys Ala Leu Val Tyr Tyr Thr Phe Gly Ala Leu Gly
 275 280 285

Gly Asn Leu Ile Ala His Met Val Leu Gly Tyr Arg Tyr Trp Ala Gly
 290 295 300

Ile Gly Val Leu Gln Ser Cys Glu Ser Ala Leu Thr His Tyr Arg Leu
 305 310 315 320

Val Ala Asn His Val Ala Ser Asp Ile Ser Leu Thr Gly Gly Ser Val
 325 330 335

Val Gln Arg Ile Arg Leu Pro Asp Glu Val Glu Asn Pro Gly Met Asn
 340 345 350

Ser Gly Met Leu Glu Glu Asp Leu Ile Gln Tyr Tyr Gln Phe Leu Ala
 355 360 365

Glu Lys Gly Asp Val Gln Ala Gln Val Gly Leu Gly Gln Leu His Leu
 370 375 380

His Gly Gly Arg Gly Val Glu Gln Asn His Gln Arg Ala Phe Asp Tyr
 385 390 395 400

Phe Asn Leu Ala Ala Asn Ala Gly Asn Ser His Ala Met Ala Phe Leu
 405 410 415

Gly Lys Met Tyr Ser Glu Gly Ser Asp Ile Val Pro Gln Ser Asn Glu
 420 425 430

Thr Ala Leu His Tyr Phe Lys Lys Ala Ala Asp Met Gly Asn Pro Val
 435 440 445

Gly Gln Ser Gly Leu Gly Met Ala Tyr Leu Tyr Gly Arg Gly Val Gln
 450 455 460

Val Asn Tyr Asp Leu Ala Leu Lys Tyr Phe Gln Lys Ala Ala Glu Gln
 465 470 475 480

Gly Trp Val Asp Gly Gln Leu Gln Leu Gly Ser Met Tyr Tyr Asn Gly
 485 490 495

Ile Gly Val Lys Arg Asp Tyr Lys Gln Ala Leu Lys Tyr Phe Asn Leu
 500 505 510

Ala ser Gln Gly Gly His Ile Leu Ala Phe Tyr Asn Leu Ala Gln Met
 515 520 525

His Ala Ser Gly Thr Gly Val Met Arg Ser Cys His Thr Ala Val Glu
 530 535 540

Leu phe Lys Asn Val Cys Glu Arg Gly Arg Trp Ser Glu Arg Leu Met
 545 550 555 560

Thr Ala Tyr Asn Ser Tyr Lys Asp Gly Asp Tyr Asn Ala Ala Val Ile
 565 570 575

Gln Tyr Leu Leu Leu Ala Glu Gln Gly Tyr Glu Val Ala Gln Ser Asn
 580 585 590

Ala Ala Phe Ile Leu Asp Gln Arg Glu Ala Ser Ile Val Gly Glu Asn
 595 600 605

Glu Thr Tyr Pro Arg Ala Leu Leu His Trp Asn Arg Ala Ala Ser Gln
 610 615 620

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Gly Tyr Thr Val Ala Arg Ile Lys Leu Gly Asp Tyr His Phe Tyr Gly
625 630 635 640

Phe Gly Thr Asp Val Asp Tyr Glu Thr Ala Phe Ile His Tyr Arg Leu
645 650 655

Ala Ser Glu Gln Gln His Ser Ala Gln Ala Met Phe Asn Leu Gly Tyr
660 665 670

Met His Glu Lys Gly Leu Gly Ile Lys Gln Asp Ile His Leu Ala Lys
675 680 685

Arg Phe Tyr Asp Met Ala Ala Glu Ala Ser Pro Asp Ala Gln Val Pro
690 695 700

Val Phe Leu Ala Leu Cys Lys Leu Gly Val Val Tyr Phe Leu Gln Tyr
705 710 715 720

Ile Arg Glu Thr Asn Ile Arg Asp Met Phe Thr Gln Leu Asp Met Asp
725 730 735

Gln Leu Leu Gly Pro Glu Trp Asp Leu Tyr Leu Met Thr Ile Ile Ala
740 745 750

Leu Leu Leu Gly Thr Val Ile Ala Tyr Arg Gln Arg Gln His Gln Asp
755 760 765

Met Pro Ala Pro Arg Pro Pro Gly Pro Arg Pro Ala Pro Pro Gln Gln
770 775 780

Glu Gly Pro Pro Glu Gln Gln Pro Pro Gln
785 790

<210> 96
<211> 583
<212> PRT
<213> Homo sapiens

<400> 96

Met Asp Leu Leu Pro Pro Lys Pro Lys Tyr Asn Pro Leu Arg Asn Glu
1 5 10 15

Ser Leu Ser Ser Leu Glu Glu Gly Ala Ser Gly Ser Thr Pro Pro Glu
20 25 30

Glu Leu Pro Ser Pro Ser Ala Ser Ser Leu Gly Pro Ile Leu Pro Pro
35 40 45

Leu Pro Gly Asp Asp Ser Pro Thr Thr Leu Cys Ser Phe Phe Pro Arg
50 55 60

Met Ser Asn Leu Arg Leu Ala Asn Pro Ala Gly Gly Arg Pro Gly Ser
65 70 75 80

Lys Gly Glu Pro Gly Arg Ala Ala Asp Asp Gly Glu Gly Ile Asp Gly
85 90 95

Ala Ala Met Pro Glu Ser Gly Pro Leu Pro Leu Leu Gln Asp Met Asn
100 105 110

Lys Leu Ser Gly Gly Gly Gly Arg Arg Thr Arg Val Glu Gly Gly Gln
115 120 125

Leu Gly Gly Glu Glu Trp Thr Arg His Gly Ser Phe Val Asn Lys Pro

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Thr Arg Gly Trp Leu His Pro Asn Asp Lys Val Met Gly Pro Gly Val
 130 135 140 145 150 155 160
 Ser Tyr Leu Val Arg Tyr Met Gly Cys Val Glu Val Leu Gln Ser Met
 165 170 175
 Arg Ala Leu Asp Phe Asn Thr Arg Thr Gln Val Thr Arg Glu Ala Ile
 180 185 190
 Ser Leu Val Cys Glu Ala Val Pro Gly Ala Lys Gly Ala Thr Arg Arg
 195 200 205
 Arg Lys Pro Cys Ser Arg Pro Leu Ser Ser Ile Leu Gly Arg Ser Asn
 210 215 220
 Leu Lys Phe Ala Gly Met Pro Ile Thr Leu Thr Val Ser Thr Ser Ser
 225 230 235 240
 Leu Asn Leu Met Ala Ala Asp Cys Lys Gln Ile Ile Ala Asn His His
 245 250 255
 Met Gln Ser Ile Ser Phe Ala Ser Gly Gly Asp Pro Asp Thr Ala Glu
 260 265 270
 Tyr Val Ala Tyr Val Ala Lys Asp Pro Val Asn Gln Arg Ala Cys His
 275 280 285
 Ile Leu Glu Cys Pro Glu Gly Leu Ala Gln Asp Val Ile Ser Thr Ile
 290 295 300
 Gly Gln Ala Phe Glu Leu Arg Phe Lys Gln Tyr Leu Arg Asn Pro Pro
 305 310 315 320
 Lys Leu Val Thr Pro His Asp Arg Met Ala Gly Phe Asp Gly Ser Ala
 325 330 335
 Trp Asp Glu Glu Glu Glu Pro Pro Asp His Gln Tyr Tyr Asn Asp
 340 345 350
 Phe Pro Gly Lys Glu Pro Pro Leu Gly Gly Val Val Asp Met Arg Leu
 355 360 365
 Arg Glu Gly Ala Ala Pro Gly Ala Ala Arg Pro Thr Ala Pro Asn Ala
 370 375 380
 Gln Thr Pro Ser His Leu Gly Ala Thr Leu Pro Val Gly Gln Pro Val
 385 390 395 400
 Gly Gly Asp Pro Glu Val Arg Lys Gln Met Pro Pro Pro Pro Cys
 405 410 415
 Pro Gly Arg Glu Leu Phe Asp Asp Pro Ser Tyr Val Asn Val Gln Asn
 420 425 430
 Leu Asp Lys Ala Arg Gln Ala Val Gly Gly Ala Gly Pro Pro Asn Pro
 435 440 445
 Ala Ile Asn Gly Ser Ala Pro Arg Asp Leu Phe Asp Met Lys Pro Phe
 450 455 460
 Glu Asp Ala Leu Arg Val Pro Pro Pro Pro Gln Ser Val Ser Met Ala
 465 470 475 480

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Glu Gln Leu Arg Gly Glu Pro Trp Phe His Gly Lys Leu Ser Arg Arg
485 490 495

Glu Ala Glu Ala Leu Leu Gln Leu Asn Gly Asp Phe Leu Val Arg Glu
500 505 510

Ser Thr Thr Thr Pro Gly Gln Tyr Val Leu Thr Gly Leu Gln Ser Gly
515 520 525

Gln Pro Lys His Leu Leu Leu Val Asp Pro Glu Gly Val Val Arg Thr
530 535 540

Lys Asp His Arg Phe Glu Ser Val Ser His Leu Ile Ser Tyr His Met
545 550 555 560

Asp Asn His Leu Pro Ile Ile Ser Ala Gly Ser Glu Leu Cys Leu Gln
565 570 575

Gln Pro Val Glu Arg Lys Leu
580

<210> 97
<211> 238
<212> PRT
<213> Homo sapiens

<400> 97

Met Met Leu Met Ala Phe His Leu Tyr Leu Pro Met Val Glu Val Met
1 5 10 15

Ser Tyr Leu Thr His Glu Phe Gly Arg Thr Leu Pro Phe Gly Ala Ser
20 25 30

Arg Pro Tyr Lys Gln Met Gly Ala Gly Leu Leu Ser Gln Pro Val Gly
35 40 45

Leu Leu Ala Gly Gly Val Val Thr Ala Ile Ser Lys Ala Ala Gly Ala
50 55 60

Pro Ile Glu Trp Leu Lys Leu Leu Leu Gln Val Gln His Ala Thr Lys
65 70 75 80

Glu Ile Thr Thr Asp Lys Gln Tyr Lys His Ile Ile Asp Cys Val Val
85 90 95

Cys Ile Pro Lys Glu Glu Arg Val Leu Ser Phe Trp Arg Gly Ala Leu
100 105 110

Asn Phe Ala Phe Glu Ile Ser Thr Ser Arg Ser Ser Trp Val Val Trp
115 120 125

Thr Arg Gly Pro Thr Phe Ser Thr Met Leu Gln Gly Thr Trp His Gln
130 135 140

Ala Cys Ala Gly Ala Thr Ser Leu Cys Phe Val Tyr Pro Leu Asp Phe
145 150 155 160

Val Cys Thr Asn Leu Pro Val Asp Val Gly Lys Ala Gly Ala Lys Arg
165 170 175

Glu Phe Arg Ser Leu Gly Asp Cys Leu Val Lys Ile Tyr Lys Ser Asn
180 185 190

Arg Ile Lys Gly Leu His Gln Gly Phe Thr Met Ser Val Gln Gly Ile
195 200 205

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ser Ile Tyr Pro Ala Ala Tyr Phe Ser Ile Cys Asp Thr Ala Lys Gly
210 215 220

Met Leu Pro Asp Ser Lys Ser Thr Thr Ser Ser Ser Ala Glu
225 230 235

<210> 98
<211> 337
<212> PRT
<213> Homo sapiens

<400> 98

Met Ser Leu Glu Gln Glu Glu Thr Gln Pro Gly Arg Leu Leu Gly
1 5 10 15

Arg Arg Asp Ala Val Pro Ala Phe Ile Glu Pro Asn Val Arg Phe Trp
20 25 30

Ile Thr Glu Arg Gln Ser Phe Ile Arg Arg Phe Leu Gln Trp Thr Glu
35 40 45

Leu Leu Asp Pro Thr Asn Val Phe Ile Ser Val Glu Ser Ile Glu Asn
50 55 60

Ser Arg Gln Leu Leu Cys Thr Asn Glu Asp Val Ser Ser Pro Ala Ser
65 70 75 80

Ala Asp Gln Arg Ile Gln Glu Ala Trp Lys Arg Ser Leu Ala Thr Val
85 90 95

His Pro Asp Ser Ser Asn Leu Ile Pro Lys Leu Phe Arg Pro Ala Ala
100 105 110

Phe Leu Pro Phe Met Ala Pro Thr Val Phe Leu Ser Met Thr Pro Leu
115 120 125

Lys Gly Ile Lys Ser Val Ile Leu Pro Gln Val Phe Leu Cys Ala Tyr
130 135 140

Met Ala Ala Phe Asn Ser Ile Asn Gly Asn Arg Ser Tyr Thr Cys Lys
145 150 155 160

Pro Leu Glu Arg Ser Leu Leu Met Ala Gly Ala Val Ala Ser Ser Thr
165 170 175

Phe Leu Gly Val Ile Pro Gln Phe Val Gln Met Lys Tyr Gly Leu Thr
180 185 190

Gly Pro Trp Ile Lys Arg Leu Leu Pro Val Ile Phe Leu Val Gln Ala
195 200 205

Ser Gly Met Asn Val Tyr Met Ser Arg Ser Leu Glu Ser Ile Lys Gly
210 215 220

Ile Ala Val Met Asp Lys Glu Gly Asn Val Leu Gly His Ser Arg Ile
225 230 235 240

Ala Gly Thr Lys Ala Val Arg Glu Thr Leu Ala Ser Arg Ile Val Leu
245 250 255

Phe Gly Thr Ser Ala Leu Ile Pro Glu Val Phe Thr Tyr Phe Phe Lys
260 265 270

Arg Thr Gln Tyr Phe Arg Lys Asn Pro Gly Ser Leu Trp Ile Leu Lys

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 275 280 285

Leu Ser Cys Thr Val Leu Ala Met Gly Leu Met Val Pro Phe Ser Phe
 290 295 300

Ser Ile Phe Pro Gln Ile Gly Gln Ile Gln Tyr Cys Ser Leu Glu Glu
 305 310 315 320

Lys Ile Gln Ser Pro Thr Glu Glu Thr Glu Ile Phe Tyr His Arg Gly
 325 330 335

Val

<210> 99
 <211> 654
 <212> PRT
 <213> Homo sapiens

<400> 99

Met Asn Gly His Leu Glu Ala Glu Glu Gln Gln Asp Gln Arg Pro Asp
 1 5 10 15

Gln Glu Leu Thr Gly Ser Trp Gly His Gly Pro Arg Ser Thr Leu Val
 20 25 30

Arg Ala Lys Ala Met Ala Pro Pro Pro Pro Pro Leu Ala Ala Ser Thr
 35 40 45

Pro Leu Leu His Gly Glu Phe Gly Ser Tyr Pro Ala Arg Gly Pro Arg
 50 55 60

Phe Ala Leu Thr Leu Thr Ser Gln Ala Leu His Ile Gln Arg Leu Arg
 65 70 75 80

Pro Lys Pro Glu Ala Arg Pro Arg Gly Gly Leu Val Pro Leu Ala Glu
 85 90 95

Val Ser Gly Cys Cys Thr Leu Arg Ser Arg Ser Pro Ser Asp Ser Ala
 100 105 110

Ala Tyr Phe Cys Ile Tyr Thr Tyr Pro Arg Gly Arg Arg Gly Ala Arg
 115 120 125

Arg Arg Ala Thr Arg Thr Phe Arg Ala Asp Gly Ala Ala Thr Tyr Glu
 130 135 140

Glu Asn Arg Ala Glu Ala Gln Arg Trp Ala Thr Ala Leu Thr Cys Leu
 145 150 155 160

Leu Arg Gly Leu Pro Leu Pro Gly Asp Gly Glu Ile Thr Pro Asp Leu
 165 170 175

Leu Pro Arg Pro Pro Arg Leu Leu Leu Leu Val Asn Pro Phe Gly Gly
 180 185 190

Arg Gly Leu Ala Trp Gln Trp Cys Lys Asn His Val Leu Pro Met Ile
 195 200 205

Ser Glu Ala Gly Leu Ser Phe Asn Leu Ile Gln Thr Glu Arg Gln Asn
 210 215 220

His Ala Arg Glu Leu Val Gln Gly Leu Ser Leu Ser Glu Trp Asp Gly
 225 230 235 240

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ile Val Thr Val Ser Gly Asp Gly Leu Leu His Glu Val Leu Asn Gly
 245 250 255
 Leu Leu Asp Arg Pro Asp Trp Glu Glu Ala Val Lys Met Pro Val Gly
 260 265 270
 Ile Leu Pro Cys Gly Ser Gly Asn Ala Leu Ala Gly Ala Val Asn Gln
 275 280 285
 His Gly Gly Phe Glu Pro Ala Leu Gly Leu Asp Leu Leu Leu Asn Cys
 290 295 300
 Ser Leu Leu Leu Cys Arg Gly Gly Gly His Pro Leu Asp Leu Leu Ser
 305 310 315 320
 Val Thr Leu Ala Ser Gly Ser Arg Cys Phe Ser Phe Leu Ser Val Ala
 325 330 335
 Trp Gly Phe Val Ser Asp Val Asp Ile Gln Ser Glu Arg Phe Arg Ala
 340 345 350
 Leu Gly Ser Ala Arg Phe Thr Leu Gly Thr Val Leu Gly Leu Ala Thr
 355 360 365
 Leu His Thr Tyr Arg Gly Arg Leu Ser Tyr Leu Pro Ala Thr Val Glu
 370 375 380
 Pro Ala Ser Pro Thr Pro Ala His Ser Leu Pro Arg Ala Lys Ser Glu
 385 390 395 400
 Leu Thr Leu Thr Pro Asp Pro Ala Pro Pro Met Ala His Ser Pro Leu
 405 410 415
 His Arg Ser Val Ser Asp Leu Pro Leu Pro Leu Pro Gln Pro Ala Leu
 420 425 430
 Ala Ser Pro Gly Ser Pro Glu Pro Leu Pro Ile Leu Ser Leu Asn Gly
 435 440 445
 Gly Gly Pro Glu Leu Ala Gly Asp Trp Gly Gly Ala Gly Asp Ala Pro
 450 455 460
 Leu Ser Pro Asp Pro Leu Leu Ser Ser Pro Pro Gly Ser Pro Lys Ala
 465 470 475 480
 Ala Leu His Ser Pro Val Ser Glu Gly Ala Pro Val Ile Pro Pro Ser
 485 490 495
 Ser Gly Leu Pro Leu Pro Thr Pro Asp Ala Arg Val Gly Ala Ser Thr
 500 505 510
 Cys Gly Pro Pro Asp His Leu Leu Pro Pro Leu Gly Thr Pro Leu Pro
 515 520 525
 Pro Asp Trp Val Thr Leu Glu Gly Asp Phe Val Leu Met Leu Ala Ile
 530 535 540
 Ser Pro Ser His Leu Gly Ala Asp Leu Val Ala Ala Pro His Ala Arg
 545 550 555 560
 Phe Asp Asp Gly Leu Val His Leu Cys Trp Val Arg Ser Gly Ile Ser
 565 570 575
 Arg Ala Ala Leu Leu Arg Leu Phe Leu Ala Met Glu Arg Gly Ser His
 580 585 590

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Phe Ser Leu Gly Cys Pro Gln Leu Gly Tyr Ala Ala Ala Arg Ala Phe
595 600 605

Arg Leu Glu Pro Leu Thr Pro Arg Gly Val Leu Thr Val Asp Gly Glu
610 615 620

Gln Val Glu Tyr Gly Pro Leu Gln Ala Gln Met His Pro Gly Ile Gly
625 630 635 640

Thr Leu Leu Thr Gly Pro Pro Gly Cys Pro Gly Arg Glu Pro
645 650

<210> 100
<211> 760
<212> PRT
<213> Homo sapiens

<400> 100

Met Met Asp Gln Ala Arg Ser Ala Phe Ser Asn Leu Phe Gly Gly Glu
1 5 10 15

Pro Leu Ser Tyr Thr Arg Phe Ser Leu Ala Arg Gln Val Asp Gly Asp
20 25 30

Asn Ser His Val Glu Met Lys Leu Ala Val Asp Glu Glu Glu Asn Ala
35 40 45

Asp Asn Asn Thr Lys Ala Asn Val Thr Lys Pro Lys Arg Cys Ser Gly
50 55 60

Ser Ile Cys Tyr Gly Thr Ile Ala Val Ile Val Phe Phe Leu Ile Gly
65 70 75 80

Phe Met Ile Gly Tyr Leu Gly Tyr Cys Lys Gly Val Glu Pro Lys Thr
85 90 95

Glu Cys Glu Arg Leu Ala Gly Thr Glu Ser Pro Val Arg Glu Glu Pro
100 105 110

Gly Glu Asp Phe Pro Ala Ala Arg Arg Leu Tyr Trp Asp Asp Leu Lys
115 120 125

Arg Lys Leu Ser Glu Lys Leu Asp Ser Thr Asp Phe Thr Gly Thr Ile
130 135 140

Lys Leu Leu Asn Glu Asn Ser Tyr Val Pro Arg Glu Ala Gly Ser Gln
145 150 155 160

Lys Asp Glu Asn Leu Ala Leu Tyr Val Glu Asn Gln Phe Arg Glu Phe
165 170 175

Lys Leu Ser Lys Val Trp Arg Asp Gln His Phe Val Lys Ile Gln Val
180 185 190

Lys Asp Ser Ala Gln Asn Ser Val Ile Ile Val Asp Lys Asn Gly Arg
195 200 205

Leu Val Tyr Leu Val Glu Asn Pro Gly Gly Tyr Val Ala Tyr Ser Lys
210 215 220

Ala Ala Thr Val Thr Gly Lys Leu Val His Ala Asn Phe Gly Thr Lys
225 230 235 240

Lys Asp Phe Glu Asp Leu Tyr Thr Pro Val Asn Gly Ser Ile Val Ile

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 245 250 255

Val Arg Ala Gly Lys Ile Thr Phe Ala Glu Lys Val Ala Asn Ala Glu
 260 265 270

Ser Leu Asn Ala Ile Gly Val Leu Ile Tyr Met Asp Gln Thr Lys Phe
 275 280 285

Pro Ile Val Asn Ala Glu Leu Ser Phe Phe Gly His Ala His Leu Gly
 290 295 300

Thr Gly Asp Pro Tyr Thr Pro Gly Phe Pro Ser Phe Asn His Thr Gln
 305 310 315 320

Phe Pro Pro Ser Arg Ser Ser Gly Leu Pro Asn Ile Pro Val Gln Thr
 325 330 335

Ile Ser Arg Ala Ala Ala Glu Lys Leu Phe Gly Asn Met Glu Gly Asp
 340 345 350

Cys Pro Ser Asp Trp Lys Thr Asp Ser Thr Cys Arg Met Val Thr Ser
 355 360 365

Glu Ser Lys Asn Val Lys Leu Thr Val Ser Asn Val Leu Lys Glu Ile
 370 375 380

Lys Ile Leu Asn Ile Phe Gly Val Ile Lys Gly Phe Val Glu Pro Asp
 385 390 395 400

His Tyr Val Val Val Gly Ala Gln Arg Asp Ala Trp Gly Pro Gly Ala
 405 410 415

Ala Lys Ser Gly Val Gly Thr Ala Leu Leu Leu Lys Leu Ala Gln Met
 420 425 430

Phe Ser Asp Met Val Leu Lys Asp Gly Phe Gln Pro Ser Arg Ser Ile
 435 440 445

Ile Phe Ala Ser Trp Ser Ala Gly Asp Phe Gly Ser Val Gly Ala Thr
 450 455 460

Glu Trp Leu Glu Gly Tyr Leu Ser Ser Leu His Leu Lys Ala Phe Thr
 465 470 475 480

Tyr Ile Asn Leu Asp Lys Ala Val Leu Gly Thr Ser Asn Phe Lys Val
 485 490 495

Ser Ala Ser Pro Leu Leu Tyr Thr Leu Ile Glu Lys Thr Met Gln Asn
 500 505 510

Val Lys His Pro Val Thr Gly Gln Phe Leu Tyr Gln Asp Ser Asn Trp
 515 520 525

Ala Ser Lys Val Glu Lys Leu Thr Leu Asp Asn Ala Ala Phe Pro Phe
 530 535 540

Leu Ala Tyr Ser Gly Ile Pro Ala Val Ser Phe Cys Phe Cys Glu Asp
 545 550 555 560

Thr Asp Tyr Pro Tyr Leu Gly Thr Thr Met Asp Thr Tyr Lys Glu Leu
 565 570 575

Ile Glu Arg Ile Pro Glu Leu Asn Lys Val Ala Arg Ala Ala Ala Glu
 580 585 590

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Val Ala Gly Gln Phe Val Ile Lys Leu Thr His Asp Val Glu Leu Asn
595 600 605

Leu Asp Tyr Glu Arg Tyr Asn Ser Gln Leu Leu Ser Phe Val Arg Asp
610 615 620

Leu Asn Gln Tyr Arg Ala Asp Ile Lys Glu Met Gly Leu Ser Leu Gln
625 630 635 640

Trp Leu Tyr Ser Ala Arg Gly Asp Phe Phe Arg Ala Thr Ser Arg Leu
645 650 655

Thr Thr Asp Phe Gly Asn Ala Glu Lys Thr Asp Arg Phe Val Met Lys
660 665 670

Lys Leu Asn Asp Arg Val Met Arg Val Glu Tyr His Phe Leu Ser Pro
675 680 685

Tyr Val Ser Pro Lys Glu Ser Pro Phe Arg His Val Phe Trp Gly Ser
690 695 700

Gly Ser His Thr Leu Pro Ala Leu Leu Glu Asn Leu Lys Leu Arg Lys
705 710 715 720

Gln Asn Asn Gly Ala Phe Asn Glu Thr Leu Phe Arg Asn Gln Leu Ala
725 730 735

Leu Ala Thr Trp Thr Ile Gln Gly Ala Ala Asn Ala Leu Ser Gly Asp
740 745 750

Val Trp Asp Ile Asp Asn Glu Phe
755 760

<210> 101
<211> 760
<212> PRT
<213> Homo sapiens

<400> 101

Met Met Asp Gln Ala Arg Ser Ala Phe Ser Asn Leu Phe Gly Gly Glu
1 5 10 15

Pro Leu Ser Tyr Thr Arg Phe Ser Leu Ala Arg Gln Val Asp Gly Asp
20 25 30

Asn Ser His Val Glu Met Lys Leu Ala Val Asp Glu Glu Glu Asn Ala
35 40 45

Asp Asn Asn Thr Lys Ala Asn Val Thr Lys Pro Lys Arg Cys Ser Gly
50 55 60

Ser Ile Cys Tyr Gly Thr Ile Ala Val Ile Val Phe Phe Leu Ile Gly
65 70 75 80

Phe Met Ile Gly Tyr Leu Gly Tyr Cys Lys Gly Val Glu Pro Lys Thr
85 90 95

Glu Cys Glu Arg Leu Ala Gly Thr Glu Ser Pro Val Arg Glu Glu Pro
100 105 110

Gly Glu Asp Phe Pro Ala Ala Arg Arg Leu Tyr Trp Asp Asp Leu Lys
115 120 125

Arg Lys Leu Ser Glu Lys Leu Asp Ser Thr Asp Phe Thr Ser Thr Ile
130 135 140

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Lys Leu Leu Asn Glu Asn Ser Tyr Val Pro Arg Glu Ala Gly Ser Gln
145 150 155 160

Lys Asp Glu Asn Leu Ala Leu Tyr Val Glu Asn Gln Phe Arg Glu Phe
165 170 175

Lys Leu Ser Lys Val Trp Arg Asp Gln His Phe Val Lys Ile Gln Val
180 185 190

Lys Asp Ser Ala Gln Asn Ser Val Ile Ile Val Asp Lys Asn Gly Arg
195 200 205

Leu Val Tyr Leu Val Glu Asn Pro Gly Gly Tyr Val Ala Tyr Ser Lys
210 215 220

Ala Ala Thr Val Thr Gly Lys Leu Val His Ala Asn Phe Gly Thr Lys
225 230 235 240

Lys Asp Phe Glu Asp Leu Tyr Thr Pro Val Asn Gly Ser Ile Val Ile
245 250 255

Val Arg Ala Gly Lys Ile Thr Phe Ala Glu Lys Val Ala Asn Ala Glu
260 265 270

Ser Leu Asn Ala Ile Gly Val Leu Ile Tyr Met Asp Gln Thr Lys Phe
275 280 285

Pro Ile Val Asn Ala Glu Leu Ser Phe Phe Gly His Ala His Leu Gly
290 295 300

Thr Gly Asp Pro Tyr Thr Pro Gly Phe Pro Ser Phe Asn His Thr Gln
305 310 315 320

Phe Pro Pro Ser Arg Ser Ser Gly Leu Pro Asn Ile Pro Val Gln Thr
325 330 335

Ile Ser Arg Ala Ala Ala Glu Lys Leu Phe Gly Asn Met Glu Gly Asp
340 345 350

Cys Pro Ser Asp Trp Lys Thr Asp Ser Thr Cys Arg Met Val Thr Ser
355 360 365

Glu Ser Lys Asn Val Lys Leu Thr Val Ser Asn Val Leu Lys Glu Ile
370 375 380

Lys Ile Leu Asn Ile Phe Gly Val Ile Lys Gly Phe Val Glu Pro Asp
385 390 395 400

His Tyr Val Val Val Gly Ala Gln Arg Asp Ala Trp Gly Pro Gly Ala
405 410 415

Ala Lys Ser Gly Val Gly Thr Ala Leu Leu Leu Lys Leu Ala Gln Met
420 425 430

Phe Ser Asp Met Val Leu Lys Asp Gly Phe Gln Pro Ser Arg Ser Ile
435 440 445

Ile Phe Ala Ser Trp Ser Ala Gly Asp Phe Gly Ser Val Gly Ala Thr
450 455 460

Glu Trp Leu Glu Gly Tyr Leu Ser Ser Leu His Leu Lys Ala Phe Thr
465 470 475 480

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Tyr Ile Asn Leu Asp Lys Ala Val Leu Gly Thr Ser Asn Phe Lys Val
 485 490 495

Ser Ala Ser Pro Leu Leu Tyr Thr Leu Ile Glu Lys Thr Met Gln Asn
 500 505 510

Val Lys His Pro Val Thr Gly Gln Phe Leu Tyr Gln Asp Ser Asn Trp
 515 520 525

Ala Ser Lys Val Glu Lys Leu Thr Leu Asp Asn Ala Ala Phe Pro Phe
 530 535 540

Leu Ala Tyr Ser Gly Ile Pro Ala Val Ser Phe Cys Phe Cys Glu Asp
 545 550 555 560

Thr Asp Tyr Pro Tyr Leu Gly Thr Thr Met Asp Thr Tyr Lys Glu Leu
 565 570 575

Ile Glu Arg Ile Pro Glu Leu Asn Lys Val Ala Arg Ala Ala Ala Glu
 580 585 590

Val Ala Gly Gln Phe Val Ile Lys Leu Thr His Asp Val Glu Leu Asn
 595 600 605

Leu Asp Tyr Glu Arg Tyr Asn Ser Gln Leu Leu Ser Phe Val Arg Asp
 610 615 620

Leu Asn Gln Tyr Arg Ala Asp Ile Lys Glu Met Gly Leu Ser Leu Gln
 625 630 635 640

Trp Leu Tyr Ser Ala Arg Gly Asp Phe Phe Arg Ala Thr Ser Arg Leu
 645 650 655

Thr Thr Asp Phe Gly Asn Ala Glu Lys Thr Asp Arg Phe Val Met Lys
 660 665 670

Lys Leu Asn Asp Arg Val Met Arg Val Glu Tyr His Phe Leu Ser Pro
 675 680 685

Tyr Val Ser Pro Lys Glu Ser Pro Phe Arg His Val Phe Trp Gly Ser
 690 695 700

Gly Ser His Thr Leu Pro Ala Leu Leu Glu Asn Leu Lys Leu Arg Lys
 705 710 715 720

Gln Asn Asn Gly Ala Phe Asn Glu Thr Leu Phe Arg Asn Gln Leu Ala
 725 730 735

Leu Ala Thr Trp Thr Ile Gln Gly Ala Ala Asn Ala Leu Ser Gly Asp
 740 745 750

Val Trp Asp Ile Asp Asn Glu Phe
 755 760

<210> 102
 <211> 1140
 <212> PRT
 <213> Homo sapiens

<400> 102

Met Ser Tyr Asn Tyr Val Val Thr Ala Gln Lys Pro Thr Ala Val Asn
 1 5 10 15

Gly Cys Val Thr Gly His Phe Thr Ser Ala Glu Asp Leu Asn Leu Leu
 20 25 30

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ile Ala Lys Asn Thr Arg Leu Glu Ile Tyr Val Val Thr Ala Glu Gly
35 40 45

Leu Arg Pro Val Lys Glu Val Gly Met Tyr Gly Lys Ile Ala Val Met
50 55 60

Glu Leu Phe Arg Pro Lys Gly Glu Ser Lys Asp Leu Leu Phe Ile Leu
65 70 75 80

Thr Ala Lys Tyr Asn Ala Cys Ile Leu Glu Tyr Lys Gln Ser Gly Glu
85 90 95

Ser Ile Asp Ile Ile Thr Arg Ala His Gly Asn Val Gln Asp Arg Ile
100 105 110

Gly Arg Pro Ser Glu Thr Gly Ile Ile Gly Ile Ile Asp Pro Glu Cys
115 120 125

Arg Met Ile Gly Leu Arg Leu Tyr Asp Gly Leu Phe Lys Val Ile Pro
130 135 140

Leu Asp Arg Asp Asn Lys Glu Leu Lys Ala Phe Asn Ile Arg Leu Glu
145 150 155 160

Glu Leu His Val Ile Asp Val Lys Phe Leu Tyr Gly Cys Gln Ala Pro
165 170 175

Thr Ile Cys Phe Val Tyr Gln Asp Pro Gln Gly Arg His Val Lys Thr
180 185 190

Tyr Glu Val Ser Leu Arg Glu Lys Glu Phe Asn Lys Gly Pro Trp Lys
195 200 205

Gln Glu Asn Val Glu Ala Glu Ala Ser Met Val Ile Ala Val Pro Glu
210 215 220

Pro Phe Gly Gly Ala Ile Ile Ile Gly Gln Glu Ser Ile Thr Tyr His
225 230 235 240

Asn Gly Asp Lys Tyr Leu Ala Ile Ala Pro Pro Ile Ile Lys Gln Ser
245 250 255

Thr Ile Val Cys His Asn Arg Val Asp Pro Asn Gly Ser Arg Tyr Leu
260 265 270

Leu Gly Asp Met Glu Gly Arg Leu Phe Met Leu Leu Leu Glu Lys Glu
275 280 285

Glu Gln Met Asp Gly Thr Val Thr Leu Lys Asp Leu Arg Val Glu Leu
290 295 300

Leu Gly Glu Thr Ser Ile Ala Glu Cys Leu Thr Tyr Leu Asp Asn Gly
305 310 315 320

Val Val Phe Val Gly Ser Arg Leu Gly Asp Ser Gln Leu Val Lys Leu
325 330 335

Asn Val Asp Ser Asn Glu Gln Gly Ser Tyr Val Val Ala Met Glu Thr
340 345 350

Phe Thr Asn Leu Gly Pro Ile Val Asp Met Cys Val Val Asp Leu Glu
355 360 365

Arg Gln Gly Gln Gly Gln Leu Val Thr Cys Ser Gly Ala Phe Lys Glu

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 370 375 380

Gly Ser Leu Arg Ile Ile Arg Asn Gly Ile Gly Ile His Glu His Ala
 385 390 395 400

Ser Ile Asp Leu Pro Gly Ile Lys Gly Leu Trp Pro Leu Arg Ser Asp
 405 410 415

Pro Asn Arg Glu Thr Tyr Asp Thr Leu Val Leu Ser Phe Val Gly Gln
 420 425 430

Thr Arg Val Leu Met Leu Asn Gly Glu Glu Val Glu Glu Thr Glu Leu
 435 440 445

Met Gly Phe Val Asp Asp Gln Gln Thr Phe Phe Cys Gly Asn Val Ala
 450 455 460

His Gln Gln Leu Ile Gln Ile Thr Ser Ala Ser Val Arg Leu Val Ser
 465 470 475 480

Gln Glu Pro Lys Ala Leu Val Ser Glu Trp Lys Glu Pro Gln Ala Lys
 485 490 495

Asn Ile Ser Val Ala Ser Cys Asn Ser Ser Gln Val Val Val Ala Val
 500 505 510

Gly Arg Ala Leu Tyr Tyr Leu Gln Ile His Pro Gln Glu Leu Arg Gln
 515 520 525

Ile Ser His Thr Glu Met Glu His Glu Val Ala Cys Leu Asp Ile Thr
 530 535 540

Pro Leu Gly Asp Ser Asn Gly Leu Ser Pro Leu Cys Ala Ile Gly Leu
 545 550 555 560

Trp Thr Asp Ile Ser Ala Arg Ile Leu Lys Leu Pro Ser Phe Glu Leu
 565 570 575

Leu His Lys Glu Met Leu Gly Gly Glu Ile Ile Pro Arg Ser Ile Leu
 580 585 590

Met Thr Thr Phe Glu Ser Ser His Tyr Leu Leu Cys Ala Leu Gly Asp
 595 600 605

Gly Ala Leu Phe Tyr Phe Gly Leu Asn Ile Glu Thr Gly Leu Leu Ser
 610 615 620

Asp Arg Lys Lys Val Thr Leu Gly Thr Gln Pro Thr Val Leu Arg Thr
 625 630 635 640

Phe Arg Ser Leu Ser Thr Thr Asn Val Phe Ala Cys Ser Asp Arg Pro
 645 650 655

Thr Val Ile Tyr Ser Ser Asn His Lys Leu Val Phe Ser Asn Val Asn
 660 665 670

Leu Lys Glu Val Asn Tyr Met Cys Pro Leu Asn Ser Asp Gly Tyr Pro
 675 680 685

Asp Ser Leu Ala Leu Ala Asn Asn Ser Thr Leu Thr Ile Gly Thr Ile
 690 695 700

Asp Glu Ile Gln Lys Leu His Ile Arg Thr Val Pro Leu Tyr Glu Ser
 705 710 715 720

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Pro Arg Lys Ile Cys Tyr Gln Glu Val Ser Gln Cys Phe Gly Val Leu
725 730 735

Ser Ser Arg Ile Glu Val Gln Asp Thr Ser Gly Gly Thr Thr Ala Leu
740 745 750

Arg Pro Ser Ala Ser Thr Gln Ala Leu Ser Ser Ser Val Ser Ser Ser
755 760 765

Lys Leu Phe Ser Ser Ser Thr Ala Pro His Glu Thr Ser Phe Gly Glu
770 775 780

Glu Val Glu Val His Asn Leu Leu Ile Ile Asp Gln His Thr Phe Glu
785 790 795 800

Val Leu His Ala His Gln Phe Leu Gln Asn Glu Tyr Ala Leu Ser Leu
805 810 815

Val Ser Cys Lys Leu Gly Lys Asp Pro Asn Thr Tyr Phe Ile Val Gly
820 825 830

Thr Ala Met Val Tyr Pro Glu Glu Ala Glu Pro Lys Gln Gly Arg Ile
835 840 845

Val Val Phe Gln Tyr Ser Asp Gly Lys Leu Gln Thr Val Ala Glu Lys
850 855 860

Glu Val Lys Gly Ala Val Tyr Ser Met Val Glu Phe Asn Gly Lys Leu
865 870 875 880

Leu Ala Ser Ile Asn Ser Thr Val Arg Leu Tyr Glu Trp Thr Thr Glu
885 890 895

Lys Asp Val Arg Thr Glu Cys Asn His Tyr Asn Asn Ile Met Ala Leu
900 905 910

Tyr Leu Lys Thr Lys Gly Asp Phe Ile Leu Val Gly Asp Leu Met Arg
915 920 925

Ser Val Leu Leu Leu Ala Tyr Lys Pro Met Glu Gly Asn Phe Glu Glu
930 935 940

Ile Ala Arg Asp Phe Asn Pro Asn Trp Met Ser Ala Val Glu Ile Leu
945 950 955 960

Asp Asp Asp Asn Phe Leu Gly Ala Glu Asn Ala Phe Asn Leu Phe Val
965 970 975

Cys Gln Lys Asp Ser Ala Ala Thr Thr Asp Glu Glu Arg Gln His Leu
980 985 990

Gln Glu Val Gly Leu Phe His Leu Gly Glu Phe Val Asn Val Phe Cys
995 1000 1005

His Gly Ser Leu Val Met Gln Asn Leu Gly Glu Thr Ser Thr Pro
1010 1015 1020

Thr Gln Gly Ser Val Leu Phe Gly Thr Val Asn Gly Met Ile Gly
1025 1030 1035

Leu Val Thr Ser Leu Ser Glu Ser Trp Tyr Asn Leu Leu Leu Asp
1040 1045 1050

Met Gln Asn Arg Leu Asn Lys Val Ile Lys Ser Val Gly Lys Ile

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 1055 1060 1065

Glu His Ser Phe Trp Arg Ser Phe His Thr Glu Arg Lys Thr Glu
 1070 1075 1080

Pro Ala Thr Gly Phe Ile Asp Gly Asp Leu Ile Glu Ser Phe Leu
 1085 1090 1095

Asp Ile Ser Arg Pro Lys Met Gln Glu Val Val Ala Asn Leu Gln
 1100 1105 1110

Tyr Asp Asp Gly Ser Gly Met Lys Arg Glu Ala Thr Ala Asp Asp
 1115 1120 1125

Leu Ile Lys Val Val Glu Glu Leu Thr Arg Ile His
 1130 1135 1140

<210> 103
 <211> 243
 <212> PRT
 <213> Homo sapiens

<400> 103

Met Ala Lys Val Glu Gln Val Leu Ser Leu Glu Pro Gln His Glu Leu
 1 5 10 15

Lys Phe Arg Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu Lys Leu
 20 25 30

Gly Asn Pro Thr Asp Arg Asn Val Cys Phe Lys Val Lys Thr Thr Ala
 35 40 45

Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile Ile Asp Ala Gly
 50 55 60

Ala Ser Ile Asn Val Ser Val Met Leu Gln Pro Phe Asp Tyr Asp Pro
 65 70 75 80

Asn Glu Lys Ser Lys His Lys Phe Met Val Gln Ser Met Phe Ala Pro
 85 90 95

Thr Asp Thr Ser Asp Met Glu Ala Val Trp Lys Glu Ala Lys Pro Glu
 100 105 110

Asp Leu Met Asp Ser Lys Leu Arg Cys Val Phe Glu Leu Pro Ala Glu
 115 120 125

Asn Asp Lys Pro His Asp Val Glu Ile Asn Lys Ile Ile Ser Thr Thr
 130 135 140

Ala Ser Lys Thr Glu Thr Pro Ile Val Ser Lys Ser Leu Ser Ser Ser
 145 150 155 160

Leu Asp Asp Thr Glu Val Lys Lys Val Met Glu Glu Cys Lys Arg Leu
 165 170 175

Gln Gly Glu Val Gln Arg Leu Arg Glu Glu Asn Lys Gln Phe Lys Glu
 180 185 190

Glu Asp Gly Leu Arg Met Arg Lys Thr Val Gln Ser Asn Ser Pro Ile
 195 200 205

Ser Ala Leu Ala Pro Thr Gly Lys Glu Glu Gly Leu Ser Thr Arg Leu
 210 215 220

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 Leu Ala Leu Val Val Leu Phe Phe Ile Val Gly Val Ile Ile Gly Lys
 225 230 235 240

Ile Ala Leu

<210> 104
 <211> 878
 <212> PRT
 <213> Homo sapiens

<400> 104

Met Glu Gln Trp Arg Gln Cys Gly Arg Trp Leu Ile Asp Cys Lys Val
 1 5 10 15

Leu Pro Pro Asn His Arg Val Val Trp Pro Ser Ala Val Val Phe Asp
 20 25 30

Leu Ala Gln Ala Leu Arg Asp Gly Val Leu Leu Cys Gln Leu Leu His
 35 40 45

Asn Leu Ser Pro Gly Ser Ile Asp Leu Lys Asp Ile Asn Phe Arg Pro
 50 55 60

Gln Met Ser Gln Phe Leu Cys Leu Lys Asn Ile Arg Thr Phe Leu Lys
 65 70 75 80

Val Cys His Asp Lys Phe Gly Leu Arg Asn Ser Glu Leu Phe Asp Pro
 85 90 95

Phe Asp Leu Phe Asp Val Arg Asp Phe Gly Lys Val Ile Ser Ala Val
 100 105 110

Ser Arg Leu Ser Leu His Ser Ile Ala Gln Asn Lys Gly Ile Arg Pro
 115 120 125

Phe Pro Ser Glu Glu Thr Thr Glu Asn Asp Asp Asp Val Tyr Arg Ser
 130 135 140

Leu Glu Glu Leu Ala Asp Glu His Asp Leu Gly Glu Asp Ile Tyr Asp
 145 150 155 160

Cys Val Pro Cys Glu Asp Gly Gly Asp Asp Ile Tyr Glu Asp Ile Ile
 165 170 175

Lys Val Glu Val Gln Gln Pro Met Ile Arg Tyr Met Gln Lys Met Gly
 180 185 190

Met Thr Glu Asp Asp Lys Arg Asn Cys Cys Leu Leu Glu Ile Gln Glu
 195 200 205

Thr Glu Ala Lys Tyr Tyr Arg Thr Leu Glu Asp Ile Glu Lys Asn Tyr
 210 215 220

Met Ser Pro Leu Arg Leu Val Leu Ser Pro Ala Asp Met Ala Ala Val
 225 230 235 240

Phe Ile Asn Leu Glu Asp Leu Ile Lys Val His His Ser Phe Leu Arg
 245 250 255

Ala Ile Asp Val Ser Val Met Val Gly Gly Ser Thr Leu Ala Lys Val
 260 265 270

Phe Leu Asp Phe Lys Glu Arg Leu Leu Ile Tyr Gly Glu Tyr Cys Ser
 275 280 285

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

His Met Glu His Ala Gln Asn Thr Leu Asn Gln Leu Leu Ala Ser Arg
290 295 300

Glu Asp Phe Arg Gln Lys Val Glu Glu Cys Thr Leu Lys Val Gln Asp
305 310 315 320

Gly Lys Phe Lys Leu Gln Asp Leu Leu Val Val Pro Met Gln Arg Val
325 330 335

Leu Lys Tyr His Leu Leu Leu Lys Glu Leu Leu Ser His Ser Ala Glu
340 345 350

Arg Pro Glu Arg Gln Gln Leu Lys Glu Ala Leu Glu Ala Met Gln Asp
355 360 365

Leu Ala Met Tyr Ile Asn Glu Val Lys Arg Asp Lys Glu Thr Leu Arg
370 375 380

Lys Ile Ser Glu Phe Gln Ser Ser Ile Glu Asn Leu Gln Val Lys Leu
385 390 395 400

Glu Glu Phe Gly Arg Pro Lys Ile Asp Gly Glu Leu Lys Val Arg Ser
405 410 415

Ile Val Asn His Thr Lys Gln Asp Arg Tyr Leu Phe Leu Phe Asp Lys
420 425 430

Val Val Ile Val Cys Lys Arg Lys Gly Tyr Ser Tyr Glu Leu Lys Glu
435 440 445

Ile Ile Glu Leu Leu Phe His Lys Met Thr Asp Asp Pro Met Asn Asn
450 455 460

Lys Asp Val Lys Lys Ser His Gly Lys Met Trp Ser Tyr Gly Phe Tyr
465 470 475 480

Leu Ile His Leu Gln Gly Lys Gln Gly Phe Gln Phe Phe Cys Lys Thr
485 490 495

Glu Asp Met Lys Arg Lys Trp Met Glu Gln Phe Glu Met Ala Met Ser
500 505 510

Asn Ile Lys Pro Asp Lys Ala Asn Ala Asn His His Ser Phe Gln Met
515 520 525

Tyr Thr Phe Asp Lys Thr Thr Asn Cys Lys Ala Cys Lys Met Phe Leu
530 535 540

Arg Gly Thr Phe Tyr Gln Gly Tyr Met Cys Thr Lys Cys Gly Val Gly
545 550 555 560

Ala His Lys Glu Cys Leu Glu Val Ile Pro Pro Cys Lys Phe Thr Ser
565 570 575

Pro Ala Asp Leu Asp Ala Ser Gly Ala Gly Pro Gly Pro Lys Met Val
580 585 590

Ala Val Gln Asn Tyr His Gly Asn Pro Ala Pro Pro Gly Lys Pro Val
595 600 605

Leu Thr Phe Gln Thr Gly Asp Val Leu Glu Leu Leu Arg Gly Asp Pro
610 615 620

Glu ser Pro Trp Trp Glu Gly Arg Leu Val Gln Thr Arg Lys Ser Gly

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 625 630 635 640

Tyr Phe Pro Ser Ser Ser Val Lys Pro Cys Pro Val Asp Gly Arg Pro
 645 650 655

Pro Ile Ser Arg Pro Pro Ser Arg Glu Ile Asp Tyr Thr Ala Tyr Pro
 660 665 670

Trp Phe Ala Gly Asn Met Glu Arg Gln Gln Thr Asp Asn Leu Leu Lys
 675 680 685

Ser His Ala Ser Gly Thr Tyr Leu Ile Arg Glu Arg Pro Ala Glu Ala
 690 695 700

Glu Arg Phe Ala Ile Ser Ile Lys Phe Asn Asp Glu Val Lys His Ile
 705 710 715 720

Lys Val Val Glu Lys Asp Asn Trp Ile His Ile Thr Glu Ala Lys Lys
 725 730 735

Phe Asp Ser Leu Leu Glu Leu Val Glu Tyr Tyr Gln Cys His Ser Leu
 740 745 750

Lys Glu Ser Phe Lys Gln Leu Asp Thr Thr Leu Lys Tyr Pro Tyr Lys
 755 760 765

Ser Arg Glu Arg Ser Ala Ser Arg Ala Ser Ser Arg Ser Pro Ala Ser
 770 775 780

Cys Ala Ser Tyr Asn Phe Ser Phe Leu Ser Pro Gln Gly Leu Ser Phe
 785 790 795 800

Ala Ser Gln Gly Pro Ser Ala Pro Phe Trp Ser Val Phe Thr Pro Arg
 805 810 815

Val Ile Gly Thr Ala Val Ala Arg Tyr Asn Phe Ala Ala Arg Asp Met
 820 825 830

Arg Glu Leu Ser Leu Arg Glu Gly Asp Val Val Arg Ile Tyr Ser Arg
 835 840 845

Ile Gly Gly Asp Gln Gly Trp Trp Lys Gly Glu Thr Asn Gly Arg Ile
 850 855 860

Gly Trp Phe Pro Ser Thr Tyr Val Glu Glu Glu Gly Ile Gln
 865 870 875

<210> 105
 <211> 847
 <212> PRT
 <213> Homo sapiens

<400> 105

Met Glu Pro Trp Lys Gln Cys Ala Gln Trp Leu Ile His Cys Lys Val
 1 5 10 15

Leu Pro Thr Asn His Arg Val Thr Trp Asp Ser Ala Gln Val Phe Asp
 20 25 30

Leu Ala Gln Thr Leu Arg Asp Gly Val Leu Leu Cys Gln Leu Leu Asn
 35 40 45

Asn Leu Arg Ala His Ser Ile Asn Leu Lys Glu Ile Asn Leu Arg Pro
 50 55 60

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Gln Met Ser Gln Phe Leu Cys Leu Lys Asn Ile Arg Thr Phe Leu Thr
65 70 75 80

Ala Cys Cys Glu Thr Phe Gly Met Arg Lys Ser Glu Leu Phe Glu Ala
85 90 95

Phe Asp Leu Phe Asp Val Arg Asp Phe Gly Lys Val Ile Glu Thr Leu
100 105 110

Ser Arg Leu Ser Arg Thr Pro Ile Ala Leu Ala Thr Gly Ile Arg Pro
115 120 125

Phe Pro Thr Glu Glu Ser Ile Asn Asp Glu Asp Ile Tyr Lys Gly Leu
130 135 140

Pro Asp Leu Ile Asp Glu Thr Leu Val Glu Asp Glu Glu Asp Leu Tyr
145 150 155 160

Asp Cys Val Tyr Gly Glu Asp Glu Gly Gly Glu Val Tyr Glu Asp Leu
165 170 175

Met Lys Ala Glu Glu Ala His Gln Pro Lys Cys Pro Glu Asn Asp Ile
180 185 190

Arg Ser Cys Cys Leu Ala Glu Ile Lys Gln Thr Glu Glu Lys Tyr Thr
195 200 205

Glu Thr Leu Glu Ser Ile Glu Lys Tyr Phe Met Ala Pro Leu Lys Arg
210 215 220

Phe Leu Thr Ala Ala Glu Phe Asp Ser Val Phe Ile Asn Ile Pro Glu
225 230 235 240

Leu Val Lys Leu His Arg Asn Leu Met Gln Glu Ile His Asp Ser Ile
245 250 255

Val Asn Lys Asn Asp Gln Asn Leu Tyr Gln Val Phe Ile Asn Tyr Lys
260 265 270

Glu Arg Leu Val Ile Tyr Gly Gln Tyr Cys Ser Gly Val Glu Ser Ala
275 280 285

Ile Ser Ser Leu Asp Tyr Ile Ser Lys Thr Lys Glu Asp Val Lys Leu
290 295 300

Lys Leu Glu Glu Cys Ser Lys Arg Ala Asn Asn Gly Lys Phe Thr Leu
305 310 315 320

Arg Asp Leu Leu Val Val Pro Met Gln Arg Val Leu Lys Tyr His Leu
325 330 335

Leu Leu Gln Glu Leu Val Lys His Thr Thr Asp Pro Thr Glu Lys Ala
340 345 350

Asn Leu Lys Leu Ala Leu Asp Ala Met Lys Asp Leu Ala Gln Tyr Val
355 360 365

Asn Glu Val Lys Arg Asp Asn Glu Thr Leu Arg Glu Ile Lys Gln Phe
370 375 380

Gln Leu Ser Ile Glu Asn Leu Asn Gln Pro Val Leu Leu Phe Gly Arg
385 390 395 400

Pro Gln Gly Asp Gly Glu Ile Arg Ile Thr Thr Leu Asp Lys His Thr
405 410 415

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Lys Gln Glu Arg His Ile Phe Leu Phe Asp Leu Ala Val Ile Val Cys
420 425 430

Lys Arg Lys Gly Asp Asn Tyr Glu Met Lys Glu Ile Ile Asp Leu Gln
435 440 445

Gln Tyr Lys Ile Ala Asn Asn Pro Thr Thr Asp Lys Glu Asn Lys Lys
450 455 460

Trp Ser Tyr Gly Phe Tyr Leu Ile His Thr Gln Gly Gln Asn Gly Leu
465 470 475 480

Glu Phe Tyr Cys Lys Thr Lys Asp Leu Lys Lys Lys Trp Leu Glu Gln
485 490 495

Phe Glu Met Ala Leu Ser Asn Ile Arg Pro Asp Tyr Ala Asp Ser Asn
500 505 510

Phe His Asp Phe Lys Met His Thr Phe Thr Arg Val Thr Ser Cys Lys
515 520 525

Val Cys Gln Met Leu Leu Arg Gly Thr Phe Tyr Gln Gly Tyr Leu Cys
530 535 540

Phe Lys Cys Gly Ala Arg Ala His Lys Glu Cys Leu Gly Arg Val Asp
545 550 555 560

Asn Cys Gly Arg Val Asn Ser Gly Glu Gln Gly Thr Leu Lys Leu Pro
565 570 575

Glu Lys Arg Thr Asn Gly Leu Arg Arg Thr Pro Lys Gln Val Asp Pro
580 585 590

Gly Leu Pro Lys Met Gln Val Ile Arg Asn Tyr Ser Gly Thr Pro Pro
595 600 605

Pro Ala Leu His Glu Gly Pro Pro Leu Gln Leu Gln Ala Gly Asp Thr
610 615 620

Val Glu Leu Leu Lys Gly Asp Ala His Ser Leu Phe Trp Gln Gly Arg
625 630 635 640

Asn Leu Ala Ser Gly Glu Val Gly Phe Phe Pro Ser Asp Ala Val Lys
645 650 655

Pro Cys Pro Cys Val Pro Lys Pro Val Asp Tyr Ser Cys Gln Pro Trp
660 665 670

Tyr Ala Gly Ala Met Glu Arg Leu Gln Ala Glu Thr Glu Leu Ile Asn
675 680 685

Arg Val Asn Ser Thr Tyr Leu Val Arg His Arg Thr Lys Glu Ser Gly
690 695 700

Glu Tyr Ala Ile Ser Ile Lys Tyr Asn Asn Glu Ala Lys His Ile Lys
705 710 715 720

Ile Leu Thr Arg Asp Gly Phe Phe His Ile Ala Glu Asn Arg Lys Phe
725 730 735

Lys ser Leu Met Glu Leu Val Glu Tyr Tyr Lys His His Ser Leu Lys
740 745 750

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 Glu Gly Phe Arg Thr Leu Asp Thr Thr Leu Gln Phe Pro Tyr Lys Glu
 755 760 765

Pro Glu His Ser Ala Gly Gln Arg Gly Asn Arg Ala Gly Asn Ser Leu
 770 775 780

Leu Ser Pro Lys Val Leu Gly Ile Ala Ile Ala Arg Tyr Asp Phe Cys
 785 790 795 800

Ala Arg Asp Met Arg Glu Leu Ser Leu Leu Lys Gly Asp Val Val Lys
 805 810 815

Ile Tyr Thr Lys Met Ser Ala Asn Gly Trp Trp Arg Gly Glu Val Asn
 820 825 830

Gly Arg Val Gly Trp Phe Pro Ser Thr Tyr Val Glu Glu Asp Glu
 835 840 845

<210> 106
 <211> 1121
 <212> PRT
 <213> Homo sapiens

<400> 106

Met Asp Ala Leu Glu Asp Tyr Val Trp Pro Arg Ala Thr Ser Glu Leu
 1 5 10 15

Ile Leu Leu Pro Val Thr Gly Leu Glu Cys Val Gly Asp Arg Leu Leu
 20 25 30

Ala Gly Glu Gly Pro Asp Val Leu Val Tyr Ser Leu Asp Phe Gly Gly
 35 40 45

His Leu Arg Met Ile Lys Arg Val Gln Asn Leu Leu Gly His Tyr Leu
 50 55 60

Ile His Gly Phe Arg Val Arg Pro Glu Pro Asn Gly Asp Leu Asp Leu
 65 70 75 80

Glu Ala Met Val Ala Val Phe Gly Ser Lys Gly Leu Arg Val Val Lys
 85 90 95

Ile Ser Trp Gly Gln Gly His Phe Trp Glu Leu Trp Arg Ser Gly Leu
 100 105 110

Trp Asn Met Ser Asp Trp Ile Trp Asp Ala Arg Trp Leu Glu Gly Asn
 115 120 125

Ile Ala Leu Ala Leu Gly His Asn Ser Val Val Leu Tyr Asp Pro Val
 130 135 140

Val Gly Cys Ile Leu Gln Glu Val Pro Cys Thr Asp Arg Cys Thr Leu
 145 150 155 160

Ser Ser Ala Cys Leu Ile Gly Asp Ala Trp Lys Glu Leu Thr Ile Val
 165 170 175

Ala Gly Ala Val Ser Asn Gln Leu Leu Val Trp Tyr Pro Ala Thr Ala
 180 185 190

Leu Ala Asp Asn Lys Pro Val Ala Pro Asp Arg Arg Ile Ser Gly His
 195 200 205

Val Gly Ile Ile Phe Ser Met Ser Tyr Leu Glu Ser Lys Gly Leu Leu
 210 215 220

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ala Thr Ala Ser Glu Asp Arg Ser Val Arg Ile Trp Lys Val Gly Asp
225 230 235 240

Leu Arg Val Pro Gly Gly Arg Val Gln Asn Ile Gly His Cys Phe Gly
245 250 255

His Ser Ala Arg Val Trp Gln Val Lys Leu Leu Glu Asn Tyr Leu Ile
260 265 270

Ser Ala Gly Glu Asp Cys Val Cys Leu Val Trp Ser His Glu Gly Glu
275 280 285

Ile Leu Gln Ala Phe Arg Gly His Gln Gly Arg Gly Ile Arg Ala Ile
290 295 300

Ala Ala His Glu Arg Gln Ala Trp Val Ile Thr Gly Gly Asp Asp Ser
305 310 315 320

Gly Ile Arg Leu Trp His Leu Val Gly Arg Gly Tyr Arg Gly Leu Gly
325 330 335

Val Ser Ala Leu Cys Phe Lys Ser Arg Ser Arg Pro Gly Thr Leu Lys
340 345 350

Ala Val Thr Leu Ala Gly Ser Trp Arg Leu Leu Ala Val Thr Asp Thr
355 360 365

Gly Ala Leu Tyr Leu Tyr Asp Val Glu Val Lys Cys Trp Glu Gln Leu
370 375 380

Leu Glu Asp Lys His Phe Gln Ser Tyr Cys Leu Leu Glu Ala Ala Pro
385 390 395 400

Gly Pro Glu Gly Phe Gly Leu Cys Ala Met Ala Asn Gly Glu Gly Arg
405 410 415

Val Lys Val Val Pro Ile Asn Thr Pro Thr Ala Ala Val Asp Gln Thr
420 425 430

Leu Phe Pro Gly Lys Val His Ser Leu Ser Trp Ala Leu Arg Gly Tyr
435 440 445

Glu Glu Leu Leu Leu Ala Ser Gly Pro Gly Gly Val Val Ala Cys
450 455 460

Leu Glu Ile Ser Ala Ala Pro Ser Gly Lys Ala Ile Phe Val Lys Glu
465 470 475 480

Arg Cys Arg Tyr Leu Leu Pro Pro Ser Lys Gln Arg Trp His Thr Cys
485 490 495

Ser Ala Phe Leu Pro Pro Gly Asp Phe Leu Val Cys Gly Asp Arg Arg
500 505 510

Gly Ser Val Leu Leu Phe Pro Ser Arg Pro Gly Leu Leu Lys Asp Pro
515 520 525

Gly Val Gly Gly Lys Ala Arg Ala Gly Ala Gly Ala Pro Val Val Gly
530 535 540

Ser Gly Ser Ser Gly Gly Gly Asn Ala Phe Thr Gly Leu Gly Pro Val
545 550 555 560

Ser Thr Leu Pro Ser Leu His Gly Lys Gln Gly Val Thr Ser Val Thr

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 565 570 575

Cys His Gly Gly Tyr Val Tyr Thr Thr Gly Arg Asp Gly Ala Tyr Tyr
 580 585 590

Gln Leu Phe Val Arg Asp Gly Gln Leu Gln Pro Val Leu Arg Gln Lys
 595 600 605

Ser Cys Arg Gly Met Asn Trp Leu Ala Gly Leu Arg Ile Val Pro Asp
 610 615 620

Gly Ser Met Val Ile Leu Gly Phe His Ala Asn Glu Phe Val Val Trp
 625 630 635 640

Asn Pro Arg Ser His Glu Lys Leu His Ile Val Asn Cys Gly Gly Gly
 645 650 655

His Arg Ser Trp Ala Phe Ser Asp Thr Glu Ala Ala Met Ala Phe Ala
 660 665 670

Tyr Leu Lys Asp Gly Asp Val Met Leu Tyr Arg Ala Leu Gly Gly Cys
 675 680 685

Thr Arg Pro His Val Ile Leu Arg Glu Gly Leu His Gly Arg Glu Ile
 690 695 700

Thr Cys Val Lys Arg Val Gly Thr Ile Thr Leu Gly Pro Glu Tyr Gly
 705 710 715 720

Val Pro Ser Phe Met Gln Pro Asp Asp Leu Glu Pro Gly Ser Glu Gly
 725 730 735

Pro Asp Leu Thr Asp Ile Val Ile Thr Cys Ser Glu Asp Thr Thr Val
 740 745 750

Cys Val Leu Ala Leu Pro Thr Thr Thr Gly Ser Ala His Ala Leu Thr
 755 760 765

Ala Val Cys Asn His Ile Ser Ser Val Arg Ala Val Ala Val Trp Gly
 770 775 780

Ile Gly Thr Pro Gly Gly Pro Gln Asp Pro Gln Pro Gly Leu Thr Ala
 785 790 795 800

His Val Val Ser Ala Gly Gly Arg Ala Glu Met His Cys Phe Ser Ile
 805 810 815

Met Val Thr Pro Asp Pro Ser Thr Pro Ser Arg Leu Ala Cys His Val
 820 825 830

Met His Leu Ser Ser His Arg Leu Asp Glu Tyr Trp Asp Arg Gln Arg
 835 840 845

Asn Arg His Arg Met Val Lys Val Asp Pro Glu Thr Arg Tyr Met Ser
 850 855 860

Leu Ala Val Cys Glu Leu Asp Gln Pro Gly Leu Gly Pro Leu Val Ala
 865 870 875 880

Ala Ala Cys Ser Asp Gly Ala Val Arg Leu Phe Leu Leu Gln Asp Ser
 885 890 895

Gly Arg Ile Leu Gln Leu Leu Ala Glu Thr Phe His His Lys Arg Cys
 900 905 910

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Val Leu Lys Val His Ser Phe Thr His Glu Ala Pro Asn Gln Arg Arg
915 920 925

Arg Leu Leu Leu Cys Ser Ala Ala Thr Asp Gly Ser Leu Ala Phe Trp
930 935 940

Asp Leu Thr Thr Met Leu Asp His Asp Ser Thr Val Leu Glu Pro Pro
945 950 955 960

Val Asp Pro Gly Leu Pro Tyr Arg Leu Gly Thr Pro Ser Leu Thr Leu
965 970 975

Gln Ala His Ser Cys Gly Ile Asn Ser Leu His Thr Leu Pro Thr Arg
980 985 990

Glu Gly His His Leu Val Ala Ser Gly Ser Glu Asp Gly Ser Leu His
995 1000 1005

Val Phe Val Leu Ala Val Glu Met Leu Gln Leu Glu Glu Ala Val
1010 1015 1020

Gly Glu Ala Gly Leu Val Pro Gln Leu Arg Val Leu Glu Glu Tyr
1025 1030 1035

Ser Val Pro Cys Ala His Ala Ala His Val Thr Gly Leu Lys Ile
1040 1045 1050

Leu Ser Pro Ser Ile Met Val Ser Ala Ser Ile Asp Gln Arg Leu
1055 1060 1065

Thr Phe Trp Arg Leu Gly His Gly Glu Pro Thr Phe Met Asn Ser
1070 1075 1080

Thr Val Phe His Val Pro Asp Val Ala Asp Met Asp Cys Trp Pro
1085 1090 1095

Val Ser Pro Glu Phe Gly His Arg Cys Ala Leu Gly Gly Gln Gly
1100 1105 1110

Leu Glu Val Tyr Asn Trp Tyr Asp
1115 1120

<210> 107
<211> 79
<212> PRT
<213> Homo sapiens

<400> 107

Met Ala Ala Ser Gly Pro Gly Cys Arg Ser Trp Cys Leu Cys Pro Glu
1 5 10 15

Val Pro Ser Ala Thr Phe Phe Thr Ala Leu Leu Ser Leu Leu Val Ser
20 25 30

Gly Pro Arg Leu Phe Leu Leu Gln Gln Pro Leu Ala Pro Ser Gly Leu
35 40 45

Thr Leu Lys Ser Glu Ala Leu Arg Asn Trp Gln Ala Thr Met Glu Gly
50 55 60

Gly Val Arg Ile Thr Ala Glu Glu Thr Gly Thr Gln Ser Val Lys
65 70 75

<210> 108
<211> 801

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

<212> PRT
 <213> Homo sapiens

<400> 108

Met Leu Gln Asn Val Thr Pro His Asn Lys Leu Pro Gly Glu Gly Asn
 1 5 10 15

Ala Gly Leu Leu Gly Leu Gly Pro Glu Ala Ala Ala Pro Gly Lys Arg
 20 25 30

Ile Arg Lys Pro Ser Leu Leu Tyr Glu Gly Phe Glu Ser Pro Thr Met
 35 40 45

Ala Ser Val Pro Ala Leu Gln Leu Thr Pro Ala Asn Pro Pro Pro Pro
 50 55 60

Glu Val Ser Asn Pro Lys Lys Pro Gly Arg Val Thr Asn Gln Leu Gln
 65 70 75 80

Tyr Leu His Lys Val Val Met Lys Ala Leu Trp Lys His Gln Phe Ala
 85 90 95

Trp Pro Phe Arg Gln Pro Val Asp Ala Val Lys Leu Gly Leu Pro Asp
 100 105 110

Tyr His Lys Ile Ile Lys Gln Pro Met Asp Met Gly Thr Ile Lys Arg
 115 120 125

Arg Leu Glu Asn Asn Tyr Tyr Trp Ala Ala Ser Glu Cys Met Gln Asp
 130 135 140

Phe Asn Thr Met Phe Thr Asn Cys Tyr Ile Tyr Asn Lys Pro Thr Asp
 145 150 155 160

Asp Ile Val Leu Met Ala Gln Thr Leu Glu Lys Ile Phe Leu Gln Lys
 165 170 175

Val Ala Ser Met Pro Gln Glu Glu Gln Glu Leu Val Val Thr Ile Pro
 180 185 190

Lys Asn Ser His Lys Lys Gly Ala Lys Leu Ala Ala Leu Gln Gly Ser
 195 200 205

Val Thr Ser Ala His Gln Val Pro Ala Val Ser Ser Val Ser His Thr
 210 215 220

Ala Leu Tyr Thr Pro Pro Pro Glu Ile Pro Thr Thr Val Leu Asn Ile
 225 230 235 240

Pro His Pro Ser Val Ile Ser Ser Pro Leu Leu Lys Ser Leu His Ser
 245 250 255

Ala Gly Pro Pro Leu Leu Ala Val Thr Ala Ala Pro Pro Ala Gln Pro
 260 265 270

Leu Ala Lys Lys Lys Gly Val Lys Arg Lys Ala Asp Thr Thr Thr Pro
 275 280 285

Thr pro Thr Ala Ile Leu Ala Pro Gly Ser Pro Ala Ser Pro Pro Gly
 290 295 300

Ser Leu Glu Pro Lys Ala Ala Arg Leu Pro Pro Met Arg Arg Glu Ser
 305 310 315 320

Gly Arg Pro Ile Lys Pro Pro Arg Lys Asp Leu Pro Asp Ser Gln Gln

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 325 330 335

Gln His Gln Ser Ser Lys Lys Gly Lys Leu Ser Glu Gln Leu Lys His
 340 345 350

Cys Asn Gly Ile Leu Lys Glu Leu Leu Ser Lys Lys His Ala Ala Tyr
 355 360 365

Ala Trp Pro Phe Tyr Lys Pro Val Asp Ala Ser Ala Leu Gly Leu His
 370 375 380

Asp Tyr His Asp Ile Ile Lys His Pro Met Asp Leu Ser Thr Val Lys
 385 390 395 400

Arg Lys Met Glu Asn Arg Asp Tyr Arg Asp Ala Gln Glu Phe Ala Ala
 405 410 415

Asp Val Arg Leu Met Phe Ser Asn Cys Tyr Lys Tyr Asn Pro Pro Asp
 420 425 430

His Asp Val Val Ala Met Ala Arg Lys Leu Gln Asp Val Phe Glu Phe
 435 440 445

Arg Tyr Ala Lys Met Pro Asp Glu Pro Leu Glu Pro Gly Pro Leu Pro
 450 455 460

Val Ser Thr Ala Met Pro Pro Gly Leu Ala Lys Ser Ser Ser Glu Ser
 465 470 475 480

Ser Ser Glu Glu Ser Ser Glu Ser Ser Ser Glu Glu Glu Glu Glu
 485 490 495

Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Ser Glu Ser Ser Asp Ser
 500 505 510

Glu Glu Glu Arg Ala His Arg Leu Ala Glu Leu Gln Glu Gln Leu Arg
 515 520 525

Ala Val His Glu Gln Leu Ala Ala Leu Ser Gln Gly Pro Ile Ser Lys
 530 535 540

Pro Lys Arg Lys Arg Glu Lys Lys Glu Lys Lys Lys Lys Arg Lys Ala
 545 550 555 560

Glu Lys His Arg Gly Arg Ala Gly Ala Asp Glu Asp Asp Lys Gly Pro
 565 570 575

Arg Ala Pro Arg Pro Pro Gln Pro Lys Lys Ser Lys Lys Ala Ser Gly
 580 585 590

Ser Gly Gly Gly Ser Ala Ala Leu Gly Pro Ser Gly Phe Gly Pro Ser
 595 600 605

Gly Gly Ser Gly Thr Lys Leu Pro Lys Lys Ala Thr Lys Thr Ala Pro
 610 615 620

Pro Ala Leu Pro Thr Gly Tyr Asp Ser Glu Glu Glu Glu Glu Ser Arg
 625 630 635 640

Pro Met Ser Tyr Asp Glu Lys Arg Gln Leu Ser Leu Asp Ile Asn Lys
 645 650 655

Leu Pro Gly Glu Lys Leu Gly Arg Val Val His Ile Ile Gln Ala Arg
 660 665 670

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Glu Pro Ser Leu Arg Asp Ser Asn Pro Glu Glu Ile Glu Ile Asp Phe
675 680 685

Glu Thr Leu Lys Pro Ser Thr Leu Arg Glu Leu Glu Arg Tyr Val Leu
690 695 700

Ser Cys Leu Arg Lys Lys Pro Arg Lys Pro Tyr Thr Ile Lys Lys Pro
705 710 715 720

Val Gly Lys Thr Lys Glu Glu Leu Ala Leu Glu Lys Lys Arg Glu Leu
725 730 735

Glu Lys Arg Leu Gln Asp Val Ser Gly Gln Leu Asn Ser Thr Lys Lys
740 745 750

Pro Pro Lys Lys Ala Asn Glu Lys Thr Glu Ser Ser Ser Ala Gln Gln
755 760 765

Val Ala Val Ser Arg Leu Ser Ala Ser Ser Ser Ser Ser Asp Ser Ser
770 775 780

Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Thr Ser Asp Ser Asp Ser
785 790 795 800

Gly

<210> 109
<211> 1362
<212> PRT
<213> Homo sapiens

<400> 109

Met Ser Ala Glu Ser Gly Pro Gly Thr Arg Leu Arg Asn Leu Pro Val
1 5 10 15

Met Gly Asp Gly Leu Glu Thr Ser Gln Met Ser Thr Thr Gln Ala Gln
20 25 30

Ala Gln Pro Gln Pro Ala Asn Ala Ala Ser Thr Asn Pro Pro Pro Pro
35 40 45

Glu Thr Ser Asn Pro Asn Lys Pro Lys Arg Gln Thr Asn Gln Leu Gln
50 55 60

Tyr Leu Leu Arg Val Val Leu Lys Thr Leu Trp Lys His Gln Phe Ala
65 70 75 80

Trp Pro Phe Gln Gln Pro Val Asp Ala Val Lys Leu Asn Leu Pro Asp
85 90 95

Tyr Tyr Lys Ile Ile Lys Thr Pro Met Asp Met Gly Thr Ile Lys Lys
100 105 110

Arg Leu Glu Asn Asn Tyr Tyr Trp Asn Ala Gln Glu Cys Ile Gln Asp
115 120 125

Phe Asn Thr Met Phe Thr Asn Cys Tyr Ile Tyr Asn Lys Pro Gly Asp
130 135 140

Asp Ile Val Leu Met Ala Glu Ala Leu Glu Lys Leu Phe Leu Gln Lys
145 150 155 160

Ile Asn Glu Leu Pro Thr Glu Glu Thr Glu Ile Met Ile Val Gln Ala
165 170 175

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Lys Gly Arg Gly Arg Gly Arg Lys Glu Thr Gly Thr Ala Lys Pro Gly
180 185 190

Val Ser Thr Val Pro Asn Thr Thr Gln Ala Ser Thr Pro Pro Gln Thr
195 200 205

Gln Thr Pro Gln Pro Asn Pro Pro Pro Val Gln Ala Thr Pro His Pro
210 215 220

Phe Pro Ala Val Thr Pro Asp Leu Ile Val Gln Thr Pro Val Met Thr
225 230 235 240

Val Val Pro Pro Gln Pro Leu Gln Thr Pro Pro Pro Val Pro Pro Gln
245 250 255

Pro Gln Pro Pro Pro Ala Pro Ala Pro Gln Pro Val Gln Ser His Pro
260 265 270

Pro Ile Ile Ala Ala Thr Pro Gln Pro Val Lys Thr Lys Lys Gly Val
275 280 285

Lys Arg Lys Ala Asp Thr Thr Thr Pro Thr Thr Ile Asp Pro Ile His
290 295 300

Glu Pro Pro Ser Leu Pro Pro Glu Pro Lys Thr Thr Lys Leu Gly Gln
305 310 315 320

Arg Arg Glu Ser Ser Arg Pro Val Lys Pro Pro Lys Lys Asp Val Pro
325 330 335

Asp Ser Gln Gln His Pro Ala Pro Glu Lys Ser Ser Lys Val Ser Glu
340 345 350

Gln Leu Lys Cys Cys Ser Gly Ile Leu Lys Glu Met Phe Ala Lys Lys
355 360 365

His Ala Ala Tyr Ala Trp Pro Phe Tyr Lys Pro Val Asp Val Glu Ala
370 375 380

Leu Gly Leu His Asp Tyr Cys Asp Ile Ile Lys His Pro Met Asp Met
385 390 395 400

Ser Thr Ile Lys Ser Lys Leu Glu Ala Arg Glu Tyr Arg Asp Ala Gln
405 410 415

Glu Phe Gly Ala Asp Val Arg Leu Met Phe Ser Asn Cys Tyr Lys Tyr
420 425 430

Asn Pro Pro Asp His Glu Val Val Ala Met Ala Arg Lys Leu Gln Asp
435 440 445

Val Phe Glu Met Arg Phe Ala Lys Met Pro Asp Glu Pro Glu Glu Pro
450 455 460

Val Val Ala Val Ser Ser Pro Ala Val Pro Pro Pro Thr-Lys Val Val
465 470 475 480

Ala Pro Pro Ser Ser Ser Asp Ser Ser Ser Asp Ser Ser Ser Asp Ser
485 490 495

Asp Ser Ser Thr Asp Asp Ser Glu Glu Glu Arg Ala Gln Arg Leu Ala
500 505 510

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 Glu Leu Gln Glu Gln Leu Lys Ala Val His Glu Gln Leu Ala Ala Leu
 515 520 525

Ser Gln Pro Gln Gln Asn Lys Pro Lys Lys Lys Glu Lys Asp Lys Lys
 530 535 540

Glu Lys Lys Lys Glu Lys His Lys Arg Lys Glu Glu Val Glu Glu Asn
 545 550 555 560

Lys Lys Ser Lys Ala Lys Glu Pro Pro Pro Lys Lys Thr Lys Lys Asn
 565 570 575

Asn Ser Ser Asn Ser Asn Val Ser Lys Lys Glu Pro Ala Pro Met Lys
 580 585 590

Ser Lys Pro Pro Pro Thr Tyr Glu Ser Glu Glu Glu Asp Lys Cys Lys
 595 600 605

Pro Met Ser Tyr Glu Glu Lys Arg Gln Leu Ser Leu Asp Ile Asn Lys
 610 615 620

Leu Pro Gly Glu Lys Leu Gly Arg Val Val His Ile Ile Gln Ser Arg
 625 630 635 640

Glu Pro Ser Leu Lys Asn Ser Asn Pro Asp Glu Ile Glu Ile Asp Phe
 645 650 655

Glu Thr Leu Lys Pro Ser Thr Leu Arg Glu Leu Glu Arg Tyr Val Thr
 660 665 670

Ser Cys Leu Arg Lys Lys Arg Lys Pro Gln Ala Glu Lys Val Asp Val
 675 680 685

Ile Ala Gly Ser Ser Lys Met Lys Gly Phe Ser Ser Ser Glu Ser Glu
 690 695 700

Ser Ser Ser Glu Ser Ser Ser Ser Asp Ser Glu Asp Ser Glu Thr Glu
 705 710 715 720

Met Ala Pro Lys Ser Lys Lys Lys Gly His Pro Gly Arg Glu Gln Lys
 725 730 735

Lys His His His His His His Gln Gln Met Gln Gln Ala Pro Ala Pro
 740 745 750

Val Pro Gln Gln Pro Pro Pro Pro Pro Gln Gln Pro Pro Pro Pro Pro
 755 760 765

Pro Pro Gln Gln Gln Gln Gln Pro Pro Pro Pro Pro Pro Pro Ser
 770 775 780

Met Pro Gln Gln Ala Ala Pro Ala Met Lys Ser Ser Pro Pro Pro Phe
 785 790 795 800

Ile Ala Thr Gln Val Pro Val Leu Glu Pro Gln Leu Pro Gly Ser Val
 805 810 815

Phe Asp Pro Ile Gly His Phe Thr Gln Pro Ile Leu His Leu Pro Gln
 820 825 830

Pro Glu Leu Pro Pro His Leu Pro Gln Pro Pro Glu His Ser Thr Pro
 835 840 845

Pro His Leu Asn Gln His Ala Val Val Ser Pro Pro Ala Leu His Asn
 850 855 860

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ala Leu Pro Gln Gln Pro Ser Arg Pro Ser Asn Arg Ala Ala Ala Leu
865 870 875 880

Pro Pro Lys Pro Ala Arg Pro Pro Ala Val Ser Pro Ala Leu Thr Gln
885 890 895

Thr Pro Leu Leu Pro Gln Pro Pro Met Ala Gln Pro Pro Gln Val Leu
900 905 910

Leu Glu Asp Glu Glu Pro Pro Ala Pro Pro Leu Thr Ser Met Gln Met
915 920 925

Gln Leu Tyr Leu Gln Gln Leu Gln Lys Val Gln Pro Pro Thr Pro Leu
930 935 940

Leu Pro Ser Val Lys Val Gln Ser Gln Pro Pro Pro Pro Leu Pro Pro
945 950 955 960

Pro Pro His Pro Ser Val Gln Gln Gln Leu Gln Gln Gln Pro Pro Pro
965 970 975

Pro Pro Pro Pro Gln Pro Gln Pro Pro Pro Gln Gln Gln His Gln Pro
980 985 990

Pro Pro Arg Pro Val His Leu Gln Pro Met Gln Phe Ser Thr His Ile
995 1000 1005

Gln Gln Pro Pro Pro Pro Gln Gly Gln Gln Pro Pro His Pro Pro
1010 1015 1020

Pro Gly Gln Gln Pro Pro Pro Pro Gln Pro Ala Lys Pro Gln Gln
1025 1030 1035

Val Ile Gln His His His Ser Pro Arg His His Lys Ser Asp Pro
1040 1045 1050

Tyr Ser Thr Gly His Leu Arg Glu Ala Pro Ser Pro Leu Met Ile
1055 1060 1065

His Ser Pro Gln Met Ser Gln Phe Gln Ser Leu Thr His Gln Ser
1070 1075 1080

Pro Pro Gln Gln Asn Val Gln Pro Lys Lys Gln Glu Leu Arg Ala
1085 1090 1095

Ala Ser Val Val Gln Pro Gln Pro Leu Val Val Val Lys Glu Glu
1100 1105 1110

Lys Ile His Ser Pro Ile Ile Arg Ser Glu Pro Phe Ser Pro Ser
1115 1120 1125

Leu Arg Pro Glu Pro Pro Lys His Pro Glu Ser Ile Lys Ala Pro
1130 1135 1140

Val His Leu Pro Gln Arg Pro Glu Met Lys Pro Val Asp Val Gly
1145 1150 1155

Arg Pro Val Ile Arg Pro Pro Glu Gln Asn Ala Pro Pro Pro Gly
1160 1165 1170

Ala Pro Asp Lys Asp Lys Gln Lys Gln Glu Pro Lys Thr Pro Val
1175 1180 1185

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ala Pro Lys Lys Asp Leu Lys Ile Lys Asn Met Gly Ser Trp Ala
 1190 1195 1200

Ser Leu Val Gln Lys His Pro Thr Thr Pro Ser Ser Thr Ala Lys
 1205 1210 1215

Ser Ser Ser Asp Ser Phe Glu Gln Phe Arg Arg Ala Ala Arg Glu
 1220 1225 1230

Lys Glu Glu Arg Glu Lys Ala Leu Lys Ala Gln Ala Glu His Ala
 1235 1240 1245

Glu Lys Glu Lys Glu Arg Leu Arg Gln Glu Arg Met Arg Ser Arg
 1250 1255 1260

Glu Asp Glu Asp Ala Leu Glu Gln Ala Arg Arg Ala His Glu Glu
 1265 1270 1275

Ala Arg Arg Arg Gln Glu Gln Gln Gln Gln Arg Gln Glu Gln
 1280 1285 1290

Gln Gln Gln Gln Gln Gln Ala Ala Ala Val Ala Ala Ala Ala
 1295 1300 1305

Thr Pro Gln Ala Gln Ser Ser Gln Pro Gln Ser Met Leu Asp Gln
 1310 1315 1320

Gln Arg Glu Leu Ala Arg Lys Arg Glu Gln Glu Arg Arg Arg Arg
 1325 1330 1335

Glu Ala Met Ala Ala Thr Ile Asp Met Asn Phe Gln Ser Asp Leu
 1340 1345 1350

Leu Ser Ile Phe Glu Glu Asn Leu Phe
 1355 1360

<210> 110
 <211> 292
 <212> PRT
 <213> Homo sapiens

<400> 110

Met Gln Lys Tyr Glu Lys Leu Glu Lys Ile Gly Glu Gly Thr Tyr Gly
 1 5 10 15

Thr Val Phe Lys Ala Lys Asn Arg Glu Thr His Glu Ile Val Ala Leu
 20 25 30

Lys Arg Val Arg Leu Asp Asp Asp Asp Glu Gly Val Pro Ser Ser Ala
 35 40 45

Leu Arg Glu Ile Cys Leu Leu Lys Glu Leu Lys His Lys Asn Ile Val
 50 55 60

Arg Leu His Asp Val Leu His Ser Asp Lys Lys Leu Thr Leu Val Phe
 65 70 75 80

Glu Phe Cys Asp Gln Asp Leu Lys Lys Tyr Phe Asp Ser Cys Asn Gly
 85 90 95

Asp Leu Asp Pro Glu Ile Val Lys Ser Phe Leu Phe Gln Leu Leu Lys
 100 105 110

Gly Leu Gly Phe Cys His Ser Arg Asn Val Leu His Arg Asp Leu Lys
 115 120 125

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Pro Gln Asn Leu Leu Ile Asn Arg Asn Gly Glu Leu Lys Leu Ala Asp
130 135 140

Phe Gly Leu Ala Arg Ala Phe Gly Ile Pro Val Arg Cys Tyr Ser Ala
145 150 155 160

Glu Val Val Thr Leu Trp Tyr Arg Pro Pro Asp Val Leu Phe Gly Ala
165 170 175

Lys Leu Tyr Ser Thr Ser Ile Asp Met Trp Ser Ala Gly Cys Ile Phe
180 185 190

Ala Glu Leu Ala Asn Ala Gly Arg Pro Leu Phe Pro Gly Asn Asp Val
195 200 205

Asp Asp Gln Leu Lys Arg Ile Phe Arg Leu Leu Gly Thr Pro Thr Glu
210 215 220

Glu Gln Trp Pro Ser Met Thr Lys Leu Pro Asp Tyr Lys Pro Tyr Pro
225 230 235 240

Met Tyr Pro Ala Thr Thr Ser Leu Val Asn Val Val Pro Lys Leu Asn
245 250 255

Ala Thr Gly Arg Asp Leu Leu Gln Asn Leu Leu Lys Cys Asn Pro Val
260 265 270

Gln Arg Ile Ser Ala Glu Glu Ala Leu Gln His Pro Tyr Phe Ser Asp
275 280 285

Phe Cys Pro Pro
290

<210> 111
<211> 765
<212> PRT
<213> Homo sapiens

<400> 111

Met Ser Gly Asp His Leu His Asn Asp Ser Gln Ile Glu Ala Asp Phe
1 5 10 15

Arg Leu Asn Asp Ser His Lys His Lys Asp Lys His Lys Asp Arg Glu
20 25 30

His Arg His Lys Glu His Lys Lys Glu Lys Asp Arg Glu Lys Ser Lys
35 40 45

His Ser Asn Ser Glu His Lys Asp Ser Glu Lys Lys His Lys Glu Lys
50 55 60

Glu Lys Thr Lys His Lys Asp Gly Ser Ser Glu Lys His Lys Asp Lys
65 70 75 80

His Lys Asp Arg Asp Lys Glu Lys Arg Lys Glu Glu Lys Val Arg Ala
85 90 95

Ser Gly Asp Ala Lys Ile Lys Lys Glu Lys Glu Asn Gly Phe Ser Ser
100 105 110

Pro pro Gln Ile Lys Asp Glu Pro Glu Asp Asp Gly Tyr Phe Val Pro
115 120 125

Pro Lys Glu Asp Ile Lys Pro Leu Lys Arg Pro Arg Asp Glu Asp Asp
130 135 140

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ala Asp Tyr Lys Pro Lys Lys Ile Lys Thr Glu Asp Thr Lys Lys Glu
145 150 155 160

Lys Lys Arg Lys Leu Glu Glu Glu Glu Asp Gly Lys Leu Lys Lys Pro
165 170 175

Lys Asn Lys Asp Lys Asp Lys Lys Val Pro Glu Pro Asp Asn Lys Lys
180 185 190

Lys Lys Pro Lys Lys Glu Glu Glu Gln Lys Trp Lys Trp Trp Glu Glu
195 200 205

Glu Arg Tyr Pro Glu Gly Ile Lys Trp Lys Phe Leu Glu His Lys Gly
210 215 220

Pro Val Phe Ala Pro Pro Tyr Glu Pro Leu Pro Glu Asn Val Lys Phe
225 230 235 240

Tyr Tyr Asp Gly Lys Val Met Lys Leu Ser Pro Lys Ala Glu Glu Val
245 250 255

Ala Thr Phe Phe Ala Lys Met Leu Asp His Glu Tyr Thr Thr Lys Glu
260 265 270

Ile Phe Arg Lys Asn Phe Phe Lys Asp Trp Arg Lys Glu Met Thr Asn
275 280 285

Glu Glu Lys Asn Ile Ile Thr Asn Leu Ser Lys Cys Asp Phe Thr Gln
290 295 300

Met Ser Gln Tyr Phe Lys Ala Gln Thr Glu Ala Arg Lys Gln Met Ser
305 310 315 320

Lys Glu Glu Lys Leu Lys Ile Lys Glu Glu Asn Glu Lys Leu Leu Lys
325 330 335

Glu Tyr Gly Phe Cys Ile Met Asp Asn His Lys Glu Arg Ile Ala Asn
340 345 350

Phe Lys Ile Glu Pro Pro Gly Leu Phe Arg Gly Arg Gly Asn His Pro
355 360 365

Lys Met Gly Met Leu Lys Arg Arg Ile Met Pro Glu Asp Ile Ile Ile
370 375 380

Asn Cys Ser Lys Asp Ala Lys Val Pro Ser Pro Pro Gly His Lys
385 390 395 400

Trp Lys Glu Val Arg His Asp Asn Lys Val Thr Trp Leu Val Ser Trp
405 410 415

Thr Glu Asn Ile Gln Gly Ser Ile Lys Tyr Ile Met Leu Asn Pro Ser
420 425 430

Ser Arg Ile Lys Gly Glu Lys Asp Trp Gln Lys Tyr Glu Thr Ala Arg
435 440 445

Arg Leu Lys Lys Cys Val Asp Lys Ile Arg Asn Gln Tyr Arg Glu Asp
450 455 460

Trp Lys Ser Lys Glu Met Lys Val Arg Gln Arg Ala Val Ala Leu Tyr
465 470 475 480

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Phe Ile Asp Lys Leu Ala Leu Arg Ala Gly Asn Glu Lys Glu Glu Gly
485 490 495

Glu Thr Ala Asp Thr Val Gly Cys Cys Ser Leu Arg Val Glu His Ile
500 505 510

Asn Leu His Pro Glu Leu Asp Gly Gln Glu Tyr Val Val Glu Phe Asp
515 520 525

Phe Leu Gly Lys Asp Ser Ile Arg Tyr Tyr Asn Lys Val Pro Val Glu
530 535 540

Lys Arg Val Phe Lys Asn Leu Gln Leu Phe Met Glu Asn Lys Gln Pro
545 550 555 560

Glu Asp Asp Leu Phe Asp Arg Leu Asn Thr Gly Ile Leu Asn Lys His
565 570 575

Leu Gln Asp Leu Met Glu Gly Leu Thr Ala Lys Val Phe Arg Thr Tyr
580 585 590

Asn Ala Ser Ile Thr Leu Gln Gln Gln Leu Lys Glu Leu Thr Ala Pro
595 600 605

Asp Glu Asn Ile Pro Ala Lys Ile Leu Ser Tyr Asn Arg Ala Asn Arg
610 615 620

Ala Val Ala Ile Leu Cys Asn His Gln Arg Ala Pro Pro Lys Thr Phe
625 630 635 640

Glu Lys Ser Met Met Asn Leu Gln Thr Lys Ile Asp Ala Lys Lys Glu
645 650 655

Gln Leu Ala Asp Ala Arg Arg Asp Leu Lys Ser Ala Lys Ala Asp Ala
660 665 670

Lys Val Met Lys Asp Ala Lys Thr Lys Lys Val Val Glu Ser Lys Lys
675 680 685

Lys Ala Val Gln Arg Leu Glu Glu Gln Leu Met Lys Leu Glu Val Gln
690 695 700

Ala Thr Asp Arg Glu Glu Asn Lys Gln Ile Ala Leu Gly Thr Ser Lys
705 710 715 720

Leu Asn Tyr Leu Asp Pro Arg Ile Thr Val Ala Trp Cys Lys Lys Trp
725 730 735

Gly Val Pro Ile Glu Lys Ile Tyr Asn Lys Thr Gln Arg Glu Lys Phe
740 745 750

Ala Trp Ala Ile Asp Met Ala Asp Glu Asp Tyr Glu Phe
755 760 765

<210> 112
<211> 691
<212> PRT
<213> Homo sapiens

<400> 112

Met Ala Ala Gly Val Glu Ala Ala Ala Glu Val Ala Ala Thr Glu Ile
1 5 10 15

Lys Met Glu Glu Glu Ser Gly Ala Pro Gly Val Pro Ser Gly Asn Gly
20 25 30

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ala Pro Gly Pro Lys Gly Glu Gly Glu Arg Pro Ala Gln Asn Glu Lys
35 40 45

Arg Lys Glu Lys Asn Ile Lys Arg Gly Gly Asn Arg Phe Glu Pro Tyr
50 55 60

Ala Asn Pro Thr Lys Arg Tyr Arg Ala Phe Ile Thr Asn Ile Pro Phe
65 70 75 80

Asp Val Lys Trp Gln Ser Leu Lys Asp Leu Val Lys Glu Lys Val Gly
85 90 95

Glu Val Thr Tyr Val Glu Leu Leu Met Asp Ala Glu Gly Lys Ser Arg
100 105 110

Leu Tyr Ser Val Val Glu Phe Lys Met Glu Glu Ser Met Lys Lys Ala
115 120 125

Ala Glu Val Leu Asn Lys His Ser Leu Ser Gly Arg Pro Leu Lys Val
130 135 140

Lys Glu Asp Pro Asp Gly Glu His Ala Arg Arg Ala Met Gln Lys Ala
145 150 155 160

Gly Arg Leu Gly Ser Thr Val Phe Val Ala Asn Leu Asp Tyr Lys Val
165 170 175

Gly Trp Lys Lys Leu Lys Glu Val Phe Ser Met Ala Gly Val Val Val
180 185 190

Arg Ala Asp Ile Leu Glu Asp Lys Asp Gly Lys Ser Arg Gly Ile Gly
195 200 205

Thr Val Thr Phe Glu Gln Ser Ile Glu Ala Val Gln Ala Ile Ser Met
210 215 220

Phe Asn Gly Gln Leu Leu Phe Asp Arg Pro Met His Val Lys Met Asp
225 230 235 240

Glu Arg Ala Leu Pro Lys Gly Asp Phe Phe Pro Pro Glu Arg Pro Gln
245 250 255

Gln Leu Pro His Gly Leu Gly Gly Ile Gly Met Gly Leu Gly Pro Gly
260 265 270

Gly Gln Pro Ile Asp Ala Asn His Leu Asn Lys Gly Ile Gly Met Gly
275 280 285

Asn Ile Gly Pro Ala Gly Met Gly Met Glu Gly Ile Gly Phe Gly Ile
290 295 300

Asn Lys Met Gly Gly Met Glu Gly Pro Phe Gly Gly Gly Met Glu Asn
305 310 315 320

Met Gly Arg Phe Gly Ser Gly Met Asn Met Gly Arg Ile Asn Glu Ile
325 330 335

Leu Ser Asn Ala Leu Lys Arg Gly Glu Ile Ile Ala Lys Gln Gly Gly
340 345 350

Gly Gly Gly Gly Gly Ser Val Pro Gly Ile Glu Arg Met Gly Pro Gly
355 360 365

Ile Asp Arg Leu Gly Gly Ala Gly Met Glu Arg Met Gly Ala Gly Leu

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
370 375 380

Gly His Gly Met Asp Arg Val Gly Ser Glu Ile Glu Arg Met Gly Leu
385 390 395 400

Val Met Asp Arg Met Gly Ser Val Glu Arg Met Gly Ser Gly Ile Glu
405 410 415

Arg Met Gly Pro Leu Gly Leu Asp His Met Ala Ser Ser Ile Glu Arg
420 425 430

Met Gly Gln Thr Met Glu Arg Ile Gly Ser Gly Val Glu Arg Met Gly
435 440 445

Ala Gly Met Gly Phe Gly Leu Glu Arg Met Ala Ala Pro Ile Asp Arg
450 455 460

Val Gly Gln Thr Ile Glu Arg Met Gly Ser Gly Val Glu Arg Met Gly
465 470 475 480

Pro Ala Ile Glu Arg Met Gly Leu Ser Met Glu Arg Met Val Pro Ala
485 490 495

Gly Met Gly Ala Gly Leu Glu Arg Met Gly Pro Val Met Asp Arg Met
500 505 510

Ala Thr Gly Leu Glu Arg Met Gly Ala Asn Asn Leu Glu Arg Met Gly
515 520 525

Leu Glu Arg Met Gly Ala Asn Ser Leu Glu Arg Met Gly Leu Glu Arg
530 535 540

Met Gly Ala Asn Ser Leu Glu Arg Met Gly Pro Ala Met Gly Pro Ala
545 550 555 560

Leu Gly Ala Gly Ile Glu Arg Met Gly Leu Ala Met Gly Gly Gly Gly
565 570 575

Gly Ala Ser Phe Asp Arg Ala Ile Glu Met Glu Arg Gly Asn Phe Gly
580 585 590

Gly Ser Phe Ala Gly Ser Phe Gly Gly Ala Gly Gly His Ala Pro Gly
595 600 605

Val Ala Arg Lys Ala Cys Gln Ile Phe Val Arg Asn Leu Pro Phe Asp
610 615 620

Phe Thr Trp Lys Met Leu Lys Asp Lys Phe Asn Glu Cys Gly His Val
625 630 635 640

Leu Tyr Ala Asp Ile Lys Met Glu Asn Gly Lys Ser Lys Gly Cys Gly
645 650 655

Val Val Lys Phe Glu Ser Pro Glu Val Ala Glu Arg Ala Cys Arg Met
660 665 670

Met Asn Gly Met Lys Leu Ser Gly Arg Glu Ile Asp Val Arg Ile Asp
675 680 685

Arg Asn Ala
690

<210> 113
<211> 211
<212> PRT

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 <213> Homo sapiens

<400> 113

Met Ala Pro Ser Arg Asn Gly Met Val Leu Lys Pro His Phe His Lys
 1 5 10 15

Asp Trp Gln Arg Arg Val Ala Thr Trp Phe Asn Gln Pro Ala Arg Lys
 20 25 30

Ile Arg Arg Arg Lys Ala Arg Gln Ala Lys Ala Arg Arg Ile Ala Pro
 35 40 45

Arg Pro Ala Ser Gly Pro Ile Arg Pro Ile Val Arg Cys Pro Thr Val
 50 55 60

Arg Tyr His Thr Lys Val Arg Ala Gly Arg Gly Phe Ser Leu Glu Glu
 65 70 75 80

Leu Arg Val Ala Gly Ile His Lys Lys Val Ala Arg Thr Ile Gly Ile
 85 90 95

Ser Val Asp Pro Arg Arg Arg Asn Lys Ser Thr Glu Ser Leu Gln Ala
 100 105 110

Asn Val Gln Arg Leu Lys Glu Tyr Arg Ser Lys Leu Ile Leu Phe Pro
 115 120 125

Arg Lys Pro Ser Ala Pro Lys Lys Gly Asp Ser Ser Ala Glu Glu Leu
 130 135 140

Lys Leu Ala Thr Gln Leu Thr Gly Pro Val Met Pro Val Arg Asn Val
 145 150 155 160

Tyr Lys Lys Glu Lys Ala Arg Val Ile Thr Glu Glu Glu Lys Asn Phe
 165 170 175

Lys Ala Phe Ala Ser Leu Arg Met Ala Arg Ala Asn Ala Arg Leu Phe
 180 185 190

Gly Ile Arg Ala Lys Arg Ala Lys Glu Ala Ala Glu Gln Asp Val Glu
 195 200 205

Lys Lys Lys
 210

<210> 114

<211> 605

<212> PRT

<213> Homo sapiens

<400> 114

Met Phe Val Cys Ile Asp Asp Leu Gly Asp Ser Val Val Leu Pro Gly
 1 5 10 15

Arg Gln Gln His Gly Arg Met Ala Ala Ile Leu Ile Leu Ile Leu Gln
 20 25 30

Leu Thr Phe Leu Lys Met Thr Ser Gly Asp Glu Val His Gly Thr Ser
 35 40 45

Ser Ile Leu Lys His Thr Ser Val Pro Gly Lys His Gln Asp Ser Leu
 50 55 60

Tyr Thr Leu Thr Arg Cys Pro Val Val Met Glu Thr Arg Ile Leu Thr
 65 70 75 80

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Thr Lys Asp Leu Glu Gly Val Arg Gly Cys Arg Leu Ala Gly Pro Ala
85 90 95

Val Gly Lys Lys Pro Gly Glu Arg Tyr Pro Pro Ile Gly Thr Phe Tyr
100 105 110

Cys Val Leu Lys Gly Val Gln Gly Pro Gly Ser Val Phe Asp Ile Val
115 120 125

Ala Asn Ser His Lys Tyr Pro Glu His Leu Ile Pro Ser Lys Met Gly
130 135 140

Leu Ser Pro Ala Cys Leu Pro Ser Ser Tyr Asp Pro Gly Lys Asp Cys
145 150 155 160

Ser Gly Arg Cys Pro Leu Cys Gly Trp Glu Ala Ser Glu Ala Arg Leu
165 170 175

Gln Ala His Gln Arg Val Cys Gly Arg Gly His Val Ala Ala Ile Phe
180 185 190

Cys Leu Leu Val Ser Val Cys Arg His Pro Met Glu Asp Ser Met Asp
195 200 205

Met His Met Ser Pro Leu Arg Pro Gln Asn Tyr Leu Phe Ser Cys Glu
210 215 220

Leu Lys Ala Asn Lys Asp Asp His Phe Lys Val Asp Asn Asp Glu Asn
225 230 235 240

Glu His Gln Leu Ser Leu Arg Thr Cys Gly Ser Gly Pro Val His Ile
245 250 255

Ser Gly Gln His Leu Val Ala Val Glu Glu Asp Ala Glu Ser Glu Asp
260 265 270

Glu Glu Glu Glu Ser Ala Lys Leu Leu Ser Ile Ser Gly Lys Gln Ser
275 280 285

Val Pro Gly Gly Gly Ser Lys Val Pro Gln Lys Gln Asp Cys Arg Asp
290 295 300

Ser Pro Arg Gly Ala Thr Ser Asp Glu Leu Gly Lys Ala Leu Gly Trp
305 310 315 320

Val Arg Ala Gly Gln Arg Pro Pro Ile Lys Glu Trp Gly Ser Gly Met
325 330 335

Glu Ala Gly Ser Val Gly Glu Pro Gly Gly Ala Ala Gly Ser Ser Gln
340 345 350

Gln Val Glu Glu Thr Pro Tyr Leu Ser Met Gly Ala Asp Cys Gln Glu
355 360 365

Arg Gln Glu Phe Cys Glu Leu Ala Ser Val Arg Val Ala Ser Ser Ala
370 375 380

Cys Ile Gly Ser Ser Gly Asp Val Ser Ser Leu Pro Pro Ser Phe Val
385 390 395 400

Lys His Lys Phe Gln Asp Asn Ile Ile Asn Thr Phe Lys Thr Ala Ala
405 410 415

Ala Glu His Gln Thr Arg Ser Val Gln Ala Pro Lys Cys Ala Ala Arg

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 420 425 430

Glu Ala Ala Leu Arg Pro Gly Ser Pro Val Ala Thr Gly Pro Leu His
 435 440 445

Trp Glu Thr Asp Leu Gly Leu Arg Asn Leu Arg Thr Gln Met Ser Ser
 450 455 460

Pro Leu Gln Trp Ser Gln Ser Arg Tyr Ser Gln Val Arg Gly Cys Ser
 465 470 475 480

Gln Ala Leu Ser Asp Ser Thr Val Ile Gln Glu Lys His His Thr Ser
 485 490 495

Val Pro Ser Thr Val Gly His Tyr Asn Arg Arg Gly Lys Ala Arg Val
 500 505 510

Gln Thr Pro Pro Arg Thr Pro Ser Arg Pro Pro Ser Ala Gly Ala Pro
 515 520 525

Glu Arg His Ala Pro Arg Gly Ser Pro Ala Pro Ser Arg Pro Gln Ser
 530 535 540

Ala Ala Glu Arg Asn Gly Asn Trp Ala Asp Ala Arg Arg Arg Leu Thr
 545 550 555 560

Ile Arg Ala Ala Arg Arg Leu Thr Ser Pro Cys Val Asp Gln Pro Pro
 565 570 575

Glu Pro Gly Lys Arg Arg Ser Leu Ile Gly Cys Ala Gly Gly Gly Leu
 580 585 590

Gly Ala Asn Asp Arg Ala Ala Ser Gly Gly Val Trp Pro
 595 600 605

<210> 115
 <211> 579
 <212> PRT
 <213> Homo sapiens

<400> 115

Met Asn Lys Leu Tyr Ile Gly Asn Leu Ser Glu Asn Ala Ala Pro Ser
 1 5 10 15

Asp Leu Glu Ser Ile Phe Lys Asp Ala Lys Ile Pro Val Ser Gly Pro
 20 25 30

Phe Leu Val Lys Thr Gly Tyr Ala Phe Val Asp Cys Pro Asp Glu Ser
 35 40 45

Trp Ala Leu Lys Ala Ile Glu Ala Leu Ser Gly Lys Ile Glu Leu His
 50 55 60

Gly Lys Pro Ile Glu Val Glu His Ser Val Pro Lys Arg Gln Arg Ile
 65 70 75 80

Arg Lys Leu Gln Ile Arg Asn Ile Pro Pro His Leu Gln Trp Glu Val
 85 90 95

Leu Asp Ser Leu Leu Val Gln Tyr Gly Val Val Glu Ser Cys Glu Gln
 100 105 110

Val Asn Thr Asp Ser Glu Thr Ala Val Val Asn Val Thr Tyr Ser Ser
 115 120 125

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Lys Asp Gln Ala Arg Gln Ala Leu Asp Lys Leu Asn Gly Phe Gln Leu
 130 135 140

Glu Asn Phe Thr Leu Lys Val Ala Tyr Ile Pro Asp Glu Met Ala Ala
 145 150 155 160

Gln Gln Asn Pro Leu Gln Gln Pro Arg Gly Arg Arg Gly Leu Gly Gln
 165 170 175

Arg Gly Ser Ser Arg Gln Gly Ser Pro Gly Ser Val Ser Lys Gln Lys
 180 185 190

Pro Cys Asp Leu Pro Leu Arg Leu Leu Val Pro Thr Gln Phe Val Gly
 195 200 205

Ala Ile Ile Gly Lys Glu Gly Ala Thr Ile Arg Asn Ile Thr Lys Gln
 210 215 220

Thr Gln Ser Lys Ile Asp Val His Arg Lys Glu Asn Ala Gly Ala Ala
 225 230 235 240

Glu Lys Ser Ile Thr Ile Leu Ser Thr Pro Glu Gly Thr Ser Ala Ala
 245 250 255

Cys Lys Ser Ile Leu Glu Ile Met His Lys Glu Ala Gln Asp Ile Lys
 260 265 270

Phe Thr Glu Glu Ile Pro Leu Lys Ile Leu Ala His Asn Asn Phe Val
 275 280 285

Gly Arg Leu Ile Gly Lys Glu Gly Arg Asn Leu Lys Lys Ile Glu Gln
 290 295 300

Asp Thr Asp Thr Lys Ile Thr Ile Ser Pro Leu Gln Glu Leu Thr Leu
 305 310 315 320

Tyr Asn Pro Glu Arg Thr Ile Thr Val Lys Gly Asn Val Glu Thr Cys
 325 330 335

Ala Lys Ala Glu Glu Glu Ile Met Lys Lys Ile Arg Glu Ser Tyr Glu
 340 345 350

Asn Asp Ile Ala Ser Met Asn Leu Gln Ala His Leu Ile Pro Gly Leu
 355 360 365

Asn Leu Asn Ala Leu Gly Leu Phe Pro Pro Thr Ser Gly Met Pro Pro
 370 375 380

Pro Thr Ser Gly Pro Pro Ser Ala Met Thr Pro Pro Tyr Pro Gln Phe
 385 390 395 400

Glu Gln Ser Glu Thr Glu Thr Val His Gln Phe Ile Pro Ala Leu Ser
 405 410 415

Val Gly Ala Ile Ile Gly Lys Gln Gly Gln His Ile Lys Gln Leu Ser
 420 425 430

Arg Phe Ala Gly Ala Ser Ile Lys Ile Ala Pro Ala Glu Ala Pro Asp
 435 440 445

Ala Lys Val Arg Met Val Ile Ile Thr Gly Pro Pro Glu Ala Gln Phe
 450 455 460

Lys Ala Gln Gly Arg Ile Tyr Gly Lys Ile Lys Glu Glu Asn Phe Val
 465 470 475 480

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ser Pro Lys Glu Glu Val Lys Leu Glu Ala His Ile Arg Val Pro Ser
485 490 495

Phe Ala Ala Gly Arg Val Ile Gly Lys Gly Gly Lys Thr Val Asn Glu
500 505 510

Leu Gln Asn Leu Ser Ser Ala Glu Val Val Val Pro Arg Asp Gln Thr
515 520 525

Pro Asp Glu Asn Asp Gln Val Val Val Lys Ile Thr Gly His Phe Tyr
530 535 540

Ala Cys Gln Val Ala Gln Arg Lys Ile Gln Glu Ile Leu Thr Gln Val
545 550 555 560

Lys Gln His Gln Gln Gln Lys Ala Leu Gln Ser Gly Pro Pro Gln Ser
565 570 575

Arg Arg Lys

<210> 116
<211> 1328
<212> PRT
<213> Homo sapiens

<400> 116

Met Glu Ser Arg Asp Pro Ala Gln Pro Met Ser Pro Gly Glu Ala Thr
1 5 10 15

Gln Ser Gly Ala Arg Pro Ala Asp Arg Tyr Gly Leu Leu Lys His Ser
20 25 30

Arg Glu Phe Leu Asp Phe Phe Trp Asp Ile Ala Lys Pro Glu Gln Glu
35 40 45

Thr Arg Leu Ala Ala Thr Glu Lys Leu Leu Glu Tyr Leu Arg Gly Arg
50 55 60

Pro Lys Gly Ser Glu Met Lys Tyr Ala Leu Lys Arg Leu Ile Thr Gly
65 70 75 80

Leu Gly Val Gly Arg Glu Thr Ala Arg Pro Cys Tyr Ser Leu Ala Leu
85 90 95

Ala Gln Leu Leu Gln Ser Phe Glu Asp Leu Pro Leu Cys Ser Ile Leu
100 105 110

Gln Gln Ile Gln Glu Lys Tyr Asp Leu His Gln Val Lys Lys Ala Met
115 120 125

Leu Arg Pro Ala Leu Phe Ala Asn Leu Phe Gly Val Leu Ala Leu Phe
130 135 140

Gln Ser Gly Arg Leu Val Lys Asp Gln Glu Ala Leu Met Lys Ser Val
145 150 155 160

Lys Leu Leu Gln Ala Leu Ala Gln Tyr Gln Asn His Leu Gln Glu Gln
165 170 175

Pro Arg Lys Ala Leu Val Asp Ile Leu Ser Glu Val Ser Lys Ala Thr
180 185 190

Leu Gln Glu Ile Leu Pro Glu Val Leu Lys Ala Asp Leu Asn Ile Ile

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 195 200 205

Leu Ser Ser Pro Glu Gln Leu Glu Leu Phe Leu Leu Ala Gln Gln Lys
 210 215 220

Val Pro Ser Lys Leu Lys Lys Leu Val Gly Ser Val Asn Leu Phe Ser
 225 230 235 240

Asp Glu Asn Val Pro Arg Leu Val Asn Val Leu Lys Met Ala Ala Ser
 245 250 255

Ser Val Lys Lys Asp Arg Lys Leu Pro Ala Ile Ala Leu Asp Leu Leu
 260 265 270

Arg Leu Ala Leu Lys Glu Asp Lys Phe Pro Arg Phe Trp Lys Glu Val
 275 280 285

Val Glu Gln Gly Leu Leu Lys Met Gln Phe Trp Pro Ala Ser Tyr Leu
 290 295 300

Cys Phe His Leu Leu Gly Ala Ala Leu Pro Leu Leu Thr Lys Glu Gln
 305 310 315 320

Leu His Leu Val Met Gln Gly Asp Val Ile Arg His Tyr Gly Glu His
 325 330 335

Val Cys Thr Ala Lys Leu Pro Lys Gln Phe Lys Phe Ala Pro Glu Met
 340 345 350

Asp Asp Tyr Val Gly Thr Phe Leu Glu Gly Cys Gln Asp Asp Pro Glu
 355 360 365

Arg Gln Leu Ala Val Leu Val Ala Phe Ser Ser Val Thr Asn Gln Gly
 370 375 380

Leu Pro Val Thr Pro Thr Phe Trp Arg Val Val Arg Phe Leu Ser Pro
 385 390 395 400

Pro Ala Leu Gln Gly Tyr Val Ala Trp Leu Arg Ala Met Phe Leu Gln
 405 410 415

Pro Asp Leu Asp Ser Leu Val Asp Phe Ser Thr Asn Asn Gln Lys Lys
 420 425 430

Ala Gln Asp Ser Ser Leu His Met Pro Glu Arg Ala Val Phe Arg Leu
 435 440 445

Arg Lys Trp Ile Ile Phe Arg Leu Val Ser Ile Val Asp Ser Leu His
 450 455 460

Leu Glu Met Glu Glu Ala Leu Thr Glu Gln Val Ala Arg Phe Cys Leu
 465 470 475 480

Phe His Ser Phe Phe Val Thr Lys Lys Pro Thr Ser Gln Ile Pro Glu
 485 490 495

Thr Lys His Pro Phe Ser Phe Pro Leu Glu Asn Gln Ala Arg Glu Ala
 500 505 510

Val Ser Ser Ala Phe Phe Ser Leu Leu Gln Thr Leu Ser Thr Gln Phe
 515 520 525

Lys Gln Ala Pro Gly Gln Thr Gln Gly Gly Gln Pro Trp Thr Tyr His
 530 535 540

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Leu Val Gln Phe Ala Asp Leu Leu Leu Asn His Ser His Asn Val Thr
 545 550 555 560

Thr Val Thr Pro Phe Thr Ala Gln Gln His Gln Ala Trp Asp Arg Met
 565 570 575

Leu Gln Thr Leu Lys Glu Leu Glu Ala His Ser Ala Glu Ala Arg Ala
 580 585 590

Ala Ala Phe Gln His Leu Leu Leu Phe Val Gly Ile His Leu Leu Lys
 595 600 605

Ser Pro Ala Glu Ser Cys Asp Leu Leu Gly Asp Ile Gln Thr Cys Ile
 610 615 620

Arg Lys Ser Leu Gly Glu Lys Pro Arg Arg Ser Arg Thr Lys Thr Ile
 625 630 635 640

Asp Pro Gln Glu Pro Pro Trp Val Glu Val Leu Val Glu Ile Leu Leu
 645 650 655

Ala Leu Leu Ala Gln Pro Ser His Leu Met Arg Gln Val Ala Arg Ser
 660 665 670

Val Phe Gly His Ile Cys Ser His Leu Thr Pro Arg Ala Leu Gln Leu
 675 680 685

Ile Leu Asp Val Leu Asn Pro Glu Thr Ser Glu Asp Glu Asn Asp Arg
 690 695 700

Val Val Val Thr Asp Asp Ser Asp Glu Arg Arg Leu Lys Gly Ala Glu
 705 710 715 720

Asp Lys Ser Glu Glu Gly Glu Asp Asn Arg Ser Ser Glu Ser Glu Glu
 725 730 735

Glu Ser Glu Gly Glu Glu Ser Glu Glu Glu Arg Asp Gly Asp Val
 740 745 750

Asp Gln Gly Phe Arg Glu Gln Leu Met Thr Val Leu Gln Ala Gly Lys
 755 760 765

Ala Leu Gly Gly Glu Asp Ser Glu Asn Glu Glu Glu Leu Gly Asp Glu
 770 775 780

Ala Met Met Ala Leu Asp Gln Ser Leu Ala Ser Leu Phe Ala Glu Gln
 785 790 795 800

Lys Leu Arg Ile Gln Ala Arg Arg Asp Glu Lys Asn Lys Leu Gln Lys
 805 810 815

Glu Lys Ala Leu Arg Arg Asp Phe Gln Ile Arg Val Leu Asp Leu Val
 820 825 830

Glu Val Leu Val Thr Lys Gln Pro Glu Asn Ala Leu Val Leu Glu Leu
 835 840 845

Leu Glu Pro Leu Leu Ser Ile Ile Arg Arg Ser Leu Arg Ser Ser Ser
 850 855 860

Ser Lys Gln Glu Gln Asp Leu Leu His Lys Thr Ala Arg Ile Phe Thr
 865 870 875 880

His His Leu Cys Arg Ala Arg Arg Tyr Cys His Asp Leu Gly Glu Arg

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 885 890 895

Ala Gly Ala Leu His Ala Gln Val Glu Arg Leu Val Gln Gln Ala Gly
 900 905 910

Arg Gln Pro Asp Ser Pro Thr Ala Leu Tyr His Phe Asn Ala Ser Leu
 915 920 925

Tyr Leu Leu Arg Val Leu Lys Gly Asn Thr Ala Glu Gly Cys Val His
 930 935 940

Glu Thr Gln Glu Lys Gln Lys Ala Gly Thr Asp Pro Ser His Met Pro
 945 950 955 960

Thr Gly Pro Gln Ala Ala Ser Cys Leu Asp Leu Asn Leu Val Thr Arg
 965 970 975

Val Tyr Ser Thr Ala Leu Ser Ser Phe Leu Thr Lys Arg Asn Ser Pro
 980 985 990

Leu Thr Val Pro Met Phe Leu Ser Leu Phe Ser Arg His Pro Val Leu
 995 1000 1005

Cys Gln Ser Leu Leu Pro Ile Leu Val Gln His Ile Thr Gly Pro
 1010 1015 1020

Val Arg Pro Arg His Gln Ala Cys Leu Leu Leu Gln Lys Thr Leu
 1025 1030 1035

Ser Met Arg Glu Val Arg Ser Cys Phe Glu Asp Pro Glu Trp Lys
 1040 1045 1050

Gln Leu Met Gly Gln Val Leu Ala Lys Val Thr Glu Asn Leu Arg
 1055 1060 1065

Val Leu Gly Glu Ala Gln Thr Lys Ala Gln His Gln Gln Ala Leu
 1070 1075 1080

Ser Ser Leu Glu Leu Leu Asn Val Leu Phe Arg Thr Cys Lys His
 1085 1090 1095

Glu Lys Leu Thr Leu Asp Leu Thr Val Leu Leu Gly Val Leu Gln
 1100 1105 1110

Gly Gln Gln Gln Ser Leu Gln Gln Gly Ala His Ser Thr Gly Ser
 1115 1120 1125

Ser Arg Leu His Asp Leu Tyr Trp Gln Ala Met Lys Thr Leu Gly
 1130 1135 1140

Val Gln Arg Pro Lys Leu Glu Lys Lys Asp Ala Lys Glu Ile Pro
 1145 1150 1155

Ser Ala Thr Gln Ser Pro Ile Ser Lys Lys Arg Lys Lys Lys Gly
 1160 1165 1170

Phe Leu Pro Glu Thr Lys Lys Arg Lys Lys Arg Lys Ser Glu Asp
 1175 1180 1185

Gly Thr Pro Ala Glu Asp Gly Thr Pro Ala Ala Thr Gly Gly Ser
 1190 1195 1200

Gln Pro Pro Ser Met Gly Arg Lys Lys Arg Asn Arg Thr Lys Ala
 1205 1210 1215

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Lys Val Pro Ala Gln Ala Asn Gly Thr Pro Thr Thr Lys Ser Pro
1220 1225 1230

Ala Pro Gly Ala Pro Thr Arg Ser Pro Ser Thr Pro Ala Lys Ser
1235 1240 1245

Pro Lys Leu Gln Lys Lys Asn Gln Lys Pro Ser Gln Val Asn Gly
1250 1255 1260

Ala Pro Gly Ser Pro Thr Glu Pro Ala Gly Gln Lys Gln His Gln
1265 1270 1275

Lys Ala Leu Pro Lys Lys Gly Val Leu Gly Lys Ser Pro Leu Ser
1280 1285 1290

Ala Leu Ala Arg Lys Lys Ala Arg Leu Ser Leu Val Ile Arg Ser
1295 1300 1305

Pro Ser Leu Leu Gln Ser Gly Ala Lys Lys Lys Ala Gln Val Arg
1310 1315 1320

Lys Ala Gly Lys Pro
1325

<210> 117
<211> 504
<212> PRT
<213> Homo sapiens

<400> 117

Met Ser Leu Ile Cys Ser Ile Ser Asn Glu Val Pro Glu His Pro Cys
1 5 10 15

Val Ser Pro Val Ser Asn His Val Tyr Glu Arg Arg Leu Ile Glu Lys
20 25 30

Tyr Ile Ala Glu Asn Gly Thr Asp Pro Ile Asn Asn Gln Pro Leu Ser
35 40 45

Glu Glu Gln Leu Ile Asp Ile Lys Val Ala His Pro Ile Arg Pro Lys
50 55 60

Pro Pro Ser Ala Thr Ser Ile Pro Ala Ile Leu Lys Ala Leu Gln Asp
65 70 75 80

Glu Trp Asp Ala Val Met Leu His Ser Phe Thr Leu Arg Gln Gln Leu
85 90 95

Gln Thr Thr Arg Gln Glu Leu Ser His Ala Leu Tyr Gln His Asp Ala
100 105 110

Ala Cys Arg Val Ile Ala Arg Leu Thr Lys Glu Val Thr Ala Ala Arg
115 120 125

Glu Ala Leu Ala Thr Leu Lys Pro Gln Ala Gly Leu Ile Val Pro Gln
130 135 140

Ala Val Pro Ser Ser Gln Pro Ser Val Val Gly Ala Gly Glu Pro Met
145 150 155 160

Asp Leu Gly Glu Leu Val Gly Met Thr Pro Glu Ile Ile Gln Lys Leu
165 170 175

Gln Asp Lys Ala Thr Val Leu Thr Thr Glu Arg Lys Lys Arg Gly Lys
180 185 190

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Thr Val Pro Glu Glu Leu Val Lys Pro Glu Glu Leu Ser Lys Tyr Arg
 195 200 205
 Gln Val Ala Ser His Val Gly Leu His Ser Ala Ser Ile Pro Gly Ile
 210 215 220
 Leu Ala Leu Asp Leu Cys Pro Ser Asp Thr Asn Lys Ile Leu Thr Gly
 225 230 235 240
 Gly Ala Asp Lys Asn Val Val Val Phe Asp Lys Ser Ser Glu Gln Ile
 245 250 255
 Leu Ala Thr Leu Lys Gly His Thr Lys Lys Val Thr Ser Val Val Phe
 260 265 270
 His Pro Ser Gln Asp Leu Val Phe Ser Ala Ser Pro Asp Ala Thr Ile
 275 280 285
 Arg Ile Trp Ser Val Pro Asn Ala Ser Cys Val Gln Val Val Arg Ala
 290 295 300
 His Glu Ser Ala Val Thr Gly Leu Ser Leu His Ala Thr Gly Asp Tyr
 305 310 315 320
 Leu Leu Ser Ser Ser Asp Asp Gln Tyr Trp Ala Phe Ser Asp Ile Gln
 325 330 335
 Thr Gly Arg Val Leu Thr Lys Val Thr Asp Glu Thr Ser Gly Cys Ser
 340 345 350
 Leu Thr Cys Ala Gln Phe His Pro Asp Gly Leu Ile Phe Gly Thr Gly
 355 360 365
 Thr Met Asp Ser Gln Ile Lys Ile Trp Asp Leu Lys Glu Arg Thr Asn
 370 375 380
 Val Ala Asn Phe Pro Gly His Ser Gly Pro Ile Thr Ser Ile Ala Phe
 385 390 395 400
 Ser Glu Asn Gly Tyr Tyr Leu Ala Thr Ala Ala Asp Asp Ser Ser Val
 405 410 415
 Lys Leu Trp Asp Leu Arg Lys Leu Lys Asn Phe Lys Thr Leu Gln Leu
 420 425 430
 Asp Asn Asn Phe Glu Val Lys Ser Leu Ile Phe Asp Gln Ser Gly Thr
 435 440 445
 Tyr Leu Ala Leu Gly Gly Thr Asp Val Gln Ile Tyr Ile Cys Lys Gln
 450 455 460
 Trp Thr Glu Ile Leu His Phe Thr Glu His Ser Gly Leu Thr Thr Gly
 465 470 475 480
 Val Ala Phe Gly His His Ala Lys Phe Ile Ala Ser Thr Gly Met Asp
 485 490 495
 Arg ser Leu Lys Phe Tyr Ser Leu
 500

<210> 118
 <211> 596
 <212> PRT
 <213> Homo sapiens

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

<400> 118

Met Val Leu Leu His Val Leu Phe Glu His Ala Val Gly Tyr Ala Leu
1 5 10 15Val Ala Leu Lys Glu Val Glu Glu Ile Ser Leu Leu Gln Pro Gln Val
20 25 30Glu Glu Ser Val Leu Asn Leu Gly Lys Phe His Ser Ile Val Arg Leu
35 40 45Val Ala Phe Cys Pro Phe Ala Ser Ser Gln Val Ala Leu Glu Asn Ala
50 55 60Asn Ala Val Ser Glu Gly Val Val His Glu Asp Leu Arg Leu Leu Leu
65 70 75 80Glu Thr His Leu Pro Ser Lys Lys Lys Lys Val Leu Leu Gly Val Gly
85 90 95Asp Pro Lys Ile Gly Ala Ala Ile Gln Glu Glu Leu Gly Tyr Asn Cys
100 105 110Gln Thr Gly Gly Val Ile Ala Glu Ile Leu Arg Gly Val Arg Leu His
115 120 125Phe His Asn Leu Val Lys Gly Leu Thr Asp Leu Ser Ala Cys Lys Ala
130 135 140Gln Leu Gly Leu Gly His Ser Tyr Ser Arg Ala Lys Val Lys Phe Asn
145 150 155 160Val Asn Arg Val Asp Asn Met Ile Ile Gln Ser Ile Ser Leu Leu Asp
165 170 175Gln Leu Asp Lys Asp Ile Asn Thr Phe Ser Met Arg Val Arg Glu Trp
180 185 190Tyr Gly Tyr His Phe Pro Glu Leu Val Lys Ile Ile Asn Asp Asn Ala
195 200 205Thr Tyr Cys Arg Leu Ala Gln Phe Ile Gly Asn Arg Arg Glu Leu Asn
210 215 220Glu Asp Lys Leu Glu Lys Leu Glu Glu Leu Thr Met Asp Gly Ala Lys
225 230 235 240Ala Lys Ala Ile Leu Asp Ala Ser Arg Ser Ser Met Gly Met Asp Ile
245 250 255Ser Ala Ile Asp Leu Ile Asn Ile Glu Ser Phe Ser Ser Arg Val Val
260 265 270Ser Leu Ser Glu Tyr Arg Gln Ser Leu His Thr Tyr Leu Arg Ser Lys
275 280 285Met Ser Gln Val Ala Pro Ser Leu Ser Ala Leu Ile Gly Glu Ala Val
290 295 300Gly Ala Arg Leu Ile Ala His Ala Gly Ser Leu Thr Asn Leu Ala Lys
305 310 315 320Tyr Pro Ala Ser Thr Val Gln Ile Leu Gly Ala Glu Lys Ala Leu Phe
325 330 335

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Arg Ala Leu Lys Thr Arg Gly Asn Thr Pro Lys Tyr Gly Leu Ile Phe
340 345 350

His Ser Thr Phe Ile Gly Arg Ala Ala Ala Lys Asn Lys Gly Arg Ile
355 360 365

Ser Arg Tyr Leu Ala Asn Lys Cys Ser Ile Ala Ser Arg Ile Asp Cys
370 375 380

Phe Ser Glu Val Pro Thr Ser Val Phe Gly Glu Lys Leu Arg Glu Gln
385 390 395 400

Val Glu Glu Arg Leu Ser Phe Tyr Glu Thr Gly Glu Ile Pro Arg Lys
405 410 415

Asn Leu Asp Val Met Lys Glu Ala Met Val Gln Ala Glu Ala Glu Glu
420 425 430

Ala Ala Ala Glu Ile Thr Arg Lys Leu Glu Lys Gln Glu Lys Lys Arg
435 440 445

Leu Lys Lys Glu Lys Lys Arg Leu Ala Ala Leu Ala Leu Ala Ser Ser
450 455 460

Glu Asn Ser Ser Ser Thr Pro Glu Glu Cys Glu Glu Met Ser Glu Lys
465 470 475 480

Pro Lys Lys Lys Lys Lys Gln Lys Pro Gln Glu Val Pro Gln Glu Asn
485 490 495

Gly Met Glu Asp Pro Ser Ile Ser Phe Ser Lys Pro Lys Lys Lys Lys
500 505 510

Ser Phe Ser Lys Glu Glu Leu Met Ser Ser Asp Leu Glu Glu Thr Ala
515 520 525

Gly Ser Thr Ser Ile Pro Lys Arg Lys Lys Ser Thr Pro Lys Glu Glu
530 535 540

Thr Val Asn Asp Pro Glu Glu Ala Gly His Arg Ser Gly Ser Lys Lys
545 550 555 560

Lys Arg Lys Phe Ser Lys Glu Glu Pro Val Ser Ser Gly Pro Glu Glu
565 570 575

Ala Val Gly Lys Ser Ser Ser Lys Lys Lys Lys Lys Phe His Lys Ala
580 585 590

Ser Gln Glu Asp
595

<210> 119
<211> 715
<212> PRT
<213> Homo sapiens

<400> 119

Met Asn Ser Pro Lys Ser Lys Lys Ala Lys Lys Lys Glu Glu Pro Ser
1 5 10 15

Gln Asn Asp Ile Ser Pro Lys Thr Lys Ser Leu Arg Lys Lys Lys Glu
20 25 30

Pro Ile Glu Lys Lys Val Val Ser Ser Lys Thr Lys Lys Val Thr Lys
35 40 45

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Asn Glu Glu Pro Ser Glu Glu Glu Ile Asp Ala Pro Lys Pro Lys Lys
50 55 60

Met Lys Lys Glu Lys Glu Met Asn Gly Glu Thr Arg Glu Lys Ser Pro
65 70 75 80

Lys Leu Lys Asn Gly Phe Pro His Pro Glu Pro Asp Cys Asn Pro Ser
85 90 95

Glu Ala Ala Ser Glu Glu Ser Asn Ser Glu Ile Glu Gln Glu Ile Pro
100 105 110

Val Glu Gln Lys Glu Gly Ala Phe Ser Asn Phe Pro Ile Ser Glu Glu
115 120 125

Thr Ile Lys Leu Leu Lys Gly Arg Gly Val Thr Phe Leu Phe Pro Ile
130 135 140

Gln Ala Lys Thr Phe His His Val Tyr Ser Gly Lys Asp Leu Ile Ala
145 150 155 160

Gln Ala Arg Thr Gly Thr Gly Lys Thr Phe Ser Phe Ala Ile Pro Leu
165 170 175

Ile Glu Lys Leu His Gly Glu Leu Gln Asp Arg Lys Arg Gly Arg Ala
180 185 190

Pro Gln Val Leu Val Leu Ala Pro Thr Arg Glu Leu Ala Asn Gln Val
195 200 205

Ser Lys Asp Phe Ser Asp Ile Thr Lys Lys Leu Ser Val Ala Cys Phe
210 215 220

Tyr Gly Gly Thr Pro Tyr Gly Gly Gln Phe Glu Arg Met Arg Asn Gly
225 230 235 240

Ile Asp Ile Leu Val Gly Thr Pro Gly Arg Ile Lys Asp His Ile Gln
245 250 255

Asn Gly Lys Leu Asp Leu Thr Lys Leu Lys His Val Val Leu Asp Glu
260 265 270

Val Asp Gln Met Leu Asp Met Gly Phe Ala Asp Gln Val Glu Glu Ile
275 280 285

Leu Ser Val Ala Tyr Lys Lys Asp Ser Glu Asp Asn Pro Gln Thr Leu
290 295 300

Leu Phe Ser Ala Thr Cys Pro His Trp Val Phe Asn Val Ala Lys Lys
305 310 315 320

Tyr Met Lys Ser Thr Tyr Glu Gln Val Asp Leu Ile Gly Lys Lys Thr
325 330 335

Gln Lys Thr Ala Ile Thr Val Glu His Leu Ala Ile Lys Cys His Trp
340 345 350

Thr Gln Arg Ala Ala Val Ile Gly Asp Val Ile Arg Val Tyr Ser Gly
355 360 365

His Gln Gly Arg Thr Ile Ile Phe Cys Glu Thr Lys Lys Glu Ala Gln
370 375 380

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Glu Leu Ser Gln Asn Ser Ala Ile Lys Gln Asp Ala Gln Ser Leu His
385 390 395 400

Gly Asp Ile Pro Gln Lys Gln Arg Glu Ile Thr Leu Lys Gly Phe Arg
405 410 415

Asn Gly ser Phe Gly Val Leu Val Ala Thr Asn Val Ala Ala Arg Gly
420 425 430

Leu Asp Ile Pro Glu Val Asp Leu Val Ile Gln Ser Ser Pro Pro Lys
435 440 445

Asp Val Glu Ser Tyr Ile His Arg Ser Gly Arg Thr Gly Arg Ala Gly
450 455 460

Arg Thr Gly Val Cys Ile Cys Phe Tyr Gln His Lys Glu Glu Tyr Gln
465 470 475 480

Leu Val Gln Val Glu Gln Lys Ala Gly Ile Lys Phe Lys Arg Ile Gly
485 490 495

Val Pro Ser Ala Thr Glu Ile Ile Lys Ala Ser Ser Lys Asp Ala Ile
500 505 510

Arg Leu Leu Asp Ser Val Pro Pro Thr Ala Ile Ser His Phe Lys Gln
515 520 525

Ser Ala Glu Lys Leu Ile Glu Glu Lys Gly Ala Val Glu Ala Leu Ala
530 535 540

Ala Ala Leu Ala His Ile Ser Gly Ala Thr Ser Val Asp Gln Arg Ser
545 550 555 560

Leu Ile Asn Ser Asn Val Gly Phe Val Thr Met Ile Leu Gln Cys Ser
565 570 575

Ile Glu Met Pro Asn Ile Ser Tyr Ala Trp Lys Glu Leu Lys Glu Gln
580 585 590

Leu Gly Glu Glu Ile Asp Ser Lys Val Lys Gly Met Val Phe Leu Lys
595 600 605

Gly Lys Leu Gly Val Cys Phe Asp Val Pro Thr Ala Ser Val Thr Glu
610 615 620

Ile Gln Glu Lys Trp His Asp Ser Arg Arg Trp Gln Leu Ser Val Ala
625 630 635 640

Thr Glu Gln Pro Glu Leu Glu Gly Pro Arg Glu Gly Tyr Gly Gly Phe
645 650 655

Arg Gly Gln Arg Glu Gly Ser Arg Gly Phe Arg Gly Gln Arg Asp Gly
660 665 670

Asn Arg Arg Phe Arg Gly Gln Arg Glu Gly Ser Arg Gly Pro Arg Gly
675 680 685

Gln Arg Ser Gly Gly Gly Asn Lys Ser Asn Arg Ser Gln Asn Lys Gly
690 695 700

Gln Lys Arg Ser Phe Ser Lys Ala Phe Gly Gln
705 710 715

<210> 120
<211> 294

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

<212> PRT

<213> Homo sapiens

<400> 120

Met Glu Asp Ser Met Asp Met Asp Met Ser Pro Leu Arg Pro Gln Asn
1 5 10 15Tyr Leu Phe Gly Cys Glu Leu Lys Ala Asp Lys Asp Tyr His Phe Lys
20 25 30Val Asp Asn Asp Glu Asn Glu His Gln Leu Ser Leu Arg Thr Val Ser
35 40 45Leu Gly Ala Gly Ala Lys Asp Glu Leu His Ile Val Glu Ala Glu Ala
50 55 60Met Asn Tyr Glu Gly Ser Pro Ile Lys Val Thr Leu Ala Thr Leu Lys
65 70 75 80Met Ser Val Gln Pro Thr Val Ser Leu Gly Gly Phe Glu Ile Thr Pro
85 90 95Pro Val Val Leu Arg Leu Lys Cys Gly Ser Gly Pro Val His Ile Ser
100 105 110Gly Gln His Leu Val Ala Val Glu Glu Asp Ala Glu Ser Glu Asp Glu
115 120 125Glu Glu Glu Asp Val Lys Leu Leu Ser Ile Ser Gly Lys Arg Ser Ala
130 135 140Pro Gly Gly Gly Ser Lys Val Pro Gln Lys Lys Val Lys Leu Ala Ala
145 150 155 160Asp Glu Asp Asp Asp Asp Asp Asp Glu Glu Asp Asp Asp Glu Asp Asp
165 170 175Asp Asp Asp Asp Phe Asp Asp Glu Glu Ala Glu Glu Lys Ala Pro Val
180 185 190Lys Lys Ser Ile Arg Asp Thr Pro Ala Lys Asn Ala Gln Lys Ser Asn
195 200 205Gln Asn Gly Lys Asp Ser Lys Pro Ser Ser Thr Pro Arg Ser Lys Gly
210 215 220Gln Glu Ser Phe Lys Lys Gln Glu Lys Thr Pro Lys Thr Pro Lys Gly
225 230 235 240Pro Ser Ser Val Glu Asp Ile Lys Ala Lys Met Gln Ala Ser Ile Glu
245 250 255Lys Gly Gly Ser Leu Pro Lys Val Glu Ala Lys Phe Ile Asn Tyr Val
260 265 270Lys Asn Cys Phe Arg Met Thr Asp Gln Glu Ala Ile Gln Asp Leu Trp
275 280 285Gln Trp Arg Lys Ser Leu
290

<210> 121

<211> 178

<212> PRT

<213> Homo sapiens

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 <400> 121

Met Ala Ala Gly Thr Ala Ala Ala Leu Ala Phe Leu Ser Gln Glu Ser
 1 5 10 15

Arg Thr Arg Ala Gly Gly Val Gly Gly Leu Arg Val Pro Ala Pro Val
 20 25 30

Thr Met Asp Ser Phe Phe Phe Gly Cys Glu Leu Ser Gly His Thr Arg
 35 40 45

Ser Phe Thr Phe Lys Val Glu Glu Glu Asp Asp Ala Glu His Val Leu
 50 55 60

Ala Leu Thr Met Leu Cys Leu Thr Glu Gly Ala Lys Asp Glu Cys Asn
 65 70 75 80

Val Val Glu Val Val Ala Arg Asn His Asp His Gln Glu Ile Ala Val
 85 90 95

Pro Val Ala Asn Leu Lys Leu Ser Cys Gln Pro Met Leu Ser Leu Asp
 100 105 110

Asp Phe Gln Leu Gln Pro Pro Val Thr Phe Arg Leu Lys Ser Gly Ser
 115 120 125

Gly Pro Val Arg Ile Thr Gly Arg His Gln Ile Val Thr Met Ser Asn
 130 135 140

Asp Val Ser Glu Glu Glu Ser Glu Glu Glu Glu Glu Asp Ser Asp Glu
 145 150 155 160

Glu Glu Val Glu Leu Cys Pro Ile Leu Pro Ala Lys Lys Gln Gly Gly
 165 170 175

Arg Pro

<210> 122
 <211> 802
 <212> PRT
 <213> Homo sapiens

<400> 122

Met Pro Arg Ile Met Ile Lys Gly Gly Val Trp Arg Asn Thr Glu Asp
 1 5 10 15

Glu Ile Leu Lys Ala Ala Val Met Lys Tyr Gly Lys Asn Gln Trp Ser
 20 25 30

Arg Ile Ala Ser Leu Leu His Arg Lys Ser Ala Lys Gln Cys Lys Ala
 35 40 45

Arg Trp Tyr Glu Trp Leu Asp Pro Ser Ile Lys Lys Thr Glu Trp Ser
 50 55 60

Arg Glu Glu Glu Glu Lys Leu Leu His Leu Ala Lys Leu Met Pro Thr
 65 70 75 80

Gln Trp Arg Thr Ile Ala Pro Ile Ile Gly Arg Thr Ala Ala Gln Cys
 85 90 95

Leu Glu His Tyr Glu Phe Leu Leu Asp Lys Ala Ala Gln Arg Asp Asn
 100 105 110

Glu Glu Glu Thr Thr Asp Asp Pro Arg Lys Leu Lys Pro Gly Glu Ile

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 115 120 125

Asp Pro Asn Pro Glu Thr Lys Pro Ala Arg Pro Asp Pro Ile Asp Met
 130 135 140

Asp Glu Asp Glu Leu Glu Met Leu Ser Glu Ala Arg Ala Arg Leu Ala
 145 150 155 160

Asn Thr Gln Gly Lys Lys Ala Lys Arg Lys Ala Arg Glu Lys Gln Leu
 165 170 175

Glu Glu Ala Arg Arg Leu Ala Ala Leu Gln Lys Arg Arg Glu Leu Arg
 180 185 190

Ala Ala Gly Ile Glu Ile Gln Lys Lys Arg Lys Arg Lys Arg Gly Val
 195 200 205

Asp Tyr Asn Ala Glu Ile Pro Phe Glu Lys Lys Pro Ala Leu Gly Phe
 210 215 220

Tyr Asp Thr Ser Glu Glu Asn Tyr Gln Ala Leu Asp Ala Asp Phe Arg
 225 230 235 240

Lys Leu Arg Gln Gln Asp Leu Asp Gly Glu Leu Arg Ser Glu Lys Glu
 245 250 255

Gly Arg Asp Arg Lys Lys Asp Lys Gln His Leu Lys Arg Lys Lys Glu
 260 265 270

Ser Asp Leu Pro Ser Ala Ile Leu Gln Thr Ser Gly Val Ser Glu Phe
 275 280 285

Thr Lys Lys Arg Ser Lys Leu Val Leu Pro Ala Pro Gln Ile Ser Asp
 290 295 300

Ala Glu Leu Gln Glu Val Val Lys Val Gly Gln Ala Ser Glu Ile Ala
 305 310 315 320

Arg Gln Thr Ala Glu Glu Ser Gly Ile Thr Asn Ser Ala Ser Ser Thr
 325 330 335

Leu Leu Ser Glu Tyr Asn Val Thr Asn Asn Ser Val Ala Leu Arg Thr
 340 345 350

Pro Arg Thr Pro Ala Ser Gln Asp Arg Ile Leu Gln Glu Ala Gln Asn
 355 360 365

Leu Met Ala Leu Thr Asn Val Asp Thr Pro Leu Lys Gly Gly Leu Asn
 370 375 380

Thr Pro Leu His Glu Ser Asp Phe Ser Gly Val Thr Pro Gln Arg Gln
 385 390 395 400

Val Val Gln Thr Pro Asn Thr Val Leu Ser Thr Pro Phe Arg Thr Pro
 405 410 415

Ser Asn Gly Ala Glu Gly Leu Thr Pro Arg Ser Gly Thr Thr Pro Lys
 420 425 430

Pro Val Ile Asn Ser Thr Pro Gly Arg Thr Pro Leu Arg Asp Lys Leu
 435 440 445

Asn Ile Asn Pro Glu Asp Gly Met Ala Asp Tyr Ser Asp Pro Ser Tyr
 450 455 460

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Val Lys Gln Met Glu Arg Glu Ser Arg Glu His Leu Arg Leu Gly Leu
465 470 475 480

Leu Gly Leu Pro Ala Pro Lys Asn Asp Phe Glu Ile Val Leu Pro Glu
485 490 495

Asn Ala Glu Lys Glu Leu Glu Glu Arg Glu Ile Asp Asp Thr Tyr Ile
500 505 510

Glu Asp Ala Ala Asp Val Asp Ala Arg Lys Gln Ala Ile Arg Asp Ala
515 520 525

Glu Arg Val Lys Glu Met Lys Arg Met His Lys Ala Val Gln Lys Asp
530 535 540

Leu Pro Arg Pro Ser Glu Val Asn Glu Thr Ile Leu Arg Pro Leu Asn
545 550 555 560

Val Glu Pro Pro Leu Thr Asp Leu Gln Lys Ser Glu Glu Leu Ile Lys
565 570 575

Lys Glu Met Ile Thr Met Leu His Tyr Asp Leu Leu His His Pro Tyr
580 585 590

Glu Pro Ser Gly Asn Lys Lys Gly Lys Thr Val Gly Phe Gly Thr Asn
595 600 605

Asn Ser Glu His Ile Thr Tyr Leu Glu His Asn Pro Tyr Glu Lys Phe
610 615 620

Ser Lys Glu Glu Leu Lys Lys Ala Gln Asp Val Leu Val Gln Glu Met
625 630 635 640

Glu Val Val Lys Gln Gly Met Ser His Gly Glu Leu Ser Ser Glu Ala
645 650 655

Tyr Asn Gln Val Trp Glu Glu Cys Tyr Ser Gln Val Leu Tyr Leu Pro
660 665 670

Gly Gln Ser Arg Tyr Thr Arg Ala Asn Leu Ala Ser Lys Lys Asp Arg
675 680 685

Ile Glu Ser Leu Glu Lys Arg Leu Glu Ile Asn Arg Gly His Met Thr
690 695 700

Thr Glu Ala Lys Arg Ala Ala Lys Met Glu Lys Lys Met Lys Ile Leu
705 710 715 720

Leu Gly Gly Tyr Gln Ser Arg Ala Met Gly Leu Met Lys Gln Leu Asn
725 730 735

Asp Leu Trp Asp Gln Ile Glu Gln Ala His Leu Glu Leu Arg Thr Phe
740 745 750

Glu Glu Leu Lys Lys His Glu Asp Ser Ala Ile Pro Arg Arg Leu Glu
755 760 765

Cys Leu Lys Glu Asp Val Gln Arg Gln Gln Glu Arg Glu Lys Glu Leu
770 775 780

Gln His Arg Tyr Ala Asp Leu Leu Leu Glu Lys Glu Thr Leu Lys Ser
785 790 795 800

Lys Phe

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

<210> 123
 <211> 855
 <212> PRT
 <213> Homo sapiens

<400> 123

Met Gly Arg Lys Leu Asp Pro Thr Lys Glu Lys Arg Gly Pro Gly Arg
 1 5 10 15

Lys Ala Arg Lys Gln Lys Gly Ala Glu Thr Glu Leu Val Arg Phe Leu
 20 25 30

Pro Ala Val Ser Asp Glu Asn Ser Lys Arg Leu Ser Ser Arg Ala Arg
 35 40 45

Lys Arg Ala Ala Lys Arg Arg Leu Gly Ser Val Glu Ala Pro Lys Thr
 50 55 60

Asn Lys Ser Pro Glu Ala Lys Pro Ser Pro Gly Lys Leu Pro Lys Gly
 65 70 75 80

Ile Ser Ala Gly Ala Val Gln Thr Ala Gly Lys Lys Gly Pro Gln Ser
 85 90 95

Leu Phe Asn Ala Pro Arg Gly Lys Lys Arg Pro Ala Pro Gly Ser Asp
 100 105 110

Glu Glu Glu Glu Glu Glu Asp Ser Glu Glu Asp Gly Met Val Asn His
 115 120 125

Gly Asp Leu Trp Gly Ser Glu Asp Asp Ala Asp Thr Val Asp Asp Tyr
 130 135 140

Gly Ala Asp Ser Asn Ser Glu Asp Glu Glu Glu Gly Glu Ala Leu Leu
 145 150 155 160

Pro Ile Glu Arg Ala Ala Arg Lys Gln Lys Ala Arg Glu Ala Ala Ala
 165 170 175

Gly Ile Gln Trp Ser Glu Glu Glu Thr Glu Asp Glu Glu Glu Glu Lys
 180 185 190

Glu Val Thr Pro Glu Ser Gly Pro Pro Lys Val Glu Glu Ala Asp Gly
 195 200 205

Gly Leu Gln Ile Asn Val Asp Glu Glu Pro Phe Val Leu Pro Pro Ala
 210 215 220

Gly Glu Met Glu Gln Asp Ala Gln Ala Pro Asp Leu Gln Arg Val His
 225 230 235 240

Lys Arg Ile Gln Asp Ile Val Gly Ile Leu Arg Asp Phe Gly Ala Gln
 245 250 255

Arg Glu Glu Gly Arg Ser Arg Ser Glu Tyr Leu Asn Arg Leu Lys Lys
 260 265 270

Asp Leu Ala Ile Tyr Tyr Ser Tyr Gly Asp Phe Leu Leu Gly Lys Leu
 275 280 285

Met Asp Leu Phe Pro Leu Ser Glu Leu Val Glu Phe Leu Glu Ala Asn
 290 295 300

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Glu Val Pro Arg Pro Val Thr Leu Arg Thr Asn Thr Leu Lys Thr Arg
305 310 315 320

Arg Arg Asp Leu Ala Gln Ala Leu Ile Asn Arg Gly Val Asn Leu Asp
325 330 335

Pro Leu Gly Lys Trp Ser Lys Thr Gly Leu Val Val Tyr Asp Ser Ser
340 345 350

Val Pro Ile Gly Ala Thr Pro Glu Tyr Leu Ala Gly His Tyr Met Leu
355 360 365

Gln Gly Ala Ser Ser Met Leu Pro Val Met Ala Leu Ala Pro Gln Glu
370 375 380

His Glu Arg Ile Leu Asp Met Cys Cys Ala Pro Gly Gly Lys Thr Ser
385 390 395 400

Tyr Met Ala Gln Leu Met Lys Asn Thr Gly Val Ile Leu Ala Asn Asp
405 410 415

Ala Asn Ala Glu Arg Leu Lys Ser Val Val Gly Asn Leu His Arg Leu
420 425 430

Gly Val Thr Asn Thr Ile Ile Ser His Tyr Asp Gly Arg Gln Phe Pro
435 440 445

Lys Val Val Gly Gly Phe Asp Arg Val Leu Leu Asp Ala Pro Cys Ser
450 455 460

Gly Thr Gly Val Ile Ser Lys Asp Pro Ala Val Lys Thr Asn Lys Asp
465 470 475 480

Glu Lys Asp Ile Leu Arg Cys Ala His Leu Gln Lys Glu Leu Leu Leu
485 490 495

Ser Ala Ile Asp Ser Val Asn Ala Thr Ser Lys Thr Gly Gly Tyr Leu
500 505 510

Val Tyr Cys Thr Cys Ser Ile Thr Val Glu Glu Asn Glu Trp Val Val
515 520 525

Asp Tyr Ala Leu Lys Lys Arg Asn Val Arg Leu Val Pro Thr Gly Leu
530 535 540

Asp Phe Gly Gln Glu Gly Phe Thr Arg Phe Arg Glu Arg Arg Phe His
545 550 555 560

Pro Ser Leu Arg Ser Thr Arg Arg Phe Tyr Pro His Thr His Asn Met
565 570 575

Asp Gly Phe Phe Ile Ala Lys Phe Lys Lys Phe Ser Asn Ser Ile Pro
580 585 590

Gln Ser Gln Thr Gly Asn Ser Glu Thr Ala Thr Pro Thr Asn Val Asp
595 600 605

Leu Pro Gln Val Ile Pro Lys Ser Glu Asn Ser Ser Gln Pro Ala Lys
610 615 620

Lys Ala Lys Gly Ala Ala Lys Thr Lys Gln Gln Leu Gln Lys Gln Gln
625 630 635 640

His Pro Lys Lys Ala Ser Phe Gln Lys Leu Asn Gly Ile Ser Lys Gly
645 650 655

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ala Asp Ser Glu Leu Ser Thr Val Pro Ser Val Thr Lys Thr Gln Ala
660 665 670

Ser Ser Ser Phe Gln Asp Ser Ser Gln Pro Ala Gly Lys Ala Glu Gly
675 680 685

Ile Arg Glu Pro Lys Val Thr Gly Lys Leu Lys Gln Arg Ser Pro Lys
690 695 700

Leu Gln Ser Ser Lys Lys Val Ala Phe Leu Arg Gln Asn Ala Pro Pro
705 710 715 720

Lys Gly Thr Asp Thr Gln Thr Pro Ala Val Leu Ser Pro Ser Lys Thr
725 730 735

Gln Ala Thr Leu Lys Pro Lys Asp His His Gln Pro Leu Gly Arg Ala
740 745 750

Lys Gly Val Glu Lys Gln Gln Phe Ala Glu Gln Pro Phe Glu Lys Ala
755 760 765

Ala Phe Gln Lys Gln Asn Asp Thr Pro Lys Gly Leu Ser Leu Pro Leu
770 775 780

Cys Leu Pro Ser Val Pro Ala Ala Pro His Gln Gln Arg Gly Arg Asn
785 790 795 800

Leu Ser Pro Gly Ala Thr Ala Ser Cys Cys Tyr Leu Arg Trp Leu Lys
805 810 815

Thr Arg Arg Val Ala His Cys His Cys His Gln Val Gly Thr Leu Ala
820 825 830

Ser Val Arg Met Pro Ser Leu Leu Cys Ile Pro Met Lys Phe Asn Thr
835 840 845

His Phe Lys Thr Ser Gly His
850 855

<210> 124
<211> 1884
<212> PRT
<213> Homo sapiens

<400> 124

Val Ala Gly Cys Arg Arg Arg Gly Ala Gly Asp Pro Asn Met Ala Asn
1 5 10 15

Leu Glu Glu Ser Phe Pro Arg Gly Gly Thr Arg Lys Ile His Lys Pro
20 25 30

Glu Lys Ala Phe Gln Gln Ser Val Glu Gln Asp Asn Leu Phe Asp Ile
35 40 45

Ser Thr Glu Glu Gly Ser Thr Lys Arg Lys Lys Ser Gln Lys Gly Pro
50 55 60

Ala Lys Thr Lys Lys Leu Lys Ile Glu Lys Arg Glu Ser Ser Lys Ser
65 70 75 80

Ala Arg Glu Lys Phe Glu Ile Leu Ser Val Glu Ser Leu Cys Glu Gly
85 90 95

Met Arg Ile Leu Gly Cys Val Lys Glu Val Asn Glu Leu Glu Leu Val

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 100 105 110

Ile Ser Leu Pro Asn Gly Leu Gln Gly Phe Val Gln Val Thr Glu Ile
 115 120 125

Cys Asp Ala Tyr Thr Lys Lys Leu Asn Glu Gln Val Thr Gln Glu Gln
 130 135 140

Pro Leu Lys Asp Leu Leu His Leu Pro Glu Leu Phe Ser Pro Gly Met
 145 150 155 160

Leu Val Arg Cys Val Val Ser Ser Leu Gly Ile Thr Asp Arg Gly Lys
 165 170 175

Lys Ser Val Lys Leu Ser Leu Asn Pro Lys Asn Val Asn Arg Val Leu
 180 185 190

Ser Ala Glu Ala Leu Lys Pro Gly Met Leu Leu Thr Gly Thr Val Ser
 195 200 205

Ser Leu Glu Asp His Gly Tyr Leu Val Asp Ile Gly Val Asp Gly Thr
 210 215 220

Arg Ala Phe Leu Pro Leu Leu Lys Ala Gln Glu Tyr Ile Arg Gln Lys
 225 230 235 240

Asn Lys Gly Ala Lys Leu Lys Val Gly Gln Tyr Leu Asn Cys Ile Val
 245 250 255

Glu Lys Val Lys Gly Asn Gly Gly Val Val Ser Leu Ser Val Gly His
 260 265 270

Ser Glu Val Ser Thr Ala Ile Ala Thr Glu Gln Gln Ser Trp Asn Leu
 275 280 285

Asn Asn Leu Leu Pro Gly Leu Val Val Lys Ala Gln Val Gln Lys Val
 290 295 300

Thr Pro Phe Gly Leu Thr Leu Asn Phe Leu Thr Phe Phe Thr Gly Val
 305 310 315 320

Val Asp Phe Met His Leu Asp Pro Lys Lys Ala Gly Thr Tyr Phe Ser
 325 330 335

Asn Gln Ala Val Arg Ala Cys Ile Leu Cys Val His Pro Arg Thr Arg
 340 345 350

Val Val His Leu Ser Leu Arg Pro Ile Phe Leu Gln Pro Gly Arg Pro
 355 360 365

Leu Thr Arg Leu Ser Cys Gln Asn Leu Gly Ala Val Leu Asp Asp Val
 370 375 380

Pro Val Gln Gly Phe Phe Lys Lys Ala Gly Ala Thr Phe Arg Leu Lys
 385 390 395 400

Asp Gly Val Leu Ala Tyr Ala Arg Leu Ser His Leu Ser Asp Ser Lys
 405 410 415

Asn Val Phe Asn Pro Glu Ala Phe Lys Pro Gly Asn Thr His Lys Cys
 420 425 430

Arg Ile Ile Asp Tyr Ser Gln Met Asp Glu Leu Ala Leu Leu Ser Leu
 435 440 445

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Arg Thr Ser Ile Ile Glu Ala Gln Tyr Leu Arg Tyr His Asp Ile Glu
450 455 460

Pro Gly Ala Val Val Lys Gly Thr Val Leu Thr Ile Lys Ser Tyr Gly
465 470 475 480

Met Leu Val Lys Val Gly Glu Gln Met Arg Gly Leu Val Pro Pro Met
485 490 495

His Leu Ala Asp Ile Leu Met Lys Asn Pro Glu Lys Lys Tyr His Ile
500 505 510

Gly Asp Glu Val Lys Cys Arg Val Leu Leu Cys Asp Pro Glu Ala Lys
515 520 525

Lys Leu Met Met Thr Leu Lys Lys Thr Leu Ile Glu Ser Lys Leu Pro
530 535 540

Val Ile Thr Cys Tyr Ala Asp Ala Lys Pro Gly Leu Gln Thr His Gly
545 550 555 560

Phe Ile Ile Arg Val Lys Asp Tyr Gly Cys Ile Val Lys Phe Tyr Asn
565 570 575

Asn Val Gln Gly Leu Val Pro Lys His Glu Leu Ser Thr Glu Tyr Ile
580 585 590

Pro Asp Pro Glu Arg Val Phe Tyr Thr Gly Gln Val Val Lys Val Val
595 600 605

Val Leu Asn Cys Glu Pro Ser Lys Glu Arg Met Leu Leu Ser Phe Lys
610 615 620

Leu Ser Ser Asp Pro Glu Pro Lys Lys Glu Pro Ala Gly His Ser Gln
625 630 635 640

Lys Lys Gly Lys Ala Ile Asn Ile Gly Gln Leu Val Asp Val Lys Val
645 650 655

Leu Glu Lys Thr Lys Asp Gly Leu Glu Val Ala Val Leu Pro His Asn
660 665 670

Ile Arg Ala Phe Leu Pro Thr Ser His Leu Ser Asp His Val Ala Asn
675 680 685

Gly Pro Leu Leu His His Trp Leu Gln Ala Gly Asp Ile Leu His Arg
690 695 700

Val Leu Cys Leu Ser Gln Ser Glu Gly Arg Val Leu Leu Cys Arg Lys
705 710 715 720

Pro Ala Leu Val Ser Thr Val Glu Gly Gly Gln Asp Pro Lys Asn Phe
725 730 735

Ser Glu Ile His Pro Gly Met Leu Leu Ile Gly Phe Val Lys Ser Ile
740 745 750

Lys Asp Tyr Gly Val Phe Ile Gln Phe Pro Ser Gly Leu Ser Gly Leu
755 760 765

Ala Pro Lys Ala Ile Met Ser Asp Lys Phe Val Thr Ser Thr Ser Asp
770 775 780

His Phe Val Glu Gly Gln Thr Val Ala Ala Lys Val Thr Asn Val Asp

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 785 790 795 800

Glu Glu Lys Gln Arg Met Leu Leu Ser Leu Arg Leu Ser Asp Cys Gly
 805 810 815
 Leu Gly Asp Leu Ala Ile Thr Ser Leu Leu Leu Asn Gln Cys Leu
 820 825 830
 Glu Glu Leu Gln Gly Val Arg Ser Leu Met Ser Asn Arg Asp Ser Val
 835 840 845
 Leu Ile Gln Thr Leu Ala Glu Met Thr Pro Gly Met Phe Leu Asp Leu
 850 855 860
 Val Val Gln Glu Val Leu Glu Asp Gly Ser Val Val Phe Ser Gly Gly
 865 870 875 880
 Pro Val Pro Asp Leu Val Leu Lys Ala Ser Arg Tyr His Arg Ala Gly
 885 890 895
 Gln Glu Val Glu Ser Gly Gln Lys Lys Lys Val Val Ile Leu Asn Val
 900 905 910
 Asp Leu Leu Lys Leu Glu Val His Val Ser Leu His Gln Asp Leu Val
 915 920 925
 Asn Arg Lys Ala Arg Lys Leu Arg Lys Gly Ser Glu His Gln Ala Ile
 930 935 940
 Val Gln His Leu Glu Lys Ser Phe Ala Ile Ala Ser Leu Val Glu Thr
 945 950 955 960
 Gly His Leu Ala Ala Phe Ser Leu Thr Ser His Leu Asn Asp Thr Phe
 965 970 975
 Arg Phe Asp Ser Glu Lys Leu Gln Val Gly Gln Gly Val Ser Leu Thr
 980 985 990
 Leu Lys Thr Thr Glu Pro Gly Val Thr Gly Leu Leu Leu Ala Val Glu
 995 1000 1005
 Gly Pro Ala Ala Lys Arg Thr Met Arg Pro Thr Gln Lys Asp Ser
 1010 1015 1020
 Glu Thr Val Asp Glu Asp Glu Glu Val Asp Pro Ala Leu Thr Val
 1025 1030 1035
 Gly Thr Ile Lys Lys His Thr Leu Ser Ile Gly Asp Met Val Thr
 1040 1045 1050
 Gly Thr Val Lys Ser Ile Lys Pro Thr His Val Val Val Thr Leu
 1055 1060 1065
 Glu Asp Gly Ile Ile Gly Cys Ile His Ala Ser His Ile Leu Asp
 1070 1075 1080
 Asp Val Pro Glu Gly Thr Ser Pro Thr Thr Lys Leu Lys Val Gly
 1085 1090 1095
 Lys Thr Val Thr Ala Arg Val Ile Gly Gly Arg Asp Met Lys Thr
 1100 1105 1110
 Phe Lys Tyr Leu Pro Ile Ser His Pro Arg Phe Val Arg Thr Ile
 1115 1120 1125

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Pro Glu Leu Ser Val Arg Pro Ser Glu Leu Glu Asp Gly His Thr
 1130 1135 1140
 Ala Leu Asn Thr His Ser Val Ser Pro Met Glu Lys Ile Lys Gln
 1145 1150 1155
 Tyr Gln Ala Gly Gln Thr Val Thr Cys Phe Leu Lys Lys Tyr Asn
 1160 1165 1170
 Val Val Lys Lys Trp Leu Glu Val Glu Ile Ala Pro Asp Ile Arg
 1175 1180 1185
 Gly Arg Ile Pro Leu Leu Leu Thr Ser Leu Ser Phe Lys Val Leu
 1190 1195 1200
 Lys His Pro Asp Lys Lys Phe Arg Val Gly Gln Ala Leu Arg Ala
 1205 1210 1215
 Thr Val Val Gly Pro Asp Ser Ser Lys Thr Phe Leu Cys Leu Ser
 1220 1225 1230
 Leu Thr Gly Pro His Lys Leu Glu Glu Gly Glu Val Ala Met Gly
 1235 1240 1245
 Arg Val Val Lys Val Thr Pro Asn Glu Gly Leu Thr Val Ser Phe
 1250 1255 1260
 Pro Phe Gly Lys Ile Gly Thr Val Ser Ile Phe His Met Ser Asp
 1265 1270 1275
 Ser Tyr Ser Glu Thr Pro Leu Glu Asp Phe Val Pro Gln Lys Val
 1280 1285 1290
 Val Arg Cys Tyr Ile Leu Ser Thr Ala Asp Asn Val Leu Thr Leu
 1295 1300 1305
 Ser Leu Arg Ser Ser Arg Thr Asn Pro Glu Thr Lys Ser Lys Val
 1310 1315 1320
 Glu Asp Pro Glu Ile Asn Ser Ile Gln Asp Ile Lys Glu Gly Gln
 1325 1330 1335
 Leu Leu Arg Gly Tyr Val Gly Ser Ile Gln Pro His Gly Val Phe
 1340 1345 1350
 Phe Arg Leu Gly Pro Ser Val Val Gly Leu Ala Arg Tyr Ser His
 1355 1360 1365
 Val Ser Gln His Ser Pro Ser Lys Lys Ala Leu Tyr Asn Lys His
 1370 1375 1380
 Leu Pro Glu Gly Lys Leu Leu Thr Ala Arg Val Leu Arg Leu Asn
 1385 1390 1395
 His Gln Lys Asn Leu Val Glu Leu Ser Phe Leu Pro Gly Asp Thr
 1400 1405 1410
 Gly Lys Pro Asp Val Leu Ser Ala Ser Leu Glu Gly Gln Leu Thr
 1415 1420 1425
 Lys Gln Glu Glu Arg Lys Thr Glu Ala Glu Glu Arg Asp Gln Lys
 1430 1435 1440
 Gly Glu Lys Lys Asn Gln Lys Arg Asn Glu Lys Lys Asn Gln Lys

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 1445 1450 1455

Gly Gln Glu Glu Val Glu Met Pro Ser Lys Glu Lys Gln Gln Pro
 1460 1465 1470
 Gln Lys Pro Gln Ala Gln Lys Arg Gly Gly Arg Glu Cys Arg Glu
 1475 1480 1485
 Ser Gly Ser Glu Gln Glu Arg Val Ser Lys Lys Pro Lys Lys Ala
 1490 1495 1500
 Gly Leu Ser Glu Glu Asp Asp Ser Leu Val Asp Val Tyr Tyr Arg
 1505 1510 1515
 Glu Gly Lys Glu Glu Ala Glu Glu Thr Asn Val Leu Pro Lys Glu
 1520 1525 1530
 Lys Gln Thr Lys Pro Ala Glu Ala Pro Arg Leu Gln Leu Ser Ser
 1535 1540 1545
 Gly Phe Ala Trp Asn Val Gly Leu Asp Ser Leu Thr Pro Ala Leu
 1550 1555 1560
 Pro Pro Leu Ala Glu Ser Ser Asp Ser Glu Glu Asp Glu Lys Pro
 1565 1570 1575
 His Gln Ala Thr Ile Lys Lys Ser Lys Lys Glu Arg Glu Leu Glu
 1580 1585 1590
 Lys Gln Lys Ala Glu Lys Glu Leu Ser Arg Ile Glu Glu Ala Leu
 1595 1600 1605
 Met Asp Pro Gly Arg Gln Pro Glu Ser Ala Asp Asp Phe Asp Arg
 1610 1615 1620
 Leu Val Leu Ser Ser Pro Asn Ser Ser Ile Leu Trp Leu Gln Tyr
 1625 1630 1635
 Met Ala Phe His Leu Gln Ala Thr Glu Ile Glu Lys Ala Arg Ala
 1640 1645 1650
 Val Ala Glu Arg Ala Leu Lys Thr Ile Ser Phe Arg Glu Glu Gln
 1655 1660 1665
 Glu Lys Leu Asn Val Trp Val Ala Leu Leu Asn Leu Glu Asn Met
 1670 1675 1680
 Tyr Gly Ser Gln Glu Ser Leu Thr Lys Val Phe Glu Arg Ala Val
 1685 1690 1695
 Gln Tyr Asn Glu Pro Leu Lys Val Phe Leu His Leu Ala Asp Ile
 1700 1705 1710
 Tyr Ala Lys Ser Glu Lys Phe Gln Glu Ala Gly Glu Leu Tyr Asn
 1715 1720 1725
 Arg Met Leu Lys Arg Phe Arg Gln Glu Lys Ala Val Trp Ile Lys
 1730 1735 1740
 Tyr Gly Ala Phe Leu Leu Arg Arg Ser Gln Ala Ala Ala Ser His
 1745 1750 1755
 Arg Val Leu Gln Arg Ala Leu Glu Cys Leu Pro Ser Lys Glu His
 1760 1765 1770

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Val Asp Val Ile Ala Lys Phe Ala Gln Leu Glu Phe Gln Leu Gly
 1775 1780 1785

Asp Ala Glu Arg Ala Lys Ala Ile Phe Glu Asn Thr Leu Ser Thr
 1790 1795 1800

Tyr Pro Lys Arg Thr Asp Val Trp Ser Val Tyr Ile Asp Met Thr
 1805 1810 1815

Ile Lys His Gly Ser Gln Lys Asp Val Arg Asp Ile Phe Glu Arg
 1820 1825 1830

Val Ile His Leu Ser Leu Ala Pro Lys Arg Met Lys Phe Phe Phe
 1835 1840 1845

Lys Arg Tyr Leu Asp Tyr Glu Lys Gln His Gly Thr Glu Lys Asp
 1850 1855 1860

Val Gln Ala Val Lys Ala Lys Ala Leu Glu Tyr Val Glu Ala Lys
 1865 1870 1875

Ser Ser Val Leu Glu Asp
 1880

<210> 125
 <211> 308
 <212> PRT
 <213> Homo sapiens

<400> 125

Lys Arg Lys Arg Glu Trp Ser Asp Glu Ser Glu Glu Glu Pro Glu Lys
 1 5 10 15

Glu Leu Ala Pro Glu Pro Glu Glu Thr Trp Val Val Glu Thr Leu Cys
 20 25 30

Gly Leu Lys Met Lys Leu Lys Gln Gln Arg Val Ser Pro Ile Leu Leu
 35 40 45

Glu His His Lys Asp Phe Asn Ser Gln Leu Ala Pro Gly Val Asp Pro
 50 55 60

Ser Pro Pro His Arg Ser Phe Cys Trp Lys Arg Lys Met Glu Trp Trp
 65 70 75 80

Asp Lys Ser Glu Glu Ser Glu Glu Glu Pro Arg Lys Val Leu Ala Pro
 85 90 95

Glu Pro Glu Glu Ile Trp Val Ala Glu Met Leu Cys Gly Leu Lys Met
 100 105 110

Lys Leu Lys Arg Arg Arg Val Ser Leu Val Leu Pro Glu His His Glu
 115 120 125

Ala Phe Asn Arg Leu Leu Glu Asp Pro Val Ile Lys Arg Phe Leu Ala
 130 135 140

Trp Asp Lys Asp Leu Arg Val Ser Asp Lys Tyr Leu Leu Ala Met Val
 145 150 155 160

Ile Ala Tyr Phe Ser Arg Ala Gly Phe Pro Ser Trp Gln Tyr Gln Arg
 165 170 175

Leu His Phe Phe Leu Ala Leu Tyr Leu Ala Asn Asp Met Glu Glu Asp
 180 185 190

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Asp Glu Asp Ser Lys Gln Asn Ile Phe His Phe Leu Tyr Gly Lys Asn
195 200 205

Arg Ser Arg Ile Pro Leu Leu Arg Lys Arg Arg Phe Gln Leu Tyr Arg
210 215 220

Ser Met Asn Pro Arg Ala Arg Lys Asn Arg Ser His Ile Pro Leu Val
225 230 235 240

Arg Lys Arg Arg Phe Gln Leu Arg Arg Cys Met Asn Pro Arg Ala Arg
245 250 255

Lys Asn Arg Ser Gln Ile Val Leu Phe Gln Lys Arg Arg Phe His Phe
260 265 270

Phe Cys Ser Met Ser Cys Arg Ala Trp Val Ser Pro Glu Glu Leu Glu
275 280 285

Glu Ile Gln Ala Tyr Asp Pro Glu His Trp Val Trp Ala Arg Asp Arg
290 295 300

Ala Arg Leu Ser
305

<210> 126
<211> 198
<212> PRT
<213> Homo sapiens

<400> 126

Met Gln His Leu Leu Glu Lys Gln Phe Leu Pro Pro Ser Ser Ile Ile
1 5 10 15

Gly His Arg Glu Lys Asn Ile Glu Pro Gln Arg Phe Ser Thr Leu Thr
20 25 30

Lys Asp Arg Leu Ile Ala Asp Gly Arg Thr Glu Ala Glu Ile His Asn
35 40 45

Pro Cys Ile Leu Gln Leu Ser Leu Gln Lys Ser Lys Glu Asp Asn Val
50 55 60

Ala Pro Val Leu Ala Val Thr Lys Gln Gln Glu Ala Lys Thr Val Leu
65 70 75 80

Asn Pro Leu Phe Glu Lys Ser Pro Lys Asn Phe Gly Ile Gly Glu Asp
85 90 95

Ile Gln Pro Lys Lys Thr Pro Thr His Phe Gly Asn Asp Pro Thr Ile
100 105 110

Ser Glu Asn Ile Pro Gln Leu Val Met Ile Ala His Asp Met Asp Ser
115 120 125

Ile Lys Leu Val Val Phe Leu Pro Val Leu Cys Tyr Lys Ile Lys Ile
130 135 140

Pro Tyr Cys Ile Ile Lys Gly Lys Glu Arg Leu Gly Gln Val Val Tyr
145 150 155 160

Arg Lys Thr Cys Thr Asn Val Thr Ile Thr Gln Val Asn Ser Glu Glu
165 170 175

Lys Arg Ser Leu Val Lys Leu Val Glu Ala Ile Arg Thr Asn Tyr Lys

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 180 185 190

Asp Arg Tyr Glu Glu Ile
 195

<210> 127
 <211> 276
 <212> PRT
 <213> Homo sapiens

<400> 127

Met Gln Asp Leu Arg Met Leu Met Pro His Ser Lys Ala Asp Thr Lys
 1 5 10 15

Met Asp Arg Lys Asp Lys Leu Phe Val Ile Asn Glu Val Cys Glu Met
 20 25 30

Lys Asn Cys Asn Lys Cys Ile Tyr Phe Glu Ala Lys Lys Lys Gln Asp
 35 40 45

Leu Tyr Met Trp Leu Ser Asn Ser Pro His Gly Pro Ser Ala Lys Phe
 50 55 60

Leu Val Gln Asn Ile His Thr Leu Ala Glu Leu Lys Met Thr Gly Asn
 65 70 75 80

Cys Leu Lys Gly Ser Arg Pro Leu Leu Ser Phe Asp Pro Ala Phe Asp
 85 90 95

Glu Leu Pro His Tyr Ala Leu Leu Lys Glu Leu Leu Ile Gln Ile Phe
 100 105 110

Ser Thr Pro Arg Tyr His Pro Lys Ser Gln Pro Phe Val Asp His Val
 115 120 125

Phe Thr Phe Thr Ile Leu Asp Asn Arg Ile Trp Phe Arg Asn Phe Gln
 130 135 140

Ile Ile Glu Glu Asp Ala Ala Leu Val Glu Ile Gly Pro Arg Phe Val
 145 150 155 160

Leu Asn Leu Ile Lys Ile Phe Gln Gly Ser Phe Gly Gly Pro Thr Leu
 165 170 175

Tyr Glu Asn Pro His Tyr Gln Ser Pro Asn Met His Arg Arg Val Ile
 180 185 190

Arg Ser Ile Thr Ala Ala Lys Tyr Arg Glu Lys Gln Gln Val Lys Asp
 195 200 205

Val Gln Lys Leu Arg Lys Lys Glu Pro Lys Thr Leu Leu Pro His Asp
 210 215 220

Pro Thr Ala Asp Val Phe Val Thr Pro Ala Glu Glu Lys Pro Ile Glu
 225 230 235 240

Ile Gln Trp Val Lys Pro Glu Pro Lys Val Asp Leu Lys Ala Arg Lys
 245 250 255

Lys Arg Ile Tyr Lys Arg Gln Arg Lys Met Lys Gln Arg Met Asp Ser
 260 265 270

Gly Lys Thr Lys
 275

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

<210> 128

<211> 297

<212> PRT

<213> Homo sapiens

<400> 128

Met Glu Asp Tyr Thr Lys Ile Glu Lys Ile Gly Glu Gly Thr Tyr Gly
1 5 10 15Val Val Tyr Lys Gly Arg His Lys Thr Thr Gly Gln Val Val Ala Met
20 25 30Lys Lys Ile Arg Leu Glu Ser Glu Glu Glu Gly Val Pro Ser Thr Ala
35 40 45Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu Arg His Pro Asn Ile Val
50 55 60Ser Leu Gln Asp Val Leu Met Gln Asp Ser Arg Leu Tyr Leu Ile Phe
65 70 75 80Glu Phe Leu Ser Met Asp Leu Lys Lys Tyr Leu Asp Ser Ile Pro Pro
85 90 95Gly Gln Tyr Met Asp Ser Ser Leu Val Lys Ser Tyr Leu Tyr Gln Ile
100 105 110Leu Gln Gly Ile Val Phe Cys His Ser Arg Arg Val Leu His Arg Asp
115 120 125Leu Lys Pro Gln Asn Leu Leu Ile Asp Asp Lys Gly Thr Ile Lys Leu
130 135 140Ala Asp Phe Gly Leu Ala Arg Ala Phe Gly Ile Pro Ile Arg Val Tyr
145 150 155 160Thr His Glu Val Val Thr Leu Trp Tyr Arg Ser Pro Glu Val Leu Leu
165 170 175Gly Ser Ala Arg Tyr Ser Thr Pro Val Asp Ile Trp Ser Ile Gly Thr
180 185 190Ile Phe Ala Glu Leu Ala Thr Lys Lys Pro Leu Phe His Gly Asp Ser
195 200 205Glu Ile Asp Gln Leu Phe Arg Ile Phe Arg Ala Leu Gly Thr Pro Asn
210 215 220Asn Glu Val Trp Pro Glu Val Glu Ser Leu Gln Asp Tyr Lys Asn Thr
225 230 235 240Phe Pro Lys Trp Lys Pro Gly Ser Leu Ala Ser His Val Lys Asn Leu
245 250 255Asp Glu Asn Gly Leu Asp Leu Leu Ser Lys Met Leu Ile Tyr Asp Pro
260 265 270Ala Lys Arg Ile Ser Gly Lys Met Ala Leu Asn His Pro Tyr Phe Asn
275 280 285Asp Leu Asp Asn Gln Ile Lys Lys Met
290 295

<210> 129

<211> 298

<212> PRT

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 <213> Homo sapiens

<400> 129

Met Glu Asn Phe Gln Lys Val Glu Lys Ile Gly Glu Gly Thr Tyr Gly
 1 5 10 15

Val Val Tyr Lys Ala Arg Asn Lys Leu Thr Gly Glu Val Val Ala Leu
 20 25 30

Lys Lys Ile Arg Leu Asp Thr Glu Thr Glu Gly Val Pro Ser Thr Ala
 35 40 45

Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu Asn His Pro Asn Ile Val
 50 55 60

Lys Leu Leu Asp Val Ile His Thr Glu Asn Lys Leu Tyr Leu Val Phe
 65 70 75 80

Glu Phe Leu His Gln Asp Leu Lys Lys Phe Met Asp Ala Ser Ala Leu
 85 90 95

Thr Gly Ile Pro Leu Pro Leu Ile Lys Ser Tyr Leu Phe Gln Leu Leu
 100 105 110

Gln Gly Leu Ala Phe Cys His Ser His Arg Val Leu His Arg Asp Leu
 115 120 125

Lys Pro Gln Asn Leu Leu Ile Asn Thr Glu Gly Ala Ile Lys Leu Ala
 130 135 140

Asp Phe Gly Leu Ala Arg Ala Phe Gly Val Pro Val Arg Thr Tyr Thr
 145 150 155 160

His Glu Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Ile Leu Leu Gly
 165 170 175

Cys Lys Tyr Tyr Ser Thr Ala Val Asp Ile Trp Ser Leu Gly Cys Ile
 180 185 190

Phe Ala Glu Met Val Thr Arg Arg Ala Leu Phe Pro Gly Asp Ser Glu
 195 200 205

Ile Asp Gln Leu Phe Arg Ile Phe Arg Thr Leu Gly Thr Pro Asp Glu
 210 215 220

Val Val Trp Pro Gly Val Thr Ser Met Pro Asp Tyr Lys Pro Ser Phe
 225 230 235 240

Pro Lys Trp Ala Arg Gln Asp Phe Ser Lys Val Val Pro Pro Leu Asp
 245 250 255

Glu Asp Gly Arg Ser Leu Leu Ser Gln Met Leu His Tyr Asp Pro Asn
 260 265 270

Lys Arg Ile Ser Ala Lys Ala Ala Leu Ala His Pro Phe Phe Gln Asp
 275 280 285

Val Thr Lys Pro Val Pro His Leu Arg Leu
 290 295

<210> 130
 <211> 1238
 <212> PRT
 <213> Homo sapiens

<400> 130

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Met Asp Ala Leu Cys Gly Ser Gly Glu Leu Gly Ser Lys Phe Trp Asp
1 5 10 15

Ser Asn Leu Ser Val His Thr Glu Asn Pro Asp Leu Thr Pro Cys Phe
20 25 30

Gln Asn Ser Leu Leu Ala Trp Val Pro Cys Ile Tyr Leu Trp Val Ala
35 40 45

Leu Pro Cys Tyr Leu Leu Tyr Leu Arg His His Cys Arg Gly Tyr Ile
50 55 60

Ile Leu Ser His Leu Ser Lys Leu Lys Met Val Leu Gly Val Leu Leu
65 70 75 80

Trp Cys Val Ser Trp Ala Asp Leu Phe Tyr Ser Phe His Gly Leu Val
85 90 95

His Gly Arg Ala Pro Ala Pro Val Phe Phe Val Thr Pro Leu Val Val
100 105 110

Gly Val Thr Met Leu Leu Ala Thr Leu Leu Ile Gln Tyr Glu Arg Leu
115 120 125

Gln Gly Val Gln Ser Ser Gly Val Leu Ile Ile Phe Trp Phe Leu Cys
130 135 140

Val Val Cys Ala Ile Val Pro Phe Arg Ser Lys Ile Leu Leu Ala Lys
145 150 155 160

Ala Glu Gly Glu Ile Ser Asp Pro Phe Arg Phe Thr Thr Phe Tyr Ile
165 170 175

His Phe Ala Leu Val Leu Ser Thr Leu Ile Leu Ala Cys Phe Arg Glu
180 185 190

Lys Pro Pro Phe Phe Ser Ala Lys Asn Val Asp Pro Asn Pro Tyr Pro
195 200 205

Glu Thr Ser Ala Gly Phe Leu Ser Arg Leu Phe Phe Trp Trp Phe Thr
210 215 220

Lys Met Ala Ile Tyr Gly Tyr Arg His Pro Leu Glu Glu Lys Asp Leu
225 230 235 240

Trp Ser Leu Lys Glu Glu Asp Arg Ser Gln Met Val Val Gln Gln Leu
245 250 255

Leu Glu Ala Trp Arg Lys Gln Glu Lys Gln Thr Ala Arg His Lys Ala
260 265 270

Ser Ala Ala Pro Gly Lys Asn Ala Ser Gly Glu Asp Glu Val Leu Leu
275 280 285

Gly Ala Arg Pro Arg Pro Arg Lys Pro Ser Phe Leu Lys Ala Leu Leu
290 295 300

Ala Thr Phe Gly Ser Ser Phe Leu Ile Ser Ala Cys Phe Lys Leu Ile
305 310 315 320

Gln Asp Leu Leu Ser Phe Ile Asn Pro Gln Leu Leu Ser Ile Leu Ile
325 330 335

Arg Phe Ile Ser Asn Pro Met Ala Pro Ser Trp Trp Gly Phe Leu Val

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 340 345 350

Ala Gly Leu Met Phe Leu Cys Ser Met Met Gln Ser Leu Ile Leu Gln
 355 360 365

His Tyr Tyr His Tyr Ile Phe Val Thr Gly Val Lys Phe Arg Thr Gly
 370 375 380

Ile Met Gly Val Ile Tyr Arg Lys Ala Leu Val Ile Thr Asn Ser Val
 385 390 395 400

Lys Arg Ala Ser Thr Val Gly Glu Ile Val Asn Leu Met Ser Val Asp
 405 410 415

Ala Gln Arg Phe Met Asp Leu Ala Pro Phe Leu Asn Leu Leu Trp Ser
 420 425 430

Ala Pro Leu Gln Ile Ile Leu Ala Ile Tyr Phe Leu Trp Gln Asn Leu
 435 440 445

Gly Pro Ser Val Leu Ala Gly Val Ala Phe Met Val Leu Leu Ile Pro
 450 455 460

Leu Asn Gly Ala Val Ala Val Lys Met Arg Ala Phe Gln Val Lys Gln
 465 470 475 480

Met Lys Leu Lys Asp Ser Arg Ile Lys Leu Met Ser Glu Ile Leu Asn
 485 490 495

Gly Ile Lys Val Leu Lys Leu Tyr Ala Trp Glu Pro Ser Phe Leu Lys
 500 505 510

Gln Val Glu Gly Ile Arg Gln Gly Glu Leu Gln Leu Leu Arg Thr Ala
 515 520 525

Ala Tyr Leu His Thr Thr Thr Thr Phe Thr Trp Met Cys Ser Pro Phe
 530 535 540

Leu Val Thr Leu Ile Thr Leu Trp Val Tyr Val Tyr Val Asp Pro Asn
 545 550 555 560

Asn Val Leu Asp Ala Glu Lys Ala Phe Val Ser Val Ser Leu Phe Asn
 565 570 575

Ile Leu Arg Leu Pro Leu Asn Met Leu Pro Gln Leu Ile Ser Asn Leu
 580 585 590

Thr Gln Ala Ser Val Ser Leu Lys Arg Ile Gln Gln Phe Leu Ser Gln
 595 600 605

Glu Glu Leu Asp Pro Gln Ser Val Glu Arg Lys Thr Ile Ser Pro Gly
 610 615 620

Tyr Ala Ile Thr Ile His Ser Gly Thr Phe Thr Trp Ala Gln Asp Leu
 625 630 635 640

Pro Pro Thr Leu His Ser Leu Asp Ile Gln Val Pro Lys Gly Ala Leu
 645 650 655

Val Ala Val Val Gly Pro Val Gly Cys Gly Lys Ser Ser Leu Val Ser
 660 665 670

Ala Leu Leu Gly Glu Met Glu Lys Leu Glu Gly Lys Val His Met Lys
 675 680 685

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Gly Ser Val Ala Tyr Val Pro Gln Gln Ala Trp Ile Gln Asn Cys Thr
690 695 700

Leu Gln Glu Asn Val Leu Phe Gly Lys Ala Leu Asn Pro Lys Arg Tyr
705 710 715 720

Gln Gln Thr Leu Glu Ala Cys Ala Leu Leu Ala Asp Leu Glu Met Leu
725 730 735

Pro Gly Gly Asp Gln Thr Glu Ile Gly Glu Lys Gly Ile Asn Leu Ser
740 745 750

Gly Gly Gln Arg Gln Arg Val Ser Leu Ala Arg Ala Val Tyr Ser Asp
755 760 765

Ala Asp Ile Phe Leu Leu Asp Asp Pro Leu Ser Ala Val Asp Ser His
770 775 780

Val Ala Lys His Ile Phe Asp His Val Ile Gly Pro Glu Gly Val Leu
785 790 795 800

Ala Gly Lys Thr Arg Val Leu Val Thr His Gly Ile Ser Phe Leu Pro
805 810 815

Gln Thr Asp Phe Ile Ile Val Leu Ala Asp Gly Gln Val Ser Glu Met
820 825 830

Gly Pro Tyr Pro Ala Leu Leu Gln Arg Asn Gly Ser Phe Ala Asn Phe
835 840 845

Leu Cys Asn Tyr Ala Pro Asp Glu Asp Gln Gly His Leu Glu Asp Ser
850 855 860

Trp Thr Ala Leu Glu Gly Ala Glu Asp Lys Glu Ala Leu Leu Ile Glu
865 870 875 880

Asp Thr Leu Ser Asn His Thr Asp Leu Thr Asp Asn Asp Pro Val Thr
885 890 895

Tyr Val Val Gln Lys Gln Phe Met Arg Gln Leu Ser Ala Leu Ser Ser
900 905 910

Asp Gly Glu Gly Gln Gly Arg Pro Val Pro Arg Arg His Leu Gly Pro
915 920 925

Ser Glu Lys Val Gln Val Thr Glu Ala Lys Ala Asp Gly Ala Leu Thr
930 935 940

Gln Glu Glu Lys Ala Ala Ile Gly Thr Val Glu Leu Ser Val Phe Trp
945 950 955 960

Asp Tyr Ala Lys Ala Val Gly Leu Cys Thr Thr Leu Ala Ile Cys Leu
965 970 975

Leu Tyr Val Gly Gln Ser Ala Ala Ala Ile Gly Ala Asn Val Trp Leu
980 985 990

Ser Ala Trp Thr Asn Asp Ala Met Ala Asp Ser Arg Gln Asn Asn Thr
995 1000 1005

Ser Leu Arg Leu Gly Val Tyr Ala Ala Leu Gly Ile Leu Gln Gly
1010 1015 1020

Phe Leu Val Met Leu Ala Ala Met Ala Met Ala Ala Gly Gly Ile

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 1025 1030 1035

Gln Ala Ala Arg Val Leu His Gln Ala Leu Leu His Asn Lys Ile
 1040 1045 1050

Arg Ser Pro Gln Ser Phe Phe Asp Thr Thr Pro Ser Gly Arg Ile
 1055 1060 1065

Leu Asn Cys Phe Ser Lys Asp Ile Tyr Val Val Asp Glu Val Leu
 1070 1075 1080

Ala Pro Val Ile Leu Met Leu Leu Asn Ser Phe Phe Asn Ala Ile
 1085 1090 1095

Ser Thr Leu Val Val Ile Met Ala Ser Thr Pro Leu Phe Thr Val
 1100 1105 1110

Val Ile Leu Pro Leu Ala Val Leu Tyr Thr Leu Val Gln Arg Phe
 1115 1120 1125

Tyr Ala Ala Thr Ser Arg Gln Leu Lys Arg Leu Glu Ser Val Ser
 1130 1135 1140

Arg Ser Pro Ile Tyr Ser His Phe Ser Glu Thr Val Thr Gly Ala
 1145 1150 1155

Ser Val Ile Arg Ala Tyr Asn Arg Ser Arg Asp Phe Glu Ile Ile
 1160 1165 1170

Ser Asp Thr Lys Val Asp Ala Asn Gln Arg Ser Cys Tyr Pro Tyr
 1175 1180 1185

Ile Ile Ser Asn Arg Ser Glu Ala Ala Ser Leu Ala Pro Cys Ser
 1190 1195 1200

Ser Arg Asn Ser Gln Gln Ala Leu Trp Cys Ser Gly Ser Leu Ser
 1205 1210 1215

Leu Leu Ser Pro Lys Gln Lys Thr Gly Pro Ala Leu Pro Leu Pro
 1220 1225 1230

His Phe Leu Leu Ile
 1235

<210> 131
 <211> 418
 <212> PRT
 <213> Homo sapiens

<400> 131

Met Ala Gly Arg Leu Pro Ala Cys Val Val Asp Cys Gly Thr Gly Tyr
 1 5 10 15

Thr Lys Leu Gly Tyr Ala Gly Asn Thr Glu Pro Gln Phe Ile Ile Pro
 20 25 30

Ser Cys Ile Ala Ile Lys Glu Ser Ala Lys Val Gly Asp Gln Ala Gln
 35 40 45

Arg Arg Val Met Lys Gly Val Asp Asp Leu Asp Phe Phe Ile Gly Asp
 50 55 60

Glu Ala Ile Glu Lys Pro Thr Tyr Ala Thr Lys Trp Pro Ile Arg His
 65 70 75 80

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Gly Ile Val Glu Asp Trp Asp Leu Met Glu Arg Phe Met Glu Gln Val
 85 90 95

Ile Phe Lys Tyr Leu Arg Ala Glu Pro Glu Asp His Tyr Phe Leu Leu
 100 105 110

Thr Glu Pro Pro Leu Asn Thr Pro Glu Asn Arg Glu Tyr Thr Ala Glu
 115 120 125

Ile Met Phe Glu Ser Phe Asn Val Pro Gly Leu Tyr Ile Ala Val Gln
 130 135 140

Ala Val Leu Ala Leu Ala Ala Ser Trp Thr Ser Arg Gln Val Gly Glu
 145 150 155 160

Arg Thr Leu Thr Gly Thr Val Ile Asp Ser Gly Asp Gly Val Thr His
 165 170 175

Val Ile Pro Val Ala Glu Gly Tyr Val Ile Gly Ser Cys Ile Lys His
 180 185 190

Ile Pro Ile Ala Gly Arg Asp Ile Thr Tyr Phe Ile Gln Gln Leu Leu
 195 200 205

Arg Asp Arg Glu Val Gly Ile Pro Pro Glu Gln Ser Leu Glu Thr Ala
 210 215 220

Lys Ala Val Lys Glu Arg Tyr Ser Tyr Val Cys Pro Asp Leu Val Lys
 225 230 235 240

Glu Phe Asn Lys Tyr Asp Thr Asp Gly Ser Lys Trp Ile Lys Gln Tyr
 245 250 255

Thr Gly Ile Asn Ala Ile Ser Lys Lys Glu Phe Ser Ile Asp Val Gly
 260 265 270

Tyr Glu Arg Phe Leu Gly Pro Glu Ile Phe Phe His Pro Glu Phe Ala
 275 280 285

Asn Pro Asp Phe Thr Gln Pro Ile Ser Glu Val Val Asp Glu Val Ile
 290 295 300

Gln Asn Cys Pro Ile Asp Val Arg Arg Pro Leu Tyr Lys Asn Ile Val
 305 310 315 320

Leu Ser Gly Gly Ser Thr Met Phe Arg Asp Phe Gly Arg Arg Leu Gln
 325 330 335

Arg Asp Leu Lys Arg Thr Val Asp Ala Arg Leu Lys Leu Ser Glu Glu
 340 345 350

Leu Ser Gly Gly Arg Leu Lys Pro Lys Pro Ile Asp Val Gln Val Ile
 355 360 365

Thr His His Met Gln Arg Tyr Ala Val Trp Phe Gly Gly Ser Met Leu
 370 375 380

Ala Ser Thr Pro Glu Phe Tyr Gln Val Cys His Thr Lys Lys Asp Tyr
 385 390 395 400

Glu Glu Ile Gly Pro Ser Ile Cys Arg His Asn Pro Val Phe Gly Val
 405 410 415

Met Ser

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

<210> 132
 <211> 210
 <212> PRT
 <213> Homo sapiens

<400> 132

Met Phe Glu Ser Phe Asn Val Pro Gly Leu Tyr Ile Ala Val Gln Ala
 1 5 10 15

Val Leu Ala Leu Ala Ala Ser Trp Thr Ser Arg Gln Val Gly Glu Arg
 20 25 30

Thr Leu Thr Gly Ile Val Ile Asp Ser Gly Asp Gly Val Thr His Val
 35 40 45

Ile Pro Val Ala Glu Gly Tyr Val Ile Gly Ser Cys Ile Lys His Ile
 50 55 60

Pro Ile Ala Gly Arg Asp Ile Thr Tyr Phe Ile Gln Gln Leu Leu Arg
 65 70 75 80

Glu Arg Glu Val Gly Ile Pro Pro Glu Gln Ser Leu Glu Thr Ala Lys
 85 90 95

Ala Ile Lys Glu Lys Tyr Cys Tyr Ile Cys Pro Asp Ile Val Lys Glu
 100 105 110

Phe Ala Lys Tyr Asp Val Asp Pro Gln Lys Trp Ile Lys Gln Tyr Thr
 115 120 125

Gly Ile Asn Ala Ile Asn Gln Lys Lys Phe Val Ile Asp Val Gly Tyr
 130 135 140

Glu Arg Phe Leu Gly Pro Glu Ile Phe Phe His Pro Glu Phe Ala Asn
 145 150 155 160

Pro Asp Ser Met Glu Ser Ile Ser Asp Val Val Asp Glu Val Ile Gln
 165 170 175

Asn Cys Pro Ile Asp Val Arg Arg Pro Leu Tyr Lys Met Glu Gln Ile
 180 185 190

Pro Leu Ser Tyr Pro Gln Gly His Gly Phe His Pro Leu Ser Pro Pro
 195 200 205

Phe His
 210

<210> 133
 <211> 300
 <212> PRT
 <213> Homo sapiens

<400> 133

Met Ile Leu Leu Glu Val Asn Asn Arg Ile Ile Glu Glu Thr Leu Ala
 1 5 10 15

Leu Lys Phe Glu Asn Ala Ala Ala Gly Asn Lys Pro Glu Ala Val Glu
 20 25 30

Val Thr Phe Ala Asp Phe Asp Gly Val Leu Tyr His Ile Ser Asn Pro
 35 40 45

Asn Gly Asp Lys Thr Lys Val Met Val Ser Ile Ser Leu Lys Phe Tyr
 50 55 60

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Lys Glu Leu Gln Ala His Gly Ala Asp Glu Leu Leu Lys Arg Val Tyr
65 70 75 80

Gly Ser Phe Leu Val Asn Pro Glu Ser Gly Tyr Asn Val Ser Leu Leu
85 90 95

Tyr Asp Leu Glu Asn Leu Pro Ala Ser Lys Asp Ser Ile Val His Gln
100 105 110

Ala Gly Met Leu Lys Arg Asn Cys Phe Ala Ser Val Phe Glu Lys Tyr
115 120 125

Phe Gln Phe Gln Glu Glu Gly Lys Glu Gly Glu Asn Arg Ala Val Ile
130 135 140

His Tyr Arg Asp Asp Glu Thr Met Tyr Val Glu Ser Lys Lys Asp Arg
145 150 155 160

Val Thr Val Val Phe Ser Thr Val Phe Lys Asp Asp Asp Asp Val Val
165 170 175

Ile Gly Lys Val Phe Met Gln Glu Phe Lys Glu Gly Arg Arg Ala Ser
180 185 190

His Thr Ala Pro Gln Val Leu Phe Ser His Arg Glu Pro Pro Leu Glu
195 200 205

Leu Lys Asp Thr Asp Ala Ala Val Gly Asp Asn Ile Gly Tyr Ile Thr
210 215 220

Phe Val Leu Phe Pro Arg His Thr Asn Ala Ser Ala Arg Asp Asn Thr
225 230 235 240

Ile Asn Leu Ile His Thr Phe Arg Asp Tyr Leu His Tyr His Ile Lys
245 250 255

Cys Ser Lys Ala Tyr Ile His Thr Arg Met Arg Ala Lys Thr Ser Asp
260 265 270

Phe Leu Lys Val Leu Asn Arg Ala Arg Pro Asp Ala Glu Lys Lys Glu
275 280 285

Met Lys Thr Ile Thr Gly Lys Thr Phe Ser Ser Arg
290 295 300

<210> 134
<211> 418
<212> PRT
<213> Homo sapiens

<400> 134

Met Ala Gly Ser Leu Pro Pro Cys Val Val Asp Cys Gly Thr Gly Tyr
1 5 10 15

Thr Lys Leu Gly Tyr Ala Gly Asn Thr Glu Pro Gln Phe Ile Ile Pro
20 25 30

Ser Cys Ile Ala Ile Arg Glu Ser Ala Lys Val Val Asp Gln Ala Gln
35 40 45

Arg Arg Val Leu Arg Gly Val Asp Asp Leu Asp Phe Phe Ile Gly Asp
50 55 60

Glu Ala Ile Asp Lys Pro Thr Tyr Ala Thr Lys Trp Pro Ile Arg His

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

65 Gly Ile Ile Glu Asp Trp Asp Leu Met Glu Arg Phe Met Glu Gln Val
 70 85 90 95
 Val Phe Lys Tyr Leu Arg Ala Glu Pro Glu Asp His Tyr Phe Leu Met
 100 105 110
 Thr Glu Pro Pro Leu Asn Thr Pro Glu Asn Arg Glu Tyr Leu Ala Glu
 115 120 125
 Ile Met Phe Glu Ser Phe Asn Val Pro Gly Leu Tyr Ile Ala Val Gln
 130 135 140
 Ala Val Leu Ala Leu Ala Ala Ser Trp Thr Ser Arg Gln Val Gly Glu
 145 150 155 160
 Arg Thr Leu Thr Gly Ile Val Ile Asp Ser Gly Asp Gly Val Thr His
 165 170 175
 Val Ile Pro Val Ala Glu Gly Tyr Val Ile Gly Ser Cys Ile Lys His
 180 185 190
 Ile Pro Ile Ala Gly Arg Asp Ile Thr Tyr Phe Ile Gln Gln Leu Leu
 195 200 205
 Arg Glu Arg Glu Val Gly Ile Pro Pro Glu Gln Ser Leu Glu Thr Ala
 210 215 220
 Lys Ala Ile Lys Glu Lys Tyr Cys Tyr Ile Cys Pro Asp Ile Val Lys
 225 230 235 240
 Glu Phe Ala Lys Tyr Asp Val Asp Pro Arg Lys Trp Ile Lys Gln Tyr
 245 250 255
 Thr Gly Ile Asn Ala Ile Asn Gln Lys Lys Phe Val Ile Asp Val Gly
 260 265 270
 Tyr Glu Arg Phe Leu Gly Pro Glu Ile Phe Phe His Pro Glu Phe Ala
 275 280 285
 Asn Pro Asp Phe Met Glu Ser Ile Ser Asp Val Val Asp Glu Val Ile
 290 295 300
 Gln Asn Cys Pro Ile Asp Val Arg Arg Pro Leu Tyr Lys Asn Val Val
 305 310 315 320
 Leu Ser Gly Gly Ser Thr Met Phe Arg Asp Phe Gly Arg Arg Leu Gln
 325 330 335
 Arg Asp Leu Lys Arg Val Val Asp Ala Arg Leu Arg Leu Ser Glu Glu
 340 345 350
 Leu Ser Gly Gly Arg Ile Lys Pro Lys Pro Val Glu Val Gln Val Val
 355 360 365
 Thr His His Met Gln Arg Tyr Ala Val Trp Phe Gly Gly Ser Met Leu
 370 375 380
 Ala Ser Thr Pro Glu Phe Phe Gln Val Cys His Thr Lys Lys Asp Tyr
 385 390 395 400
 Glu Glu Tyr Gly Pro Ser Ile Cys Arg His Asn Pro Val Phe Gly Val
 405 410 415

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Met Ser

<210> 135
 <211> 1271
 <212> PRT
 <213> Homo sapiens
 <400> 135

Met Val Asp Pro Val Gly Phe Ala Glu Ala Trp Lys Ala Gln Phe Pro
 1 5 10 15

Asp Ser Glu Pro Pro Arg Met Glu Leu Arg Ser Val Gly Asp Ile Glu
 20 25 30

Gln Glu Leu Glu Arg Cys Lys Ala Ser Ile Arg Arg Leu Glu Gln Glu
 35 40 45

Val Asn Gln Glu Arg Phe Arg Met Ile Tyr Leu Gln Thr Leu Leu Ala
 50 55 60

Lys Glu Lys Lys Ser Tyr Asp Arg Gln Arg Trp Gly Phe Arg Arg Ala
 65 70 75 80

Ala Gln Ala Pro Asp Gly Ala Ser Glu Pro Arg Ala Ser Ala Ser Arg
 85 90 95

Pro Gln Pro Ala Pro Ala Asp Gly Ala Asp Pro Pro Pro Ala Glu Glu
 100 105 110

Pro Glu Ala Arg Pro Asp Gly Glu Gly Ser Pro Gly Lys Ala Arg Pro
 115 120 125

Gly Thr Ala Arg Arg Pro Gly Ala Ala Ala Ser Gly Glu Arg Asp Asp
 130 135 140

Arg Gly Pro Pro Ala Ser Val Ala Ala Leu Arg Ser Asn Phe Glu Arg
 145 150 155 160

Ile Arg Lys Gly His Gly Gln Pro Gly Ala Asp Ala Glu Lys Pro Phe
 165 170 175

Tyr Val Asn Val Glu Phe His His Glu Arg Gly Leu Val Lys Val Asn
 180 185 190

Asp Lys Glu Val Ser Asp Arg Ile Ser Ser Leu Gly Ser Gln Ala Met
 195 200 205

Gln Met Glu Arg Lys Lys Ser Gln His Gly Ala Gly Ser Ser Val Gly
 210 215 220

Asp Ala Ser Arg Pro Pro Tyr Arg Gly Arg Ser Ser Glu Ser Ser Cys
 225 230 235 240

Gly Val Asp Gly Asp Tyr Glu Asp Ala Glu Leu Asn Pro Arg Phe Leu
 245 250 255

Lys Asp Asn Leu Ile Asp Ala Asn Gly Gly Ser Arg Pro Pro Trp Pro
 260 265 270

Pro Leu Glu Tyr Gln Pro Tyr Gln Ser Ile Tyr Val Gly Gly Met Met
 275 280 285

Glu Gly Glu Gly Lys Gly Pro Leu Leu Arg Ser Gln Ser Thr Ser Glu
 290 295 300

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Gln Glu Lys Arg Leu Thr Trp Pro Arg Arg Ser Tyr Ser Pro Arg Ser
305 310 315 320

Phe Glu Asp Cys Gly Gly Gly Tyr Thr Pro Asp Cys Ser Ser Asn Glu
325 330 335

Asn Leu Thr Ser Ser Glu Glu Asp Phe Ser Ser Gly Gln Ser Ser Arg
340 345 350

Val Ser Pro Ser Pro Thr Thr Tyr Arg Met Phe Arg Asp Lys Ser Arg
355 360 365

Ser Pro Ser Gln Asn Ser Gln Gln Ser Phe Asp Ser Ser Ser Pro Pro
370 375 380

Thr Pro Gln Cys His Lys Arg His Arg His Cys Pro Val Val Val Ser
385 390 395 400

Glu Ala Thr Ile Val Gly Val Arg Lys Thr Gly Gln Ile Trp Pro Asn
405 410 415

Asp Gly Glu Gly Ala Phe His Gly Asp Ala Asp Gly Ser Phe Gly Thr
420 425 430

Pro Pro Gly Tyr Gly Cys Ala Ala Asp Arg Ala Glu Glu Gln Arg Arg
435 440 445

His Gln Asp Gly Leu Pro Tyr Ile Asp Asp Ser Pro Ser Ser Ser Pro
450 455 460

His Leu Ser Ser Lys Gly Arg Gly Ser Arg Asp Ala Leu Val Ser Gly
465 470 475 480

Ala Leu Glu Ser Thr Lys Ala Ser Glu Leu Asp Leu Glu Lys Gly Leu
485 490 495

Glu Met Arg Lys Trp Val Leu Ser Gly Ile Leu Ala Ser Glu Glu Thr
500 505 510

Tyr Leu Ser His Leu Glu Ala Leu Leu Leu Pro Met Lys Pro Leu Lys
515 520 525

Ala Ala Ala Thr Thr Ser Gln Pro Val Leu Thr Ser Gln Gln Ile Glu
530 535 540

Thr Ile Phe Phe Lys Val Pro Glu Leu Tyr Glu Ile His Lys Glu Phe
545 550 555 560

Tyr Asp Gly Leu Phe Pro Arg Val Gln Gln Trp Ser His Gln Gln Arg
565 570 575

Val Gly Asp Leu Phe Gln Lys Leu Ala Ser Gln Leu Gly Val Tyr Arg
580 585 590

Ala Phe Val Asp Asn Tyr Gly Val Ala Met Glu Met Ala Glu Lys Cys
595 600 605

Cys Gln Ala Asn Ala Gln Phe Ala Glu Ile Ser Glu Asn Leu Arg Ala
610 615 620

Arg Ser Asn Lys Asp Ala Lys Asp Pro Thr Thr Lys Asn Ser Leu Glu
625 630 635 640

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Thr Leu Leu Tyr Lys Pro Val Asp Arg Val Thr Arg Ser Thr Leu Val
 645 650 655

Leu His Asp Leu Leu Lys His Thr Pro Ala Ser His Pro Asp His Pro
 660 665 670

Leu Leu Gln Asp Ala Leu Arg Ile Ser Gln Asn Phe Leu Ser Ser Ile
 675 680 685

Asn Glu Glu Ile Thr Pro Arg Arg Gln Ser Met Thr Val Lys Lys Gly
 690 695 700

Glu His Arg Gln Leu Leu Lys Asp Ser Phe Met Val Glu Leu Val Glu
 705 710 715 720

Gly Ala Arg Lys Leu Arg His Val Phe Leu Phe Thr Glu Leu Leu Leu
 725 730 735

Cys Thr Lys Leu Lys Lys Gln Ser Gly Gly Lys Thr Gln Gln Tyr Asp
 740 745 750

Cys Lys Trp Tyr Ile Pro Leu Thr Asp Leu Ser Phe Gln Met Val Asp
 755 760 765

Glu Leu Glu Ala Val Pro Asn Ile Pro Leu Val Pro Asp Glu Glu Leu
 770 775 780

Asp Ala Leu Lys Ile Lys Ile Ser Gln Ile Lys Ser Asp Ile Gln Arg
 785 790 795 800

Glu Lys Arg Ala Asn Lys Gly Ser Lys Ala Thr Glu Arg Leu Lys Lys
 805 810 815

Lys Leu Ser Glu Gln Glu Ser Leu Leu Leu Met Ser Pro Ser Met
 820 825 830

Ala Phe Arg Val His Ser Arg Asn Gly Lys Ser Tyr Thr Phe Leu Ile
 835 840 845

Ser Ser Asp Tyr Glu Arg Ala Glu Trp Arg Glu Asn Ile Arg Glu Gln
 850 855 860

Gln Lys Lys Cys Phe Arg Ser Phe Ser Leu Thr Ser Val Glu Leu Gln
 865 870 875 880

Met Leu Thr Asn Ser Cys Val Lys Leu Gln Thr Val His Ser Ile Pro
 885 890 895

Leu Thr Ile Asn Lys Glu Asp Asp Glu Ser Pro Gly Leu Tyr Gly Phe
 900 905 910

Leu Asn Val Ile Val His Ser Ala Thr Gly Phe Lys Gln Ser Ser Asn
 915 920 925

Leu Tyr Cys Thr Leu Glu Val Asp Ser Phe Gly Tyr Phe Val Asn Lys
 930 935 940

Ala Lys Thr Arg Val Tyr Arg Asp Thr Ala Glu Pro Asn Trp Asn Glu
 945 950 955 960

Glu Phe Glu Ile Glu Leu Glu Gly Ser Gln Thr Leu Arg Ile Leu Cys
 965 970 975

Tyr Glu Lys Cys Tyr Asn Lys Thr Lys Ile Pro Lys Glu Asp Gly Glu
 980 985 990

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ser Thr Asp Arg Leu Met Gly Lys Gly Gln Val Gln Leu Asp Pro Gln
995 1000 1005

Ala Leu Gln Asp Arg Asp Trp Gln Arg Thr Val Ile Ala Met Asn
1010 1015 1020

Gly Ile Glu Val Lys Leu Ser Val Lys Phe Asn Ser Arg Glu Phe
1025 1030 1035

Ser Leu Lys Arg Met Pro Ser Arg Lys Gln Thr Gly Val Phe Gly
1040 1045 1050

Val Lys Ile Ala Val Val Thr Lys Arg Glu Arg Ser Lys Val Pro
1055 1060 1065

Tyr Ile Val Arg Gln Cys Val Glu Glu Ile Glu Arg Arg Gly Met
1070 1075 1080

Glu Glu Val Gly Ile Tyr Arg Val Ser Gly Val Ala Thr Asp Ile
1085 1090 1095

Gln Ala Leu Lys Ala Ala Phe Asp Val Asn Asn Lys Asp Val Ser
1100 1105 1110

Val Met Met Ser Glu Met Asp Val Asn Ala Ile Ala Gly Thr Leu
1115 1120 1125

Lys Leu Tyr Phe Arg Glu Leu Pro Glu Pro Leu Phe Thr Asp Glu
1130 1135 1140

Phe Tyr Pro Asn Phe Ala Glu Gly Ile Ala Leu Ser Asp Pro Val
1145 1150 1155

Ala Lys Glu Ser Cys Met Leu Asn Leu Leu Leu Ser Leu Pro Glu
1160 1165 1170

Ala Asn Leu Leu Thr Phe Leu Phe Leu Leu Asp His Leu Lys Arg
1175 1180 1185

Val Ala Glu Lys Glu Ala Val Asn Lys Met Ser Leu His Asn Leu
1190 1195 1200

Ala Thr Val Phe Gly Pro Thr Leu Leu Arg Pro Ser Glu Lys Glu
1205 1210 1215

Ser Lys Leu Pro Ala Asn Pro Ser Gln Pro Ile Thr Met Thr Asp
1220 1225 1230

Ser Trp Ser Leu Glu Val Met Ser Gln Val Gln Val Leu Leu Tyr
1235 1240 1245

Phe Leu Gln Leu Glu Ala Ile Pro Ala Pro Asp Ser Lys Arg Gln
1250 1255 1260

Ser Ile Leu Phe Ser Thr Glu Val
1265 1270

<210> 136
<211> 1227
<212> PRT
<213> Homo sapiens

<400> 136

Met Val Asp Pro Val Gly Phe Ala Glu Ala Trp Lys Ala Gln Phe Pro

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

```

1      5      10      15
Asp Ser Glu Pro Pro Arg Met Glu Leu Arg Ser Val Gly Asp Ile Glu
20      25      30
Gln Glu Leu Glu Arg Cys Lys Ala Ser Ile Arg Arg Leu Glu Gln Glu
35      40      45
Val Asn Gln Glu Arg Phe Arg Met Ile Tyr Leu Gln Thr Leu Leu Ala
50      55      60
Lys Glu Lys Lys Ser Tyr Asp Arg Gln Arg Trp Gly Phe Arg Arg Ala
65      70      75      80
Ala Gln Ala Pro Asp Gly Ala Ser Glu Pro Arg Ala Ser Ala Ser Arg
85      90      95
Pro Gln Pro Ala Pro Ala Asp Gly Ala Asp Pro Pro Pro Ala Glu Glu
100     105     110
Pro Glu Ala Arg Pro Asp Gly Glu Gly Ser Pro Gly Lys Ala Arg Pro
115     120     125
Gly Thr Ala Arg Arg Pro Gly Ala Ala Ala Ser Gly Glu Arg Asp Asp
130     135     140
Arg Gly Pro Pro Ala Ser Val Ala Ala Leu Arg Ser Asn Phe Glu Arg
145     150     155     160
Ile Arg Lys Gly His Gly Gln Pro Gly Ala Asp Ala Glu Lys Pro Phe
165     170     175
Tyr Val Asn Val Glu Phe His His Glu Arg Gly Leu Val Lys Val Asn
180     185     190
Asp Lys Glu Val Ser Asp Arg Ile Ser Ser Leu Gly Ser Gln Ala Met
195     200     205
Gln Met Glu Arg Lys Lys Ser Gln His Gly Ala Gly Ser Ser Val Gly
210     215     220
Asp Ala Ser Arg Pro Pro Tyr Arg Gly Arg Ser Ser Glu Ser Ser Cys
225     230     235     240
Gly Val Asp Gly Asp Tyr Glu Asp Ala Glu Leu Asn Pro Arg Phe Leu
245     250     255
Lys Asp Asn Leu Ile Asp Ala Asn Gly Gly Ser Arg Pro Pro Trp Pro
260     265     270
Pro Leu Glu Tyr Gln Pro Tyr Gln Ser Ile Tyr Val Gly Gly Ile Met
275     280     285
Glu Gly Glu Gly Lys Gly Pro Leu Leu Arg Ser Gln Ser Thr Ser Glu
290     295     300
Gln Glu Lys Arg Leu Thr Trp Pro Arg Arg Ser Tyr Ser Pro Arg Ser
305     310     315     320
Phe Glu Asp Cys Gly Gly Gly Tyr Thr Pro Asp Cys Ser Ser Asn Glu
325     330     335
Asn Leu Thr Ser Ser Glu Glu Asp Phe Ser Ser Gly Gln Ser Ser Arg
340     345     350

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Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Val Ser Pro Ser Pro Thr Thr Tyr Arg Met Phe Arg Asp Lys Ser Arg
355 360 365

Ser Pro Ser Gln Asn Ser Gln Gln Ser Phe Asp Ser Ser Ser Pro Pro
370 375 380

Thr Pro Gln Cys His Lys Arg His Arg His Cys Pro Val Val Val Ser
385 390 395 400

Glu Ala Thr Ile Val Gly Val Arg Lys Thr Gly Gln Ile Trp Pro Asn
405 410 415

Asp Asp Glu Gly Ala Phe His Gly Asp Ala Asp Gly Ser Phe Gly Thr
420 425 430

Pro Pro Gly Tyr Gly Cys Ala Ala Asp Arg Ala Glu Glu Gln Arg Arg
435 440 445

His Gln Asp Gly Leu Pro Tyr Ile Asp Asp Ser Pro Ser Ser Ser Pro
450 455 460

His Leu Ser Ser Lys Gly Arg Gly Ser Arg Asp Ala Leu Val Ser Gly
465 470 475 480

Ala Leu Lys Ser Thr Lys Ala Ser Glu Leu Asp Leu Glu Lys Gly Leu
485 490 495

Glu Met Arg Lys Trp Val Leu Ser Gly Ile Leu Ala Ser Glu Glu Thr
500 505 510

Tyr Leu Ser His Leu Glu Ala Leu Leu Leu Pro Met Lys Pro Leu Lys
515 520 525

Ala Ala Ala Thr Thr Ser Gln Pro Val Leu Thr Ser Gln Gln Ile Glu
530 535 540

Thr Ile Phe Phe Lys Val Pro Glu Leu Tyr Glu Ile His Lys Glu Ser
545 550 555 560

Tyr Asp Gly Leu Phe Pro Arg Val Gln Gln Trp Ser His Gln Gln Arg
565 570 575

Val Gly Asp Leu Phe Gln Lys Leu Ala Ser Gln Leu Gly Val Tyr Arg
580 585 590

Ala Phe Val Asp Asn Tyr Gly Val Ala Met Glu Met Ala Glu Lys Cys
595 600 605

Cys Gln Ala Asn Ala Gln Phe Ala Glu Ile Ser Glu Asn Leu Arg Ala
610 615 620

Arg Ser Asn Lys Asp Ala Lys Asp Pro Thr Thr Lys Asn Ser Leu Glu
625 630 635 640

Thr Leu Leu Tyr Lys Pro Val Asp Arg Val Thr Arg Ser Thr Leu Val
645 650 655

Leu His Asp Leu Leu Lys His Thr Pro Ala Ser His Pro Asp His Pro
660 665 670

Leu Leu Gln Asp Ala Leu Arg Ile Ser Gln Asn Phe Leu Ser Ser Ile
675 680 685

Asn Glu Glu Ile Thr Pro Arg Arg Gln Ser Met Thr Val Lys Lys Gly

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 690 695 700

Glu His Arg Gln Leu Leu Lys Asp Ser Phe Met Val Glu Leu Val Glu
 705 710 715 720

Gly Ala Arg Lys Leu Arg His Val Phe Leu Phe Thr Asp Leu Leu Leu
 725 730 735

Cys Thr Lys Leu Lys Lys Gln Ser Gly Gly Lys Thr Gln Gln Tyr Asp
 740 745 750

Cys Lys Trp Tyr Ile Pro Leu Thr Asp Leu Ser Phe Gln Met Val Asp
 755 760 765

Glu Leu Glu Ala Val Pro Asn Ile Pro Leu Val Pro Asp Glu Glu Leu
 770 775 780

Asp Ala Leu Lys Ile Lys Ile Ser Gln Ile Lys Ser Asp Ile Gln Arg
 785 790 795 800

Glu Lys Arg Ala Asn Lys Gly Ser Lys Ala Thr Glu Arg Leu Lys Lys
 805 810 815

Lys Leu Ser Glu Gln Glu Ser Leu Leu Leu Leu Met Ser Pro Ser Met
 820 825 830

Ala Phe Arg Val His Ser Arg Asn Gly Lys Ser Tyr Thr Phe Leu Ile
 835 840 845

Ser Ser Asp Tyr Glu Arg Ala Glu Trp Arg Glu Asn Ile Arg Glu Gln
 850 855 860

Gln Lys Lys Cys Phe Arg Ser Phe Ser Leu Thr Ser Val Glu Leu Gln
 865 870 875 880

Met Leu Thr Asn Ser Cys Val Lys Leu Gln Thr Val His Ser Ile Pro
 885 890 895

Leu Thr Ile Asn Lys Glu Asp Asp Glu Ser Pro Gly Leu Tyr Gly Phe
 900 905 910

Leu Asn Val Ile Val His Ser Ala Thr Gly Phe Lys Gln Ser Ser Asn
 915 920 925

Leu Tyr Cys Thr Leu Glu Val Asp Ser Phe Gly Tyr Phe Val Asn Lys
 930 935 940

Ala Lys Thr Arg Val Tyr Arg Asp Thr Ala Glu Pro Asn Trp Asn Glu
 945 950 955 960

Leu Asp Pro Gln Ala Leu Gln Asp Arg Asp Trp Gln Arg Thr Val Ile
 965 970 975

Ala Met Asn Gly Ile Glu Val Lys Leu Ser Val Lys Phe Asn Ser Arg
 980 985 990

Glu Phe Ser Leu Lys Arg Met Pro Ser Arg Lys Gln Thr Gly Val Phe
 995 1000 1005

Gly Val Lys Ile Ala Val Val Thr Lys Arg Glu Arg Ser Lys Val
 1010 1015 1020

Pro Tyr Ile Val Arg Gln Cys Val Glu Glu Ile Glu Arg Arg Gly
 1025 1030 1035

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Met Glu Glu Val Gly Ile Tyr Arg Val Ser Gly Val Ala Thr Asp
 1040 1045 1050

Ile Gln Ala Leu Lys Ala Ala Phe Asp Val Asn Asn Lys Asp Val
 1055 1060 1065

Ser Val Met Met Ser Glu Met Asp Val Asn Ala Ile Ala Gly Thr
 1070 1075 1080

Leu Lys Leu Tyr Phe Arg Glu Leu Pro Glu Pro Leu Phe Thr Asp
 1085 1090 1095

Glu Phe Tyr Pro Asn Phe Ala Glu Gly Ile Ala Leu Ser Asp Pro
 1100 1105 1110

Val Ala Lys Glu Ser Cys Met Leu Asn Leu Leu Leu Ser Leu Pro
 1115 1120 1125

Glu Ala Asn Leu Leu Thr Phe Leu Phe Leu Leu Asp His Leu Lys
 1130 1135 1140

Arg Val Ala Glu Lys Glu Ala Val Asn Lys Met Ser Leu His Asn
 1145 1150 1155

Leu Ala Thr Val Phe Gly Pro Thr Leu Leu Arg Pro Ser Glu Lys
 1160 1165 1170

Glu Ser Lys Leu Pro Ala Asn Pro Ser Gln Pro Ile Thr Met Thr
 1175 1180 1185

Asp Ser Trp Ser Leu Glu Val Met Ser Gln Val Gln Val Leu Leu
 1190 1195 1200

Tyr Phe Leu Gln Leu Glu Ala Ile Pro Ala Pro Asp Ser Lys Arg
 1205 1210 1215

Gln Ser Ile Leu Phe Ser Thr Glu Val
 1220 1225

<210> 137
 <211> 304
 <212> PRT
 <213> Homo sapiens

<400> 137

Met Ala Gly Asn Phe Asp Ser Glu Glu Arg Ser Ser Trp Tyr Trp Gly
 1 5 10 15

Arg Leu Ser Arg Gln Glu Ala Val Ala Leu Leu Gln Gly Gln Arg His
 20 25 30

Gly Val Phe Leu Val Arg Asp Ser Ser Thr Ser Pro Gly Asp Tyr Val
 35 40 45

Leu Ser Val Ser Glu Asn Ser Arg Val Ser His Tyr Ile Ile Asn Ser
 50 55 60

Ser Gly Pro Arg Pro Pro Val Pro Pro Ser Pro Ala Gln Pro Pro Pro
 65 70 75 80

Gly Val Ser Pro Ser Arg Leu Arg Ile Gly Asp Gln Glu Phe Asp Ser
 85 90 95

Leu Pro Ala Leu Leu Glu Phe Tyr Lys Ile His Tyr Trp Asp Thr Thr
 100 105 110

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Thr Leu Ile Glu Pro Val Ser Arg Ser Arg Gln Gly Ser Gly Val Ile
115 120 125

Leu Arg Gln Glu Glu Ala Glu Tyr Val Arg Ala Leu Phe Asp Phe Asn
130 135 140

Gly Asn Asp Glu Glu Asp Leu Pro Phe Lys Lys Gly Asp Ile Leu Arg
145 150 155 160

Ile Arg Asp Lys Pro Glu Glu Gln Trp Trp Asn Ala Glu Asp Ser Glu
165 170 175

Gly Lys Arg Gly Met Ile Pro Val Pro Tyr Val Glu Lys Tyr Arg Pro
180 185 190

Ala Ser Ala Ser Val Ser Ala Leu Ile Gly Gly Asn Gln Glu Gly Ser
195 200 205

His Pro Gln Pro Leu Gly Pro Pro Glu Pro Gly Pro Tyr Ala Gln Pro
210 215 220

Ser Val Asn Thr Pro Leu Pro Asn Leu Gln Asn Gly Pro Ile Tyr Ala
225 230 235 240

Arg Val Ile Gln Lys Arg Val Pro Asn Ala Tyr Asp Lys Thr Ala Leu
245 250 255

Ala Leu Glu Val Gly Glu Leu Val Lys Val Thr Lys Ile Asn Val Ser
260 265 270

Gly Gln Trp Glu Gly Gly Cys Asn Gly Lys Arg Gly His Phe Pro Phe
275 280 285

Thr His Val Arg Leu Leu Asp Gln Gln Asn Pro Asp Glu Asp Phe Ser
290 295 300

<210> 138
<211> 360
<212> PRT
<213> Homo sapiens

<400> 138

Met Ala Ala Ala Ala Ala Ala Gly Ala Gly Pro Glu Met Val Arg Gly
1 5 10 15

Gln Val Phe Asp Val Gly Pro Arg Tyr Thr Asn Leu Ser Tyr Ile Gly
20 25 30

Glu Gly Ala Tyr Gly Met Val Cys Ser Ala Tyr Asp Asn Val Asn Lys
35 40 45

Val Arg Val Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln Thr Tyr
50 55 60

Cys Gln Arg Thr Leu Arg Glu Ile Lys Ile Leu Leu Arg Phe Arg His
65 70 75 80

Glu Asn Ile Ile Gly Ile Asn Asp Ile Ile Arg Ala Pro Thr Ile Glu
85 90 95

Gln Met Lys Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr Asp Leu
100 105 110

Tyr Lys Leu Leu Lys Thr Gln His Leu Ser Asn Asp His Ile Cys Tyr

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 115 120 125

Phe Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn
 130 135 140

Val Leu His Arg Asp Leu Lys Pro Ser Asn Leu Leu Asn Thr Thr
 145 150 155 160

Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Val Ala Asp Pro
 165 170 175

Asp His Asp His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr Arg Trp
 180 185 190

Tyr Arg Ala Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr Lys Ser
 195 200 205

Ile Asp Ile Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu Ser Asn
 210 215 220

Arg Pro Ile Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn His Ile
 225 230 235 240

Leu Gly Ile Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys Ile Ile
 245 250 255

Asn Leu Lys Ala Arg Asn Tyr Leu Leu Ser Leu Pro His Lys Asn Lys
 260 265 270

Val Pro Trp Asn Arg Leu Phe Pro Asn Ala Asp Ser Lys Ala Leu Asp
 275 280 285

Leu Leu Asp Lys Met Leu Thr Phe Asn Pro His Lys Arg Ile Glu Val
 290 295 300

Glu Gln Ala Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp Pro Ser
 305 310 315 320

Asp Glu Pro Ile Ala Glu Ala Pro Phe Lys Phe Asp Met Glu Leu Asp
 325 330 335

Asp Leu Pro Lys Glu Lys Leu Lys Glu Leu Ile Phe Glu Glu Thr Ala
 340 345 350

Arg Phe Gln Pro Gly Tyr Arg Ser
 355 360

<210> 139
 <211> 694
 <212> PRT
 <213> Homo sapiens

<400> 139

Met Ser Gly Gly Glu Val Val Cys Ser Gly Trp Leu Arg Lys Ser Pro
 1 5 10 15

Pro Glu Lys Lys Leu Lys Arg Tyr Ala Trp Lys Arg Arg Trp Phe Val
 20 25 30

Leu Arg Ser Gly Arg Leu Thr Gly Asp Pro Asp Val Leu Glu Tyr Tyr
 35 40 45

Lys Asn Asp His Ala Lys Lys Pro Ile Arg Ile Ile Asp Leu Asn Leu
 50 55 60

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Cys Gln Gln Val Asp Ala Gly Leu Thr Phe Asn Lys Lys Glu Phe Glu
65 70 75 80

Asn Ser Tyr Ile Phe Asp Ile Asn Thr Ile Asp Arg Ile Phe Tyr Leu
85 90 95

Val Ala Asp Ser Glu Glu Glu Met Asn Lys Trp Val Arg Cys Ile Cys
100 105 110

Asp Ile Cys Gly Phe Asn Pro Thr Glu Glu Asp Pro Val Lys Pro Pro
115 120 125

Gly Ser Ser Leu Gln Ala Pro Ala Asp Leu Pro Leu Ala Ile Asn Thr
130 135 140

Ala Pro Pro Ser Thr Gln Ala Asp Ser Ser Ser Ala Thr Leu Pro Pro
145 150 155 160

Pro Tyr Gln Leu Ile Asn Val Pro Pro His Leu Glu Thr Leu Gly Ile
165 170 175

Gln Glu Asp Pro Gln Asp Tyr Leu Leu Leu Ile Asn Cys Gln Ser Lys
180 185 190

Lys Pro Glu Pro Thr Arg Thr His Ala Asp Ser Gly Lys Ser Thr Ser
195 200 205

Ser Glu Thr Asp Ser Asn Asp Asn Val Pro Ser His Lys Asn Pro Ala
210 215 220

Ser Ser Gln Ser Lys His Gly Met Asn Gly Phe Phe Gln Gln Gln Met
225 230 235 240

Ile Tyr Asp Ser Pro Pro Ser Arg Ala Pro Ser Ala Ser Val Asp Ser
245 250 255

Ser Leu Tyr Asn Leu Pro Arg Ser Tyr Ser His Asp Val Leu Pro Lys
260 265 270

Val Ser Pro Ser Ser Thr Glu Ala Asp Gly Glu Leu Tyr Val Phe Asn
275 280 285

Thr pro Ser Gly Thr Ser Ser Val Glu Thr Gln Met Arg His Val Ser
290 295 300

Ile Ser Tyr Asp Ile Pro Pro Thr Pro Gly Asn Thr Tyr Gln Ile Pro
305 310 315 320

Arg Thr Phe Pro Glu Gly Thr Leu Gly Gln Thr Ser Lys Leu Asp Thr
325 330 335

Ile Pro Asp Ile Pro Pro Pro Arg Pro Pro Lys Pro His Pro Ala His
340 345 350

Asp Arg Ser Pro Val Glu Thr Cys Ser Ile Pro Arg Thr Ala Ser Asp
355 360 365

Thr Asp Ser Ser Tyr Cys Ile Pro Thr Ala Gly Met Ser Pro Ser Arg
370 375 380

Ser Asn Thr Ile Ser Thr Val Asp Leu Asn Lys Leu Arg Lys Asp Ala
385 390 395 400

Ser Ser Gln Asp Cys Tyr Asp Ile Pro Arg Ala Phe Pro Ser Asp Arg
405 410 415

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ser Ser Ser Leu Glu Gly Phe His Asn His Phe Lys Val Lys Asn Val
420 425 430

Leu Thr Val Gly Ser Val Ser Ser Glu Glu Leu Asp Glu Asn Tyr Val
435 440 445

Pro Met Asn Pro Asn Ser Pro Pro Arg Gln His Ser Ser Ser Phe Thr
450 455 460

Glu Pro Ile Gln Glu Ala Asn Tyr Val Pro Met Thr Pro Gly Thr Phe
465 470 475 480

Asp Phe Ser Ser Phe Gly Met Gln Val Pro Pro Pro Ala His Met Gly
485 490 495

Phe Arg Ser Ser Pro Lys Thr Pro Pro Arg Arg Pro Val Pro Val Ala
500 505 510

Asp Cys Glu Pro Pro Pro Val Asp Arg Asn Leu Lys Pro Asp Arg Lys
515 520 525

Val Lys Pro Ala Pro Leu Glu Ile Lys Pro Leu Pro Glu Trp Glu Glu
530 535 540

Leu Gln Ala Pro Val Arg Ser Pro Ile Thr Arg Ser Phe Ala Arg Asp
545 550 555 560

Ser Ser Arg Phe Pro Met Ser Pro Arg Pro Asp Ser Val His Ser Thr
565 570 575

Thr Ser Ser Ser Asp Ser His Asp Ser Glu Glu Asn Tyr Val Pro Met
580 585 590

Asn Pro Asn Leu Ser Ser Glu Asp Pro Asn Leu Phe Gly Ser Asn Ser
595 600 605

Leu Asp Gly Gly Ser Ser Pro Met Ile Lys Pro Lys Gly Asp Lys Gln
610 615 620

Val Glu Tyr Leu Asp Leu Asp Leu Asp Ser Gly Lys Ser Thr Pro Pro
625 630 635 640

Arg Lys Gln Lys Ser Ser Gly Ser Gly Ser Ser Val Ala Asp Glu Arg
645 650 655

Val Asp Tyr Val Val Val Asp Gln Gln Lys Thr Leu Ala Leu Lys Ser
660 665 670

Thr Arg Glu Ala Trp Thr Asp Gly Arg Gln Ser Thr Glu Ser Glu Thr
675 680 685

Pro Ala Lys Ser Val Lys
690

<210> 140
<211> 284
<212> PRT
<213> Homo sapiens

<400> 140

Met Asp Ser Tyr Ser Thr Tyr Leu Ala Thr Val Lys Val Ser Gly Ser
1 5 10 15

Trp Leu Glu Glu Gln Asp Glu Asp Ile Tyr Glu Ala Glu Ser Arg Val

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 20 25 30

Pro Leu Pro His Pro Phe Pro Leu Cys Glu His Leu Asp Glu Asn Asn
 35 40 45

Ser Val Ile Val Asn Thr Ser Ile Phe His Phe Ile His Lys Arg Asn
 50 55 60

Gly His Ile Leu Lys Leu Ile Ser Lys Ile Ser Leu Pro Thr Pro Pro
 65 70 75 80

Tyr Ser Leu Glu His Ala Lys Val Thr Gln Thr Glu Leu Met Arg Glu
 85 90 95

Ser Phe Arg Gln Lys Gln Glu Ala Thr Glu Ser Leu Lys Cys Gln Glu
 100 105 110

Glu Leu Arg Glu Arg Leu His Glu Glu Ser Arg Ala Arg Glu Gln Leu
 115 120 125

Ala Val Glu Leu Ser Lys Ala Glu Gly Val Ile Asp Gly Tyr Ala Asp
 130 135 140

Glu Lys Thr Leu Phe Glu Arg Gln Ile Gln Glu Lys Thr Asp Ile Ile
 145 150 155 160

Asp Arg Leu Glu Gln Glu Leu Leu Cys Ala Ser Asn Arg Leu Gln Glu
 165 170 175

Leu Glu Ala Glu Gln Gln Gln Ile Gln Glu Glu Arg Glu Leu Leu Ser
 180 185 190

Arg Gln Lys Glu Ala Met Lys Ala Glu Ala Gly Pro Val Glu Gln Gln
 195 200 205

Leu Leu Gln Glu Thr Glu Lys Leu Met Lys Glu Lys Leu Glu Val Gln
 210 215 220

Cys Gln Ala Glu Lys Val Arg Asp Asp Leu Gln Lys Gln Val Lys Ala
 225 230 235 240

Leu Glu Ile Asp Val Glu Glu Gln Val Ser Arg Phe Ile Glu Leu Glu
 245 250 255

Gln Glu Lys Asn Thr Glu Leu Met Asp Leu Arg Gln Gln Asn Gln Ala
 260 265 270

Leu Glu Lys Gln Leu Glu Lys Lys Lys Lys Lys
 275 280

<210> 141
 <211> 1258
 <212> PRT
 <213> Homo sapiens

<400> 141

Met Ala Ser Ala Cys Gly Ala Pro Gly Pro Gly Gly Ala Leu Gly Ser
 1 5 10 15

Gln Ala Pro Ser Trp Tyr His Arg Asp Leu Ser Arg Ala Ala Ala Glu
 20 25 30

Glu Leu Leu Ala Arg Ala Gly Arg Asp Gly Ser Phe Leu Val Arg Asp
 35 40 45

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ser Glu Ser Val Ala Gly Ala Phe Ala Leu Cys Val Leu Tyr Gln Lys
 50 55 60

His Val His Thr Tyr Arg Ile Leu Pro Asp Gly Glu Asp Phe Leu Ala
 65 70 75 80

Val Gln Thr Ser Gln Gly Val Pro Val Arg Arg Phe Gln Thr Leu Gly
 85 90 95

Glu Leu Ile Gly Leu Tyr Ala Gln Pro Asn Gln Gly Leu Val Cys Ala
 100 105 110

Leu Leu Leu Pro Val Glu Gly Glu Arg Glu Pro Asp Pro Pro Asp Asp
 115 120 125

Arg Asp Ala Ser Asp Gly Glu Asp Glu Lys Pro Pro Leu Pro Pro Arg
 130 135 140

Ser Gly Ser Thr Ser Ile Ser Ala Pro Thr Gly Pro Ser Ser Pro Leu
 145 150 155 160

Pro Ala Pro Glu Thr Pro Thr Ala Pro Ala Ala Glu Ser Ala Pro Asn
 165 170 175

Gly Leu Ser Thr Val Ser His Asp Tyr Leu Lys Gly Ser Tyr Gly Leu
 180 185 190

Asp Leu Glu Ala Val Arg Gly Gly Ala Ser His Leu Pro His Leu Thr
 195 200 205

Arg Thr Leu Ala Thr Ser Cys Arg Arg Leu His Ser Glu Val Asp Lys
 210 215 220

Val Leu Ser Gly Leu Glu Ile Leu Ser Lys Val Phe Asp Gln Gln Ser
 225 230 235 240

Ser Pro Met Val Thr Arg Leu Leu Gln Gln Gln Asn Leu Pro Gln Thr
 245 250 255

Gly Glu Gln Glu Leu Glu Ser Leu Val Leu Lys Leu Ser Val Leu Lys
 260 265 270

Asp Phe Leu Ser Gly Ile Gln Lys Lys Ala Leu Lys Ala Leu Gln Asp
 275 280 285

Met Ser Ser Thr Ala Pro Pro Ala Pro Gln Pro Ser Thr Arg Lys Ala
 290 295 300

Lys Thr Ile Pro Val Gln Ala Phe Glu Val Lys Leu Asp Val Thr Leu
 305 310 315 320

Gly Asp Leu Thr Lys Ile Gly Lys Ser Gln Lys Phe Thr Leu Ser Val
 325 330 335

Asp Val Glu Gly Gly Arg Leu Val Leu Leu Arg Arg Gln Arg Asp Ser
 340 345 350

Gln Glu Asp Trp Thr Thr Phe Thr His Asp Arg Ile Arg Gln Leu Ile
 355 360 365

Lys Ser Gln Arg Val Gln Asn Lys Leu Gly Val Val Phe Glu Lys Glu
 370 375 380

Lys Asp Arg Thr Gln Arg Lys Asp Phe Ile Phe Val Ser Ala Arg Lys
 385 390 395 400

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Arg Glu Ala Phe Cys Gln Leu Leu Gln Leu Met Lys Asn Lys His Ser
405 410 415

Lys Gln Asp Glu Pro Asp Met Ile Ser Val Phe Ile Gly Thr Trp Asn
420 425 430

Met Gly Ser Val Pro Pro Pro Lys Asn Val Thr Ser Trp Phe Thr Ser
435 440 445

Lys Gly Leu Gly Lys Thr Leu Asp Glu Val Thr Val Thr Ile Pro His
450 455 460

Asp Ile Tyr Val Phe Gly Thr Gln Glu Asn Ser Val Gly Asp Arg Glu
465 470 475 480

Trp Leu Asp Leu Leu Arg Gly Gly Leu Lys Glu Leu Thr Asp Leu Asp
485 490 495

Tyr Arg Pro Ile Ala Met Gln Ser Leu Trp Asn Ile Lys Val Ala Val
500 505 510

Leu Val Lys Pro Glu His Glu Asn Arg Ile ser His Val Ser Thr Ser
515 520 525

Ser Val Lys Thr Gly Ile Ala Asn Thr Leu Gly Asn Lys Gly Ala Val
530 535 540

Gly Val Ser Phe Met Phe Asn Gly Thr Ser Phe Gly Phe Val Asn Cys
545 550 555 560

His Leu Thr Ser Gly Asn Glu Lys Thr Ala Arg Arg Asn Gln Asn Tyr
565 570 575

Leu Asp Ile Leu Arg Leu Leu Ser Leu Gly Asp Arg Gln Leu Asn Ala
580 585 590

Phe Asp Ile Ser Leu Arg Phe Thr His Leu Phe Trp Phe Gly Asp Leu
595 600 605

Asn Tyr Arg Leu Asp Met Asp Ile Gln Glu Ile Leu Asn Tyr Ile Ser
610 615 620

Arg Lys Glu Phe Glu Pro Leu Leu Arg Val Asp Gln Leu Asn Leu Glu
625 630 635 640

Arg Glu Lys His Lys Val Phe Leu Arg Phe ser Glu Glu Glu Ile Ser
645 650 655

Phe Pro Pro Thr Tyr Arg Tyr Glu Arg Gly ser Arg Asp Thr Tyr Ala
660 665 670

Trp His Lys Gln Lys Pro Thr Gly Val Arg Thr Asn Val Pro Ser Trp
675 680 685

Cys Asp Arg Ile Leu Trp Lys Ser Tyr Pro Glu Thr His Ile Ile Cys
690 695 700

Asn Ser Tyr Gly Cys Thr Asp Asp Ile Val Thr Ser Asp His Ser Pro
705 710 715 720

Val Phe Gly Thr Phe Glu Val Gly Val Thr ser Gln Phe Ile Ser Lys
725 730 735

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Lys Gly Leu Ser Lys Thr Ser Asp Gln Ala Tyr Ile Glu Phe Glu Ser
 740 745 750

Ile Glu Ala Ile Val Lys Thr Ala Ser Arg Thr Lys Phe Phe Ile Glu
 755 760 765

Phe Tyr Ser Thr Cys Leu Glu Glu Tyr Lys Lys Ser Phe Glu Asn Asp
 770 775 780

Ala Gln Ser Ser Asp Asn Ile Asn Phe Leu Lys Val Gln Trp Ser Ser
 785 790 795 800

Arg Gln Leu Pro Thr Leu Lys Pro Ile Leu Ala Asp Ile Glu Tyr Leu
 805 810 815

Gln Asp Gln His Leu Leu Leu Thr Val Lys Ser Met Asp Gly Tyr Glu
 820 825 830

Ser Tyr Gly Glu Cys Val Val Ala Leu Lys Ser Met Ile Gly Ser Thr
 835 840 845

Ala Gln Gln Phe Leu Thr Phe Leu Ser His Arg Gly Glu Glu Thr Gly
 850 855 860

Asn Ile Arg Gly Ser Met Lys Val Arg Val Pro Thr Glu Arg Leu Gly
 865 870 875 880

Thr Arg Glu Arg Leu Tyr Glu Trp Ile Ser Ile Asp Lys Asp Glu Ala
 885 890 895

Gly Ala Lys Ser Lys Ala Pro Ser Val Ser Arg Gly Ser Gln Glu Pro
 900 905 910

Arg Ser Gly Ser Arg Lys Pro Ala Phe Thr Glu Ala Ser Cys Pro Leu
 915 920 925

Ser Arg Leu Phe Glu Glu Pro Glu Lys Pro Pro Pro Thr Gly Arg Pro
 930 935 940

Pro Ala Pro Pro Arg Ala Ala Pro Arg Glu Glu Pro Leu Thr Pro Arg
 945 950 955 960

Leu Lys Pro Glu Gly Ala Pro Glu Pro Glu Gly Val Ala Ala Pro Pro
 965 970 975

Pro Lys Asn Ser Phe Asn Asn Pro Ala Tyr Tyr Val Leu Glu Gly Val
 980 985 990

Pro His Gln Leu Leu Pro Pro Glu Pro Pro Ser Pro Ala Arg Ala Pro
 995 1000 1005

Val Pro Ser Ala Thr Lys Asn Lys Val Ala Ile Thr Val Pro Ala
 1010 1015 1020

Pro Gln Leu Gly His His Arg His Pro Arg Val Gly Glu Gly Ser
 1025 1030 1035

Ser Ser Asp Glu Glu Ser Gly Gly Thr Leu Pro Pro Pro Asp Phe
 1040 1045 1050

Pro Pro Pro Pro Leu Pro Asp Ser Ala Ile Phe Leu Pro Pro Ser
 1055 1060 1065

Leu Asp Pro Leu Pro Gly Pro Val Val Arg Gly Arg Gly Gly Ala
 1070 1075 1080

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Glu Ala Arg Gly Pro Pro Pro Pro Lys Ala His Pro Arg Pro Pro
1085 1090 1095

Leu Pro Pro Gly Pro Ser Pro Ala Ser Thr Phe Leu Gly Glu Val
1100 1105 1110

Gly Ser Gly Asp Asp Arg Ser Cys Ser Val Leu Gln Met Ala Lys
1115 1120 1125

Thr Leu ser Glu Val Asp Tyr Ala Pro Ala Gly Pro Ala Arg Ser
1130 1135 1140

Ala Leu Leu Pro Gly Pro Leu Glu Leu Gln Pro Pro Arg Gly Leu
1145 1150 1155

Pro Ser Asp Tyr Gly Arg Pro Leu Ser Phe Pro Pro Pro Arg Ile
1160 1165 1170

Arg Glu Ser Ile Gln Glu Asp Leu Ala Glu Glu Ala Pro Cys Leu
1175 1180 1185

Gln Gly Gly Arg Ala Ser Gly Leu Gly Glu Ala Gly Met Ser Ala
1190 1195 1200

Trp Leu Arg Ala Ile Gly Leu Glu Arg Tyr Glu Glu Gly Leu Val
1205 1210 1215

His Asn Gly Trp Asp Asp Leu Glu Phe Leu Ser Asp Ile Thr Glu
1220 1225 1230

Glu Asp Leu Glu Glu Ala Gly Val Gln Asp Pro Ala His Lys Arg
1235 1240 1245

Leu Leu Leu Asp Thr Leu Gln Leu Ser Lys
1250 1255

<210> 142
<211> 1196
<212> PRT
<213> Homo sapiens

<400> 142

Ala Asp Asp Asp Trp Trp Pro Met Gln Ile Leu Ile Lys Cys Pro Asn
1 5 10 15

Gln Ile Val Arg Gln Met Phe Gln Arg Leu Cys Ile His Val Ile Gln
20 25 30

Arg Leu Arg Pro Val His Ala His Leu Tyr Leu Gln Pro Gly Met Glu
35 40 45

Asp Gly Ser Asp Asp Met Asp Thr Ser Val Glu Asp Ile Gly Gly Arg
50 55 60

Ser Cys Val Thr Arg Phe Val Arg Thr Leu Leu Leu Ile Met Glu His
65 70 75 80

Gly Val Lys Pro His Ser Lys His Leu Thr Glu Tyr Phe Ala Phe Leu
85 90 95

Tyr Glu Phe Ala Lys Met Gly Glu Glu Glu Ser Gln Phe Leu Leu Ser
100 105 110

Leu Gln Ala Ile Ser Thr Met Val His Phe Tyr Met Gly Thr Lys Gly

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 115 120 125

Pro Glu Asn Pro Gln Val Glu Val Leu Ser Glu Glu Glu Gly Glu Glu
 130 135 140

Glu Glu Glu Glu Glu Asp Ile Leu Ser Leu Ala Glu Glu Lys Tyr Arg
 145 150 155 160

Pro Ala Ala Leu Glu Lys Met Ile Ala Leu Val Ala Leu Leu Val Glu
 165 170 175

Gln Ser Arg Ser Glu Arg His Leu Thr Leu Ser Gln Thr Asp Met Ala
 180 185 190

Ala Leu Thr Gly Gly Lys Gly Phe Pro Phe Leu Phe Gln His Ile Arg
 195 200 205

Asp Gly Ile Asn Ile Arg Gln Thr Cys Asn Leu Ile Phe Ser Leu Cys
 210 215 220

Arg Tyr Asn Asn Arg Leu Ala Glu His Ile Val Ser Met Leu Phe Thr
 225 230 235 240

Ser Ile Ala Lys Leu Thr Pro Glu Ala Ala Asn Pro Phe Phe Lys Leu
 245 250 255

Leu Thr Met Leu Met Glu Phe Ala Gly Gly Pro Pro Gly Met Pro Pro
 260 265 270

Phe Ala Ser Tyr Ile Leu Gln Arg Ile Trp Glu Val Ile Glu Tyr Asn
 275 280 285

Pro Ser Gln Cys Leu Asp Trp Leu Ala Val Gln Thr Pro Arg Asn Lys
 290 295 300

Leu Ala His Ser Trp Val Leu Gln Asn Met Glu Asn Trp Val Glu Arg
 305 310 315 320

Phe Leu Leu Ala His Asn Tyr Pro Arg Val Arg Thr Ser Ala Ala Tyr
 325 330 335

Leu Leu Val Ser Leu Ile Pro Ser Asn Ser Phe Arg Gln Met Phe Arg
 340 345 350

Ser Thr Arg Ser Leu His Ile Pro Thr Arg Asp Leu Pro Leu Ser Pro
 355 360 365

Asp Thr Thr Val Val Leu His Gln Val Tyr Asn Val Leu Leu Gly Leu
 370 375 380

Leu Ser Arg Ala Lys Leu Tyr Val Asp Ala Ala Val His Gly Thr Thr
 385 390 395 400

Lys Leu Val Pro Tyr Phe Ser Phe Met Thr Tyr Cys Leu Ile Ser Lys
 405 410 415

Thr Glu Lys Leu Met Phe Ser Thr Tyr Phe Met Asp Leu Trp Asn Leu
 420 425 430

Phe Gln Pro Lys Leu Ser Glu Pro Ala Ile Ala Thr Asn His Asn Lys
 435 440 445

Gln Ala Leu Leu Ser Phe Trp Tyr Asn Val Cys Ala Asp Cys Pro Glu
 450 455 460

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Asn Ile Arg Leu Ile Val Gln Asn Pro Val Val Thr Lys Asn Ile Ala
465 470 475 480

Phe Asn Tyr Ile Leu Ala Asp His Asp Asp Gln Asp Val Val Leu Phe
485 490 495

Asn Arg Gly Met Leu Pro Ala Tyr Tyr Gly Ile Leu Arg Leu Cys Cys
500 505 510

Glu Gln Ser Pro Ala Phe Thr Arg Gln Leu Ala Ser His Gln Asn Ile
515 520 525

Gln Trp Ala Phe Lys Asn Leu Thr Pro His Ala Ser Gln Tyr Pro Gly
530 535 540

Ala Val Glu Glu Leu Phe Asn Leu Met Gln Leu Phe Ile Ala Gln Arg
545 550 555 560

Pro Asp Met Arg Glu Glu Glu Leu Glu Asp Ile Lys Gln Phe Lys Lys
565 570 575

Thr Thr Ile Ser Cys Tyr Leu Arg Cys Leu Asp Gly Arg Ser Cys Trp
580 585 590

Thr Thr Leu Ile Ser Ala Phe Arg Ile Leu Leu Glu Ser Asp Glu Asp
595 600 605

Arg Leu Leu Val Val Phe Asn Arg Gly Leu Ile Leu Met Thr Glu Ser
610 615 620

Phe Asn Thr Leu His Met Met Tyr His Glu Ala Thr Ala Cys His Val
625 630 635 640

Thr Gly Asp Leu Val Glu Leu Leu Ser Ile Phe Leu Ser Val Leu Lys
645 650 655

Ser Thr Arg Pro Tyr Leu Gln Arg Lys Asp Val Lys Gln Ala Leu Ile
660 665 670

Gln Trp Gln Glu Arg Ile Glu Phe Ala His Lys Leu Leu Thr Leu Leu
675 680 685

Asn Ser Tyr Ser Pro Pro Glu Leu Arg Asn Ala Cys Ile Asp Val Leu
690 695 700

Lys Glu Leu Val Leu Leu Ser Pro His Asp Phe Leu His Thr Leu Val
705 710 715 720

Pro Phe Leu Gln His Asn His Cys Thr Tyr His His Ser Asn Ile Pro
725 730 735

Met Ser Leu Gly Pro Tyr Phe Pro Cys Arg Glu Asn Ile Lys Leu Ile
740 745 750

Gly Gly Lys Ser Asn Ile Arg Pro Pro Arg Pro Glu Leu Asn Met Cys
755 760 765

Leu Leu Pro Thr Met Val Glu Thr Ser Lys Gly Lys Asp Asp Val Tyr
770 775 780

Asp Arg Met Leu Leu Asp Tyr Phe Phe Ser Tyr His Gln Phe Ile His
785 790 795 800

Leu Leu Cys Arg Val Ala Ile Asn Cys Glu Lys Phe Thr Glu Thr Leu

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 805 810 815

Val Lys Leu Ser Val Leu Val Ala Tyr Glu Gly Leu Pro Leu His Leu
 820 825 830

Ala Leu Phe Pro Lys Leu Trp Thr Glu Leu Cys Gln Thr Gln Ser Ala
 835 840 845

Met Ser Lys Asn Cys Ile Lys Leu Leu Cys Glu Asp Pro Val Phe Ala
 850 855 860

Glu Tyr Ile Lys Cys Ile Leu Met Asp Glu Arg Thr Phe Leu Asn Asn
 865 870 875 880

Asn Ile Val Tyr Thr Phe Met Thr His Phe Leu Leu Lys Val Gln Ser
 885 890 895

Gln Val Phe Ser Glu Ala Asn Cys Ala Asn Leu Ile Ser Thr Leu Ile
 900 905 910

Thr Asn Leu Ile Ser Gln Tyr Gln Asn Leu Gln Ser Asp Phe Ser Asn
 915 920 925

Arg Val Glu Ile Ser Lys Ala Ser Ala Ser Leu Asn Gly Asp Leu Arg
 930 935 940

Ala Leu Ala Leu Leu Leu Ser Val His Thr Pro Lys Gln Leu Asn Pro
 945 950 955 960

Ala Leu Ile Pro Thr Leu Gln Glu Leu Leu Ser Lys Cys Arg Thr Cys
 965 970 975

Leu Gln Gln Arg Asn Ser Leu Gln Glu Gln Glu Ala Lys Glu Arg Lys
 980 985 990

Thr Lys Asp Asp Glu Gly Ala Thr Pro Ile Lys Arg Arg Arg Val Ser
 995 1000 1005

Ser Asp Glu Glu His Thr Val Asp Ser Cys Ile Ser Asp Met Lys
 1010 1015 1020

Thr Glu Thr Arg Glu Val Leu Thr Pro Thr Ser Thr Ser Asp Asn
 1025 1030 1035

Glu Thr Arg Asp Ser Ser Ile Ile Asp Pro Gly Thr Glu Gln Asp
 1040 1045 1050

Leu Pro Ser Pro Glu Asn Ser Ser Val Lys Glu Tyr Arg Met Glu
 1055 1060 1065

Val Pro Ser Ser Phe Ser Glu Asp Met Ser Asn Ile Arg Ser Gln
 1070 1075 1080

His Ala Glu Glu Gln Ser Asn Asn Gly Arg Tyr Asp Asp Cys Lys
 1085 1090 1095

Glu Phe Lys Asp Leu His Cys Ser Lys Asp Ser Thr Leu Ala Glu
 1100 1105 1110

Glu Glu Ser Glu Phe Pro Ser Thr Ser Ile Ser Ala Val Leu Ser
 1115 1120 1125

Asp Leu Ala Asp Leu Arg Ser Cys Asp Gly Gln Ala Leu Pro Ser
 1130 1135 1140

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Gln Asp Pro Glu Val Ala Leu Ser Leu Ser Cys Gly His Ser Arg
1145 1150 1155

Gly Leu Phe Ser His Met Gln Gln His Asp Ile Leu Asp Thr Leu
1160 1165 1170

Cys Arg Thr Ile Glu Ser Thr Ile His Val Val Thr Arg Ile Ser
1175 1180 1185

Gly Lys Gly Asn Gln Ala Ala Ser
1190 1195

<210> 143
<211> 1680
<212> PRT
<213> Homo sapiens

<400> 143

Pro Gly Leu Val Gly Glu His Gly Gly His Cys Lys Val Leu Trp Leu
1 5 10 15

Ala Asn Ser Leu Tyr Ser Val Gly Leu Pro His His Ser His Gly Thr
20 25 30

Glu Pro Met Trp His Gly Asn His Val Gln Pro Gly Ala Thr His Arg
35 40 45

Pro Asn Gln Gly Leu Glu Met Leu Gln Gly Leu Gly Ile Gly Met Lys
50 55 60

Ala Phe His Asn Phe Asn Tyr Phe Leu Phe Phe Tyr Asn Val Leu Leu
65 70 75 80

Gly Leu Gly Ala Cys Leu Ser Arg Leu Leu Ile Ser Cys Leu Leu Gly
85 90 95

Met Trp Leu Ile Ala Arg Ile Asp Arg Thr Ile Met Gln Ser Gly Tyr
100 105 110

Glu Gly Ala Asp Met Gly Phe Ser Ala Trp Ile Gly Met Leu Tyr Met
115 120 125

Asp His Tyr His Ile Asn Pro Val Leu Val Ser Phe Cys His Ile Leu
130 135 140

Ile Thr Asn His Arg Glu Lys Lys Leu Gln Gln Ser Thr Lys Tyr Trp
145 150 155 160

Cys Leu Asn Gln Ser Ala Glu Ser Leu Arg Ile Cys Ala Met Arg Gly
165 170 175

Gly Glu Asn Arg Pro Pro Ala Arg Val Gln Ser Ser Ser Glu Glu Leu
180 185 190

Glu Leu Arg His Gln Ser Leu Asp Ala Phe Pro Gly Arg Arg Leu Pro
195 200 205

Gly Arg Gly Ile Gln Pro Ala Ala Lys Met Ser Ser Val Gly Lys Val
210 215 220

Thr Gln Val Pro Asn Gly Lys Ala Tyr Gln Gln Ile Phe Gln Ala Glu
225 230 235 240

Val Gln Leu Val His Ser Leu Ala Ala Thr Arg Lys Arg Ala Ala Glu
245 250 255

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Arg Ser Val Thr Leu Lys Ser Gly Arg Ile Pro Met Met Lys Lys Val
260 265 270

Glu Thr Pro Glu Gly Glu Val Met Ser Pro Arg Gln Gln Lys Trp Met
275 280 285

His Ser Leu Pro Asn Asp Trp Ile Met Glu Asn Pro Val Leu His Arg
290 295 300

Glu Lys Glu Arg Ala Lys Arg Glu Lys Ala Arg Glu Ser Glu Asn Thr
305 310 315 320

Ile Ala Ala Arg Glu Val Arg Gly Leu Met Asp Thr Ile Val Pro Glu
325 330 335

Lys Ile Ser Thr Ser Thr Phe Gln Arg Gln Ala Glu His Lys Arg Lys
340 345 350

Ser Tyr Glu Ser Ala Leu Ala Ser Phe Gln Glu Glu Ile Ala Gln Val
355 360 365

Gly Lys Glu Met Glu Pro Leu Ile Val Asp Thr Gly Gly Leu Phe Leu
370 375 380

Lys Lys Leu Thr Glu Ser Asp Glu Glu Met Asn Arg Leu Phe Leu Lys
385 390 395 400

Val Glu Asn Asp Thr Asn Leu Glu Asp Tyr Thr Ile Gln Ala Leu Leu
405 410 415

Glu Leu Trp Asp Lys Val Ala Gly Arg Leu Leu Leu Arg Lys Gln Glu
420 425 430

Ile Lys Glu Leu Asp Glu Ala Leu His Ser Leu Glu Phe Ser Arg Thr
435 440 445

Asp Lys Leu Lys Ser Val Leu Lys Lys Tyr Ala Glu Val Ile Glu Lys
450 455 460

Thr Ser Tyr Leu Met Arg Pro Glu Val Tyr Arg Leu Ile Asn Glu Glu
465 470 475 480

Ala Met Val Met Asn Tyr Ala Leu Leu Gly Asn Arg Lys Ala Leu Ala
485 490 495

Gln Leu Phe Val Asn Leu Met Glu Ser Thr Leu Gln Gln Glu Leu Asp
500 505 510

Ser Arg His Arg Trp Gln Gly Leu Val Asp Thr Trp Lys Ala Leu Lys
515 520 525

Lys Glu Ala Leu Leu Gln Ser Phe Ser Glu Phe Met Ala Ser Glu Ser
530 535 540

Ile His Thr Pro Pro Ala Val Thr Lys Glu Leu Glu Val Met Leu Lys
545 550 555 560

Thr Gln Asn Val Leu Gln Gln Arg Arg Leu Lys His Leu Cys Thr Ile
565 570 575

Cys Asp Leu Leu Pro Pro Ser Tyr Ser Lys Thr Gln Leu Thr Glu Trp
580 585 590

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

His Ser Ser Leu Asn Ser Leu Asn Lys Glu Leu Asp Thr Tyr His Val
 595 600 605

Asp Cys Met Met Trp Ile Arg Leu Leu Tyr Glu Lys Thr Trp Gln Glu
 610 615 620

Cys Leu Met His Val Gln Asn Cys Lys Lys Gln Leu Leu Asp Trp Lys
 625 630 635 640

Ala Phe Thr Glu Glu Glu Ala Glu Thr Leu Val Asn Gln Phe Phe Phe
 645 650 655

Gln Met Val Gly Ala Leu Gln Gly Lys Val Glu Glu Asp Leu Glu Leu
 660 665 670

Leu Asp Lys Ser Phe Glu Thr Leu Ala Asp Gln Thr Glu Trp Gln Ser
 675 680 685

Ser His Leu Phe Lys Tyr Phe Gln Glu Val Val Gln Leu Trp Glu Ala
 690 695 700

His Gln Ser Glu Leu Leu Val Gln Glu Leu Glu Leu Glu Lys Arg Met
 705 710 715 720

Glu Gln His Arg Gln Lys His Ser Leu Glu Ser Gln Val Gln Glu Ala
 725 730 735

His Leu Asp Arg Leu Leu Asp Gln Leu Arg Gln Gln Ser Asp Lys Glu
 740 745 750

Thr Leu Ala Phe His Leu Glu Lys Val Lys Asp Tyr Leu Lys Asn Met
 755 760 765

Lys Ser Arg Tyr Glu Cys Phe His Thr Leu Leu Thr Lys Glu Val Met
 770 775 780

Glu Tyr Pro Ala Ile Met Leu Lys Glu Leu Asn Ser Tyr Ser Ser Ala
 785 790 795 800

Leu Ser Gln Tyr Phe Phe Val Arg Glu Ile Phe Glu Gln Asn Leu Ala
 805 810 815

Gly Glu Val Ile Phe Lys Phe Arg Gln Pro Glu Ala His Glu Lys Pro
 820 825 830

Ser Gln Lys Arg Val Lys Lys Leu Arg Lys Lys Gln Gly Ser Lys Glu
 835 840 845

Asp Met Thr Arg Ser Glu Glu Ser Ile Ser Ser Gly Thr Ser Thr Ala
 850 855 860

Arg Ser Val Glu Glu Val Glu Glu Glu Asn Asp Gln Glu Met Glu Ser
 865 870 875 880

Phe Ile Thr Glu Glu Val Leu Gly Gln Gln Lys Lys Ser Pro Leu His
 885 890 895

Ala Lys Met Asp Glu Ser Lys Glu Gly Ser Ile Gln Gly Leu Glu Glu
 900 905 910

Met Gln Val Glu Arg Glu Gly Ser Leu Asn Pro Ser Leu Asn Glu Glu
 915 920 925

Asn Val Lys Gly Gln Gly Glu Lys Lys Glu Glu Ser Glu Glu Glu Asp
 930 935 940

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Glu Lys Glu Glu Glu Glu Glu Glu Lys Leu Glu Glu Glu Lys Glu
 945 950 955 960
 Glu Lys Glu Ala Gln Glu Glu Gln Glu Ser Leu Ser Val Gly Glu Glu
 965 970 975
 Glu Asp Lys Glu Glu Gly Leu Glu Glu Ile Tyr Tyr Glu Asp Met Glu
 980 985 990
 Ser Phe Thr Ile Ser Ser Gly Asn Thr Tyr Phe Val Phe Val Pro Leu
 995 1000 1005
 Glu Glu Glu His Cys Arg Lys Ser His Ser Thr Phe Ser Ala Met
 1010 1015 1020
 Phe Ile Asn Asp Thr Ser Ser Ala Lys Phe Ile Glu Gln Val Thr
 1025 1030 1035
 Ile Pro Ser Arg Leu Ile Leu Glu Ile Lys Lys Gln Leu Phe Ser
 1040 1045 1050
 Glu Gly Gly Asn Phe Ser Pro Lys Glu Ile Asn Ser Leu Cys Ser
 1055 1060 1065
 Arg Leu Glu Lys Glu Ala Ala Arg Ile Glu Leu Val Glu Ser Val
 1070 1075 1080
 Ile Met Leu Asn Met Glu Lys Leu Glu Asn Glu Tyr Leu Asp Gln
 1085 1090 1095
 Ala Asn Asp Val Ile Asn Lys Phe Glu Ser Lys Phe His Asn Leu
 1100 1105 1110
 Ser Val Asp Leu Ile Phe Ile Glu Lys Ile Gln Arg Leu Leu Thr
 1115 1120 1125
 Asn Leu Gln Val Lys Ile Lys Cys Gln Val Ala Lys Ser Asn Ser
 1130 1135 1140
 Gln Thr Asn Gly Leu Asn Phe Ser Leu Gln Gln Leu Gln Asn Lys
 1145 1150 1155
 Ile Lys Thr Cys Gln Glu Ser Arg Gly Glu Lys Thr Thr Val Thr
 1160 1165 1170
 Thr Glu Glu Leu Leu Ser Phe Val Gln Thr Trp Lys Glu Lys Leu
 1175 1180 1185
 Ser Gln Arg Ile Gln Tyr Leu Asn Cys Ser Leu Asp Arg Val Ser
 1190 1195 1200
 Met Thr Glu Leu Val Phe Thr Asn Thr Ile Leu Lys Asp Gln Glu
 1205 1210 1215
 Glu Asp Ser Asp Ile Leu Thr Ser Ser Glu Ala Leu Glu Glu Glu
 1220 1225 1230
 Ala Lys Leu Asp Val Val Thr Pro Glu Ser Phe Thr Gln Leu Ser
 1235 1240 1245
 Arg Val Gly Lys Pro Leu Ile Glu Asp Pro Ala Val Asp Val Ile
 1250 1255 1260

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Arg Lys Leu Leu Gln Leu Pro Asn Thr Lys Trp Pro Thr His His
 1265 1270 1275

Cys Asp Lys Asp Pro Ser Gln Thr Gly Phe Lys Arg His Arg Cys
 1280 1285 1290

Gln Pro Glu Asn Ser Gly Lys Lys Ala Val Pro Ser Ala Ser Ala
 1295 1300 1305

Thr Ser Ala Gly Ser Leu Gln Thr Thr His Pro Pro Leu Ser His
 1310 1315 1320

Ser Phe Thr Pro His Pro Lys Pro Asn Lys Met Glu Arg Lys Tyr
 1325 1330 1335

Arg Val Leu Gly Asp Lys Pro Pro Pro Ala Ala Glu Asp Phe Lys
 1340 1345 1350

Gly Ile Ile Leu Thr Leu Leu Trp Glu Ser Ser Glu Asn Leu Leu
 1355 1360 1365

Thr Val Ala Glu Glu Phe Tyr Arg Lys Glu Lys Arg Pro Val Thr
 1370 1375 1380

Arg Pro Asp Cys Met Cys Asp Thr Phe Asp Gln Cys Ala Glu Asn
 1385 1390 1395

Ile Ser Lys Lys Ile Leu Glu Tyr Gln Ser Gln Ala Asn Lys Tyr
 1400 1405 1410

His Asn Ser Cys Leu Ile Glu Leu Arg Ile Gln Ile Arg Arg Phe
 1415 1420 1425

Glu Glu Leu Leu Pro Gln Val Cys Trp Leu Val Met Glu Asn Phe
 1430 1435 1440

Lys Glu His His Trp Lys Lys Phe Phe Thr Ser Val Lys Glu Ile
 1445 1450 1455

Arg Gly Gln Phe Glu Glu Gln Gln Lys Arg Leu Glu Lys Arg Lys
 1460 1465 1470

Asp Lys Asn Ala Gln Lys Leu His Leu Asn Leu Gly His Pro Val
 1475 1480 1485

His Phe Gln Glu Met Glu Ser Leu His Leu Ser Glu Glu Glu Arg
 1490 1495 1500

Gln Glu Glu Leu Asp Ser Met Ile Arg Met Asn Lys Glu Lys Leu
 1505 1510 1515

Glu Glu Cys Thr Arg Arg Asn Gly Gln Val Phe Ile Thr Asn Leu
 1520 1525 1530

Ala Thr Phe Thr Glu Lys Phe Leu Leu Gln Leu Asp Glu Val Val
 1535 1540 1545

Thr Ile Asp Asp Val Gln Val Ala Arg Met Glu Pro Pro Lys Gln
 1550 1555 1560

Lys Leu Ser Met Leu Ile Arg Arg Lys Leu Ala Gly Leu Ser Leu
 1565 1570 1575

Lys Glu Glu Ser Glu Lys Pro Leu Ile Glu Arg Gly Ser Arg Lys
 1580 1585 1590

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Trp Pro Gly Ile Lys Pro Thr Glu Val Thr Ile Gln Asn Lys Ile
1595 1600 1605

Leu Leu Gln Pro Thr Ser Ser Ile Ser Thr Thr Lys Thr Thr Leu
1610 1615 1620

Gly His Leu Ala Ala Val Glu Ala Arg Asp Ala Val Tyr Leu Lys
1625 1630 1635

Tyr Leu Ala Ser Phe Glu Glu Glu Leu Lys Arg Ile Gln Asp Asp
1640 1645 1650

Cys Thr Ser Gln Ile Lys Glu Ala Gln Arg Trp Lys Asp Ser Trp
1655 1660 1665

Lys Gln Ser Leu His Thr Ile Gln Gly Leu Tyr Val
1670 1675 1680

<210> 144
<211> 968
<212> PRT
<213> Homo sapiens

<400> 144

Met Ala Phe Ala Asn Phe Arg Arg Ile Leu Arg Leu Ser Thr Phe Glu
1 5 10 15

Lys Arg Lys Ser Arg Glu Tyr Glu His Val Arg Arg Asp Leu Asp Pro
20 25 30

Asn Glu Val Trp Glu Ile Val Gly Glu Leu Gly Asp Gly Ala Phe Gly
35 40 45

Lys Val Tyr Lys Ala Lys Asn Lys Glu Thr Gly Ala Leu Ala Ala Ala
50 55 60

Lys Val Ile Glu Thr Lys Ser Glu Glu Glu Leu Glu Asp Tyr Ile Val
65 70 75 80

Glu Ile Glu Ile Leu Ala Thr Cys Asp His Pro Tyr Ile Val Lys Leu
85 90 95

Leu Gly Ala Tyr Tyr His Asp Gly Lys Leu Trp Ile Met Ile Glu Phe
100 105 110

Cys Pro Gly Gly Ala Val Asp Ala Ile Met Leu Glu Leu Asp Arg Gly
115 120 125

Leu Thr Glu Pro Gln Ile Gln Val Val Cys Arg Gln Met Leu Glu Ala
130 135 140

Leu Asn Phe Leu His Ser Lys Arg Ile Ile His Arg Asp Leu Lys Ala
145 150 155 160

Gly Asn Val Leu Met Thr Leu Glu Gly Asp Ile Arg Leu Ala Asp Phe
165 170 175

Gly Val Ser Ala Lys Asn Leu Lys Thr Leu Gln Lys Arg Asp Ser Phe
180 185 190

Ile Gly Thr Pro Tyr Trp Met Ala Pro Glu Val Val Met Cys Glu Thr
195 200 205

Met Lys Asp Thr Pro Tyr Asp Tyr Lys Ala Asp Ile Trp Ser Leu Gly

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 210 215 220

Ile Thr Leu Ile Glu Met Ala Gln Ile Glu Pro Pro His His Glu Leu
 225 230 235 240

Asn Pro Met Arg Val Leu Leu Lys Ile Ala Lys Ser Asp Pro Pro Thr
 245 250 255

Leu Leu Thr Pro Ser Lys Trp Ser Val Glu Phe Arg Asp Phe Leu Lys
 260 265 270

Ile Ala Leu Asp Lys Asn Pro Glu Thr Arg Pro Ser Ala Ala Gln Leu
 275 280 285

Leu Glu His Pro Phe Val Ser Ser Ile Thr Ser Asn Lys Ala Leu Arg
 290 295 300

Glu Leu Val Ala Glu Ala Lys Ala Glu Val Met Glu Glu Ile Glu Asp
 305 310 315 320

Gly Arg Asp Glu Gly Glu Glu Glu Asp Ala Val Asp Ala Ala Ser Thr
 325 330 335

Leu Glu Asn His Thr Gln Asn Ser Ser Glu Val Ser Pro Pro Ser Leu
 340 345 350

Asn Ala Asp Lys Pro Leu Glu Glu Ser Pro Ser Thr Pro Leu Ala Pro
 355 360 365

Ser Gln Ser Gln Asp Ser Val Asn Glu Pro Cys Ser Gln Pro Ser Gly
 370 375 380

Asp Arg Ser Leu Gln Thr Thr Ser Pro Pro Val Val Ala Pro Gly Asn
 385 390 395 400

Glu Asn Gly Leu Ala Val Pro Val Pro Leu Arg Lys Ser Arg Pro Val
 405 410 415

Ser Met Asp Ala Arg Ile Gln Val Ala Gln Glu Lys Gln Val Ala Glu
 420 425 430

Gln Gly Gly Asp Leu Ser Pro Ala Ala Asn Arg Ser Gln Lys Ala Ser
 435 440 445

Gln Ser Arg Pro Asn Ser Ser Ala Leu Glu Thr Leu Gly Gly Glu Lys
 450 455 460

Leu Ala Asn Gly Ser Leu Glu Pro Pro Ala Gln Ala Ala Pro Gly Pro
 465 470 475 480

Ser Lys Arg Asp Ser Asp Cys Ser Ser Leu Cys Thr Ser Glu Ser Met
 485 490 495

Asp Tyr Gly Thr Asn Leu Ser Thr Asp Leu Ser Leu Asn Lys Glu Met
 500 505 510

Gly Ser Leu Ser Ile Lys Asp Pro Lys Leu Tyr Lys Lys Thr Leu Lys
 515 520 525

Arg Thr Arg Lys Phe Val Val Asp Gly Val Glu Val Ser Ile Thr Thr
 530 535 540

Ser Lys Ile Ile Ser Glu Asp Glu Lys Lys Asp Glu Glu Met Arg Phe
 545 550 555 560

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Leu Arg Arg Gln Glu₅₆₅ Leu Arg Glu Leu Arg₅₇₀ Leu Leu Gln Lys Glu₅₇₅ Glu
 His Arg Asn Gln Thr Gln Leu Ser Asn₅₈₀ Lys His Glu Leu Gln₅₉₀ Leu Glu
 Gln Met His₅₉₅ Lys Arg Phe Glu Gln₆₀₀ Glu Ile Asn Ala Lys₆₀₅ Lys Lys Phe
 Phe Asp Thr Glu Leu Glu Asn₆₁₀ Leu Glu Arg Gln Gln₆₂₀ Lys Gln Gln Val
 Glu Lys Met Glu Gln Asp₆₃₀ His Ala Val Arg Arg₆₃₅ Arg Glu Glu Ala Arg₆₄₀
 Arg Ile Arg Leu Glu₆₄₅ Gln Asp Arg Asp Tyr Thr Arg Phe Gln Glu₆₅₅ Gln
 Leu Lys Leu Met₆₆₀ Lys Lys Glu Val Lys₆₆₅ Asn Glu Val Glu Lys₆₇₀ Leu Pro
 Arg Gln Gln Arg Lys Glu Ser Met₆₈₀ Lys Gln Lys Met Glu₆₈₅ Glu His Thr
 Gln Lys Lys Gln Leu Leu Asp₆₉₅ Arg Asp Phe Val Ala Lys Gln Lys Glu
 Asp Leu Glu Leu Ala Met₇₁₀ Lys Arg Leu Thr Thr₇₁₅ Asp Asn Arg Arg Glu₇₂₀
 Ile Cys Asp Lys Glu₇₂₅ Arg Glu Cys Leu Met₇₃₀ Lys Lys Gln Glu Leu₇₃₅ Leu
 Arg Asp Arg Glu Ala Ala Leu Trp Glu₇₄₅ Met Glu Glu His Gln₇₅₀ Leu Gln
 Glu Arg His Gln Leu Val Lys Gln₇₆₀ Gln Leu Lys Asp Gln Tyr Phe Leu
 Gln Arg His Glu Leu Leu Arg₇₇₅ Lys His Glu Lys Glu₇₈₀ Arg Glu Gln Met
 Gln Arg Tyr Asn Gln Arg Met Ile Glu Gln Leu₇₉₅ Lys Val Arg Gln Gln₈₀₀
 Gln Glu Lys Ala Arg₈₀₅ Leu Pro Lys Ile Gln Arg Ser Glu Gly Lys₈₁₅ Thr
 Arg Met Ala Met₈₂₀ Tyr Lys Lys Ser Leu His Ile Asn Gly Gly₈₃₀ Gly Ser
 Ala Ala Glu Gln Arg Glu Lys Ile₈₄₀ Lys Gln Phe Ser Gln Gln Glu Glu
 Lys Arg Gln Lys Ser Glu Arg₈₅₅ Leu Gln Gln Gln Gln₈₆₀ Lys His Glu Asn
 Gln Met Arg Asp Met Leu Ala Gln Cys Glu Ser₈₇₅ Asn Met Ser Glu Leu₈₈₀
 Gln Gln Leu Gln Asn Glu Lys Cys His Leu Leu Val Glu His Glu₈₉₅ Thr
 Gln Lys Leu Lys Ala Leu Asp Glu Ser His Asn Gln Asn Leu Lys Glu

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 900 905 910

Trp Arg Asp Lys Leu Arg Pro Arg Lys Lys Ala Leu Glu Glu Asp Leu
 915 920 925

Asn Gln Lys Lys Arg Glu Gln Glu Met Phe Phe Lys Leu Ser Glu Glu
 930 935 940

Ala Glu Cys Pro Asn Pro Ser Thr Pro Ser Lys Ala Ala Lys Phe Phe
 945 950 955 960

Pro Tyr Ser Ser Ala Asp Ala Ser
 965

<210> 145
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 145

Met Ala Leu Gln Leu Ser Arg Glu Gln Gly Ile Thr Leu Arg Gly Ser
 1 5 10 15

Ala Glu Ile Val Ala Glu Phe Phe Ser Phe Gly Ile Asn Ser Ile Leu
 20 25 30

Tyr Gln Arg Gly Ile Tyr Pro Ser Glu Thr Phe Thr Arg Val Gln Lys
 35 40 45

Tyr Gly Leu Thr Leu Leu Val Thr Thr Asp Leu Glu Leu Ile Lys Tyr
 50 55 60

Leu Asn Asn Val Val Glu Gln Leu Lys Asp Trp Leu Tyr Lys Cys Ser
 65 70 75 80

Val Gln Lys Leu Val Val Val Ile Ser Asn Ile Glu Ser Gly Glu Val
 85 90 95

Leu Glu Arg Trp Gln Phe Asp Ile Glu Cys Asp Lys Thr Ala Lys Asp
 100 105 110

Asp Ser Ala Pro Arg Glu Lys Ser Gln Lys Ala Ile Gln Asp Glu Ile
 115 120 125

Arg Ser Val Ile Arg Gln Ile Thr Ala Thr Val Thr Phe Leu Pro Leu
 130 135 140

Leu Glu Val Ser Cys Ser Phe Asp Leu Leu Ile Tyr Thr Asp Lys Asp
 145 150 155 160

Leu Val Val Pro Glu Lys Trp Glu Glu Ser Gly Pro Gln Phe Ile Thr
 165 170 175

Asn Ser Glu Glu Val Arg Leu Arg Ser Phe Thr Thr Thr Ile His Lys
 180 185 190

Val Asn Ser Met Val Ala Tyr Lys Ile Pro Val Asn Asp
 195 200 205

<210> 146
 <211> 591
 <212> PRT
 <213> Homo sapiens

<400> 146

Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu Ile Val Lys Ala Gln

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 1 5 10 15

Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His Asn Glu Asp Ile Thr
 20 25 30

Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val Phe Arg Gly Lys Leu
 35 40 45

Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp
 50 55 60

Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys
 65 70 75 80

Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro
 85 90 95

Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu
 100 105 110

Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu
 115 120 125

Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg
 130 135 140

Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val
 145 150 155 160

Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu
 165 170 175

Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val
 180 185 190

Ser Asp Thr Asn Ser Thr Ser Gly Asp Pro Val Glu Lys Lys Asp Glu
 195 200 205

Thr Pro Phe Gly Val Ser Val Ala Val Gly Leu Ala Val Phe Ala Cys
 210 215 220

Leu Phe Leu Ser Thr Leu Leu Leu Val Leu Asn Lys Cys Gly Arg Arg
 225 230 235 240

Asn Lys Phe Gly Ile Asn Arg Pro Ala Val Leu Ala Pro Glu Asp Gly
 245 250 255

Leu Ala Met Ser Leu His Phe Met Thr Leu Gly Gly Ser Ser Leu Ser
 260 265 270

Pro Thr Glu Gly Lys Gly Ser Gly Leu Gln Gly His Ile Ile Glu Asn
 275 280 285

Pro Gln Tyr Phe Ser Asp Ala Cys Val His His Ile Lys Arg Arg Asp
 290 295 300

Ile Val Leu Lys Trp Glu Leu Gly Glu Gly Ala Phe Gly Lys Val Phe
 305 310 315 320

Leu Ala Glu Ser His Asn Leu Leu Pro Glu Gln Asp Lys Met Leu Val
 325 330 335

Ala Val Lys Ala Leu Lys Glu Ala Ser Glu Ser Ala Arg Gln Asp Phe
 340 345 350

protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Gln Arg Glu Ala Glu Leu Leu Thr Met Leu Gln His Gln His Ile Val
355 360 365

Arg Phe Phe Gly Val Cys Thr Glu Gly Arg Pro Leu Leu Met Val Phe
370 375 380

Glu Tyr Met Arg His Gly Asp Leu Asn Arg Phe Leu Arg Ser His Gly
385 390 395 400

Pro Asp Ala Lys Leu Leu Ala Gly Gly Glu Asp Val Ala Pro Gly Pro
405 410 415

Leu Gly Leu Gly Gln Leu Leu Ala Val Ala Ser Gln Val Ala Ala Gly
420 425 430

Met Val Tyr Leu Ala Gly Leu His Phe Val His Arg Asp Leu Ala Thr
435 440 445

Arg Asn Cys Leu Val Gly Gln Gly Leu Val Val Lys Ile Gly Asp Phe
450 455 460

Gly Met Ser Arg Asp Ile Tyr Ser Thr Asp Tyr Tyr Arg Val Gly Gly
465 470 475 480

Arg Thr Met Leu Pro Ile Arg Trp Met Pro Pro Glu Ser Ile Leu Tyr
485 490 495

Arg Lys Phe Thr Thr Glu Ser Asp Val Trp Ser Phe Gly Val Val Leu
500 505 510

Trp Glu Ile Phe Thr Tyr Gly Lys Gln Pro Trp Tyr Gln Leu Ser Asn
515 520 525

Thr Glu Ala Ile Asp Cys Ile Thr Gln Gly Arg Glu Leu Glu Arg Pro
530 535 540

Arg Ala Cys Pro Pro Glu Val Tyr Ala Ile Met Arg Gly Cys Trp Gln
545 550 555 560

Arg Glu Pro Gln Gln Arg His Ser Ile Lys Asp Val His Ala Arg Leu
565 570 575

Gln Ala Leu Ala Gln Ala Pro Pro Val Tyr Leu Asp Val Leu Gly
580 585 590

<210> 147
<211> 887
<212> PRT
<213> Homo sapiens

<400> 147

Met Gly Glu Ala Glu Lys Phe His Tyr Ile Tyr Ser Cys Asp Leu Asp
1 5 10 15

Ile Asn Val Gln Leu Lys Ile Gly Ser Leu Glu Gly Lys Arg Glu Gln
20 25 30

Lys Ser Tyr Asn Ala Val Leu Glu Asp Pro Met Leu Lys Phe Ser Gly
35 40 45

Leu Tyr Gln Glu Thr Cys Ser Asp Leu Tyr Val Thr Cys Gln Val Phe
50 55 60

Ala Glu Gly Lys Pro Ser Ala Leu Pro Val Arg Thr Ser Tyr Lys Ala
65 70 75 80

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Phe Ser Thr Arg Trp Asn Trp Asn Glu Trp Leu Lys Leu Pro Val Lys
 85 90 95
 Tyr Pro Asp Leu Pro Arg Asn Ala Gln Val Ala Leu Thr Ile Trp Asp
 100 105 110
 Val Tyr Gly Pro Gly Lys Ala Val Pro Val Gly Gly Thr Thr Val Ser
 115 120 125
 Leu Phe Gly Lys Tyr Gly Met Ser Arg Gln Gly Met His Asp Leu Lys
 130 135 140
 Val Trp Pro Asn Val Glu Ala Asp Gly Ser Glu Pro Thr Asn Thr Pro
 145 150 155 160
 Gly Arg Thr Ser Ser Thr Leu Ser Glu Asp Gln Met Ser Arg Leu Ala
 165 170 175
 Lys Leu Thr Lys Ala His Arg Gln Gly His Met Val Lys Val Asp Trp
 180 185 190
 Leu Asp Arg Leu Thr Phe Arg Glu Ile Glu Met Ile Asn Glu Ser Val
 195 200 205
 Lys Arg Ser Ser Asn Phe Met Tyr Leu Met Gly Gly Phe Arg Cys Val
 210 215 220
 Lys Cys Asp Asp Lys Glu Tyr Gly Ile Val Tyr Tyr Glu Lys Asp Gly
 225 230 235 240
 Asp Glu Ser Ser Pro Ile Leu Thr Ser Phe Glu Leu Val Lys Val Pro
 245 250 255
 Asp Pro Gln Met Ser Leu Glu Asn Leu Val Glu Ser Lys His His Asn
 260 265 270
 Leu Pro Arg Ser Leu Arg Ser Gly Pro Ser Asp His Asp Leu Lys Pro
 275 280 285
 Tyr Pro Ser Pro Arg Asp Gln Leu Lys Asn Ile Val Ser Tyr Pro Pro
 290 295 300
 Ser Lys Pro Pro Thr Tyr Glu Glu Gln Asp Leu Val Trp Glu Phe Arg
 305 310 315 320
 Tyr Tyr Leu Thr Asn Gln Asp Lys Ala Leu Thr Lys Ile Leu Thr Ser
 325 330 335
 Val Ile Trp Asp Leu Pro Gln Gly Ala Lys Gln Ala Leu Ala Leu Leu
 340 345 350
 Gly Lys Trp Asn Pro Met Asp Val Glu Asp Ser Leu Glu Leu Ile Ser
 355 360 365
 Ser His Tyr Thr Asn Pro Thr Val Arg Arg Tyr Ala Val Ala Arg Leu
 370 375 380
 Arg Gln Ala Asp Asp Glu Asp Leu Leu Met Tyr Leu Ser Gln Leu Val
 385 390 395 400
 Gln Ala Leu Lys Tyr Glu Asn Phe Asp Asp Ile Lys Asn Gly Leu Glu
 405 410 415

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Pro Thr Lys Lys Asp Ser Gln Ser Ser Val Ser Gly Asn Val Ser Asn
 420 425 430

Ser Gly Ile Asn Ser Ala Glu Ile Asp Ser Ser Gln Ile Ile Thr Ser
 435 440 445

Pro Leu Pro Ser Val Ser Ser Pro Pro Pro Ala Ser Lys Thr Lys Glu
 450 455 460

Val Pro Asp Gly Glu Asn Leu Glu Gln Asp Leu Cys Thr Phe Leu Ile
 465 470 475 480

Ser Arg Ala Ser Lys Asn Ser Thr Leu Ala Asn Tyr Leu Tyr Trp Tyr
 485 490 495

Val Ile Val Glu Cys Glu Asp Gln Asp Thr Gln Gln Arg Asp Pro Lys
 500 505 510

Thr His Glu Met Tyr Leu Asn Val Met Arg Arg Phe Ser Gln Ala Leu
 515 520 525

Leu Lys Gly Asp Lys Ser Val Arg Val Met Arg Ser Leu Leu Ala Ala
 530 535 540

Gln Gln Thr Phe Val Asp Arg Leu Val His Leu Met Lys Ala Val Gln
 545 550 555 560

Arg Glu Ser Gly Asn Arg Lys Lys Lys Asn Glu Arg Leu Gln Ala Leu
 565 570 575

Leu Gly Asp Asn Glu Lys Met Asn Leu Ser Asp Val Glu Leu Ile Pro
 580 585 590

Leu Pro Leu Glu Pro Gln Val Lys Ile Arg Gly Ile Ile Pro Glu Thr
 595 600 605

Ala Thr Leu Phe Lys Ser Ala Leu Met Pro Ala Gln Leu Phe Phe Lys
 610 615 620

Thr Glu Asp Gly Gly Lys Tyr Pro Val Ile Phe Lys His Gly Asp Asp
 625 630 635 640

Leu Arg Gln Asp Gln Leu Ile Leu Gln Ile Ile Ser Leu Met Asp Lys
 645 650 655

Leu Leu Arg Lys Glu Asn Leu Asp Leu Lys Leu Thr Pro Tyr Lys Val
 660 665 670

Leu Ala Thr Ser Thr Lys His Gly Phe Met Gln Phe Ile Gln Ser Val
 675 680 685

Pro Val Ala Glu Val Leu Asp Thr Glu Gly Ser Ile Gln Asn Phe Phe
 690 695 700

Arg Lys Tyr Ala Pro Ser Glu Asn Gly Pro Asn Gly Ile Ser Ala Glu
 705 710 715 720

Val Met Asp Thr Tyr Val Lys Ser Cys Ala Gly Tyr Cys Val Ile Thr
 725 730 735

Tyr Ile Leu Gly Val Gly Asp Arg His Leu Asp Asn Leu Val Leu Thr
 740 745 750

Lys Thr Gly Lys Leu Phe His Ile Asp Phe Gly Tyr Ile Leu Gly Arg
 755 760 765

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Asp Pro Lys Pro Leu Pro Pro Pro Met Lys Leu Asn Lys Glu Met Val
770 775 780

Glu Gly Met Gly Gly Thr Gln Ser Glu Gln Tyr Gln Glu Phe Arg Lys
785 790 795 800

Gln Cys Tyr Thr Ala Phe Leu His Leu Arg Arg Tyr Ser Asn Leu Ile
805 810 815

Leu Asn Leu Phe Ser Leu Met Val Asp Pro Asn Ile Pro Asp Ile Ala
820 825 830

Leu Glu Pro Asp Lys Thr Val Lys Lys Val Gln Asp Lys Phe Arg Leu
835 840 845

Asp Leu Ser Asp Glu Glu Ala Val His Tyr Met Gln Ser Leu Ile Asp
850 855 860

Glu Ser Val His Ala Leu Phe Ala Ala Val Val Glu Gln Ile His Lys
865 870 875 880

Phe Ala Gln Tyr Trp Arg Lys
885

<210> 148
<211> 1290
<212> PRT
<213> Homo sapiens

<400> 148

Met Ala Gly Ala Ala Ser Pro Cys Ala Asn Gly Cys Gly Pro Gly Ala
1 5 10 15

Pro Ser Asp Ala Glu Val Leu His Leu Cys Arg Ser Leu Glu Val Gly
20 25 30

Thr Val Met Thr Leu Phe Tyr Ser Lys Lys Ser Gln Arg Pro Glu Arg
35 40 45

Lys Thr Phe Gln Val Lys Leu Glu Thr Arg Gln Ile Thr Trp Ser Arg
50 55 60

Gly Ala Asp Lys Ile Glu Gly Ala Ile Asp Ile Arg Glu Ile Lys Glu
65 70 75 80

Ile Arg Pro Gly Lys Thr Ser Arg Asp Phe Asp Arg Tyr Gln Glu Asp
85 90 95

Pro Ala Phe Arg Pro Asp Gln Ser His Cys Phe Val Ile Leu Tyr Gly
100 105 110

Met Glu Phe Arg Leu Lys Thr Leu Ser Leu Gln Ala Thr Ser Glu Asp
115 120 125

Glu Val Asn Met Trp Ile Lys Gly Leu Thr Trp Leu Met Glu Asp Thr
130 135 140

Leu Gln Ala Pro Thr Pro Leu Gln Ile Glu Arg Trp Leu Arg Lys Gln
145 150 155 160

Phe Tyr Ser Val Asp Arg Asn Arg Glu Asp Arg Ile Ser Ala Lys Asp
165 170 175

Leu Lys Asn Met Leu Ser Gln Val Asn Tyr Arg Val Pro Asn Met Arg

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 180 185 190

Phe Leu Arg Glu Arg Leu Thr Asp Leu Glu Gln Arg Ser Gly Asp Ile
 195 200 205

Thr Tyr Gly Gln Phe Ala Gln Leu Tyr Arg Ser Leu Met Tyr Ser Ala
 210 215 220

Gln Lys Thr Met Asp Leu Pro Phe Leu Glu Ala Ser Thr Leu Arg Ala
 225 230 235 240

Gly Glu Arg Pro Glu Leu Cys Arg Val Ser Leu Pro Glu Phe Gln Gln
 245 250 255

Phe Leu Leu Asp Tyr Gln Gly Glu Leu Trp Ala Val Asp Arg Leu Gln
 260 265 270

Val Gln Glu Phe Met Leu Ser Phe Leu Arg Asp Pro Leu Arg Glu Ile
 275 280 285

Glu Glu Pro Tyr Phe Phe Leu Asp Glu Phe Val Thr Phe Leu Phe Ser
 290 295 300

Lys Glu Asn Ser Val Trp Asn Ser Gln Leu Asp Ala Val Cys Pro Asp
 305 310 315 320

Thr Met Asn Asn Pro Leu Ser His Tyr Trp Ile Ser Ser Ser His Asn
 325 330 335

Thr Tyr Leu Thr Gly Asp Gln Phe Ser Ser Glu Ser Ser Leu Glu Ala
 340 345 350

Tyr Ala Arg Cys Leu Arg Met Gly Cys Arg Cys Ile Glu Leu Asp Cys
 355 360 365

Trp Asp Gly Pro Asp Gly Met Pro Val Ile Tyr His Gly His Thr Leu
 370 375 380

Thr Thr Lys Ile Lys Phe Ser Asp Val Leu His Thr Ile Lys Glu His
 385 390 395 400

Ala Phe Val Ala Ser Glu Tyr Pro Val Ile Leu Ser Ile Glu Asp His
 405 410 415

Cys Ser Ile Ala Gln Gln Arg Asn Met Ala Gln Tyr Phe Lys Lys Val
 420 425 430

Leu Gly Asp Thr Leu Leu Thr Lys Pro Val Glu Ile Ser Ala Asp Gly
 435 440 445

Leu Pro Ser Pro Asn Gln Leu Lys Arg Lys Ile Leu Ile Lys His Lys
 450 455 460

Lys Leu Ala Glu Gly Ser Ala Tyr Glu Glu Val Pro Thr Ser Met Met
 465 470 475 480

Tyr Ser Glu Asn Asp Ile Ser Asn Ser Ile Lys Asn Gly Ile Leu Tyr
 485 490 495

Leu Glu Asp Pro Val Asn His Glu Trp Tyr Pro His Tyr Phe Val Leu
 500 505 510

Thr Ser Ser Lys Ile Tyr Tyr Ser Glu Glu Thr Ser Ser Asp Gln Gly
 515 520 525

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Asn Glu Asp Glu Glu Glu Pro Lys Glu Val Ser Ser Ser Thr Glu Leu
530 535 540

His Ser Asn Glu Lys Trp Phe His Gly Lys Leu Gly Ala Gly Arg Asp
545 550 555 560

Gly Arg His Ile Ala Glu Arg Leu Leu Thr Glu Tyr Cys Ile Glu Thr
565 570 575

Gly Ala Pro Asp Gly Ser Phe Leu Val Arg Glu Ser Glu Thr Phe Val
580 585 590

Gly Asp Tyr Thr Leu Ser Phe Trp Arg Asn Gly Lys Val Gln His Cys
595 600 605

Arg Ile His Ser Arg Gln Asp Ala Gly Thr Pro Lys Phe Phe Leu Thr
610 615 620

Asp Asn Leu Val Phe Asp Ser Leu Tyr Asp Leu Ile Thr His Tyr Gln
625 630 635 640

Gln Val Pro Leu Arg Cys Asn Glu Phe Glu Met Arg Leu Ser Glu Pro
645 650 655

Val Pro Gln Thr Asn Ala His Glu Ser Lys Glu Trp Tyr His Ala Ser
660 665 670

Leu Thr Arg Ala Gln Ala Glu His Met Leu Met Arg Val Pro Arg Asp
675 680 685

Gly Ala Phe Leu Val Arg Lys Arg Asn Glu Pro Asn Ser Tyr Ala Ile
690 695 700

Ser Phe Arg Ala Glu Gly Lys Ile Lys His Cys Arg Val Gln Gln Glu
705 710 715 720

Gly Gln Thr Val Met Leu Gly Asn Ser Glu Phe Asp Ser Leu Val Asp
725 730 735

Leu Ile Ser Tyr Tyr Glu Lys His Pro Leu Tyr Arg Lys Met Lys Leu
740 745 750

Arg Tyr Pro Ile Asn Glu Glu Ala Leu Glu Lys Ile Gly Thr Ala Glu
755 760 765

Pro Asp Tyr Gly Ala Leu Tyr Glu Gly Arg Asn Pro Gly Phe Tyr Val
770 775 780

Glu Ala Asn Pro Met Pro Thr Phe Lys Cys Ala Val Lys Ala Leu Phe
785 790 795 800

Asp Tyr Lys Ala Gln Arg Glu Asp Glu Leu Thr Phe Ile Lys Ser Ala
805 810 815

Ile Ile Gln Asn Val Glu Lys Gln Glu Gly Gly Trp Trp Arg Gly Asp
820 825 830

Tyr Gly Gly Lys Lys Gln Leu Trp Phe Pro Ser Asn Tyr Val Glu Glu
835 840 845

Met Val Asn Pro Val Ala Leu Glu Pro Glu Arg Glu His Leu Asp Glu
850 855 860

Asn Ser Pro Leu Gly Asp Leu Leu Arg Gly Val Leu Asp Val Pro Ala

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 865 870 875 880

Cys Gln Ile Ala Ile Arg Pro Glu Gly Lys Asn Asn Arg Leu Phe Val
 885 890 895

Phe Ser Ile Ser Met Ala Ser Val Ala His Trp Ser Leu Asp Val Ala
 900 905 910

Ala Asp Ser Gln Glu Glu Leu Gln Asp Trp Val Lys Lys Ile Arg Glu
 915 920 925

Val Ala Gln Thr Ala Asp Ala Arg Leu Thr Glu Gly Lys Ile Met Glu
 930 935 940

Arg Arg Lys Lys Ile Ala Leu Glu Leu Ser Glu Leu Val Val Tyr Cys
 945 950 955 960

Arg Pro Val Pro Phe Asp Glu Glu Lys Ile Gly Thr Glu Arg Ala Cys
 965 970 975

Tyr Arg Asp Met Ser Ser Phe Pro Glu Thr Lys Ala Glu Lys Tyr Val
 980 985 990

Asn Lys Ala Lys Gly Lys Lys Phe Leu Gln Tyr Asn Arg Leu Gln Leu
 995 1000 1005

Ser Arg Ile Tyr Pro Lys Gly Gln Arg Leu Asp Ser Ser Asn Tyr
 1010 1015 1020

Asp Pro Leu Pro Met Trp Ile Cys Gly Ser Gln Leu Val Ala Leu
 1025 1030 1035

Asn Phe Gln Thr Pro Asp Lys Pro Met Gln Met Asn Gln Ala Leu
 1040 1045 1050

Phe Met Thr Gly Arg His Cys Gly Tyr Val Leu Gln Pro Ser Thr
 1055 1060 1065

Met Arg Asp Glu Ala Phe Asp Pro Phe Asp Lys Ser Ser Leu Arg
 1070 1075 1080

Gly Leu Glu Pro Cys Ala Ile Ser Ile Glu Val Leu Gly Ala Arg
 1085 1090 1095

His Leu Pro Lys Asn Gly Arg Gly Ile Val Cys Pro Phe Val Glu
 1100 1105 1110

Ile Glu Val Ala Gly Ala Glu Tyr Asp Ser Thr Lys Gln Lys Thr
 1115 1120 1125

Glu Phe Val Val Asp Asn Gly Leu Asn Pro Val Trp Pro Ala Lys
 1130 1135 1140

Pro Phe His Phe Gln Ile Ser Asn Pro Glu Phe Ala Phe Leu Arg
 1145 1150 1155

Phe Val Val Tyr Glu Glu Asp Met Phe Ser Asp Gln Asn Phe Leu
 1160 1165 1170

Ala Gln Ala Thr Phe Pro Val Lys Gly Leu Lys Thr Gly Tyr Arg
 1175 1180 1185

Ala Val Pro Leu Lys Asn Asn Tyr Ser Glu Asp Leu Glu Leu Ala
 1190 1195 1200

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ser Leu Leu Ile Lys Ile Asp Ile Phe Pro Ala Lys Glu Asn Gly
1205 1210 1215

Asp Leu Ser Pro Phe Ser Gly Thr Ser Leu Arg Glu Arg Gly Ser
1220 1225 1230

Asp Ala Ser Gly Gln Leu Phe His Gly Arg Ala Arg Glu Gly Ser
1235 1240 1245

Phe Glu Ser Arg Tyr Gln Gln Pro Phe Glu Asp Phe Arg Ile Ser
1250 1255 1260

Gln Glu His Leu Ala Asp His Phe Asp Ser Arg Glu Arg Arg Ala
1265 1270 1275

Pro Arg Arg Thr Arg Val Asn Gly Asp Asn Arg Leu
1280 1285 1290

<210> 149
<211> 200
<212> PRT
<213> Homo sapiens

<400> 149

Met Val Ser Ile Ser Leu Lys Phe Tyr Lys Glu Leu Gln Ala His Gly
1 5 10 15

Ala Asp Glu Leu Leu Lys Arg Val Tyr Gly Ser Phe Leu Val Asn Pro
20 25 30

Glu Ser Gly Tyr Asn Val Ser Leu Leu Tyr Asp Leu Glu Asn Leu Pro
35 40 45

Ala Ser Lys Asp Ser Ile Val His Gln Ala Gly Met Leu Lys Arg Asn
50 55 60

Cys Phe Ala Ser Val Phe Glu Lys Tyr Phe Gln Phe Gln Glu Glu Gly
65 70 75 80

Lys Glu Gly Glu Asn Arg Ala Val Ile His Tyr Arg Asp Asp Glu Thr
85 90 95

Met Tyr Val Glu Ser Lys Lys Asp Arg Val Thr Val Val Phe Ser Thr
100 105 110

Val Phe Lys Asp Asp Asp Asp Val Val Ile Gly Lys Val Phe Met Gln
115 120 125

Glu Phe Lys Glu Gly Arg Arg Ala Ser His Thr Ala Pro Gln Val Leu
130 135 140

Phe Ser His Arg Glu Pro Pro Leu Glu Leu Lys Asp Thr Asp Ala Ala
145 150 155 160

Val Gly Asp Asn Ile Gly Tyr Ile Thr Phe Cys Ala Val Pro Phe Val
165 170 175

His Gln Cys Gln Cys Ser Arg His Thr Ile Asn Leu Val Pro His Val
180 185 190

Pro Gly Leu Pro Pro Leu Pro His
195 200

<210> 150
<211> 36

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

<212> PRT
<213> Homo sapiens

<400> 150

Met Ala Arg Leu Arg Ala Gly Ile Tyr Leu Ala Ser Gln Phe Phe Gly
1 5 10 15Trp Lys Glu Gln Glu Ile Ser Ser Tyr Ser Pro Val Glu Arg Ser Gly
20 25 30Leu Ser Leu Gly
35<210> 151
<211> 593
<212> PRT
<213> Homo sapiens

<400> 151

Met Thr Ser Arg Arg Trp Phe His Pro Asn Ile Thr Gly Val Glu Ala
1 5 10 15Glu Asn Leu Leu Leu Thr Arg Gly Val Asp Gly Ser Phe Leu Ala Arg
20 25 30Pro Ser Lys Ser Asn Pro Gly Asp Phe Thr Leu Ser Val Arg Arg Asn
35 40 45Gly Ala Val Thr His Ile Lys Ile Gln Asn Thr Gly Asp Tyr Tyr Asp
50 55 60Leu Tyr Gly Gly Glu Lys Phe Ala Thr Leu Ala Glu Leu Val Gln Tyr
65 70 75 80Tyr Met Glu His His Gly Gln Leu Lys Glu Lys Asn Gly Asp Val Ile
85 90 95Glu Leu Lys Tyr Pro Leu Asn Cys Ala Asp Pro Thr Ser Glu Arg Trp
100 105 110Phe His Gly His Leu Ser Gly Lys Glu Ala Glu Lys Leu Leu Thr Glu
115 120 125Lys Gly Lys His Gly Ser Phe Leu Val Arg Glu Ser Gln Ser His Pro
130 135 140Gly Asp Phe Val Leu Ser Val Arg Thr Gly Asp Asp Lys Gly Glu Ser
145 150 155 160Asn Asp Gly Lys Ser Lys Val Thr His Val Met Ile Arg Cys Gln Glu
165 170 175Leu Lys Tyr Asp Val Gly Gly Gly Glu Arg Phe Asp Ser Leu Thr Asp
180 185 190Leu Val Glu His Tyr Lys Lys Asn Pro Met Val Glu Thr Leu Gly Thr
195 200 205Val Leu Gln Leu Lys Gln Pro Leu Asn Thr Thr Arg Ile Asn Ala Ala
210 215 220Glu Ile Glu Ser Arg Val Arg Glu Leu Ser Lys Leu Ala Glu Thr Thr
225 230 235 240Asp Lys Val Lys Gln Gly Phe Trp Glu Glu Phe Glu Thr Leu Gln Gln
245 250 255

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Gln Glu Cys Lys Leu Leu Tyr Ser Arg Lys Glu Gly Gln Arg Gln Glu
260 265 270

Asn Lys Asn Lys Asn Arg Tyr Lys Asn Ile Leu Pro Phe Asp His Thr
275 280 285

Arg Val Val Leu His Asp Gly Asp Pro Asn Glu Pro Val Ser Asp Tyr
290 295 300

Ile Asn Ala Asn Ile Ile Met Pro Glu Phe Glu Thr Lys Cys Asn Asn
305 310 315 320

Ser Lys Pro Lys Lys Ser Tyr Ile Ala Thr Gln Gly Cys Leu Gln Asn
325 330 335

Thr Val Asn Asp Phe Trp Arg Met Val Phe Gln Glu Asn Ser Arg Val
340 345 350

Ile Val Met Thr Thr Lys Glu Val Glu Arg Gly Lys Ser Lys Cys Val
355 360 365

Lys Tyr Trp Pro Asp Glu Tyr Ala Leu Lys Glu Tyr Gly Val Met Arg
370 375 380

Val Arg Asn Val Lys Glu Ser Ala Ala His Asp Tyr Thr Leu Arg Glu
385 390 395 400

Leu Lys Leu Ser Lys Val Gly Gln Gly Asn Thr Glu Arg Thr Val Trp
405 410 415

Gln Tyr His Phe Arg Thr Trp Pro Asp His Gly Val Pro Ser Asp Pro
420 425 430

Gly Gly Val Leu Asp Phe Leu Glu Glu Val His His Lys Gln Glu Ser
435 440 445

Ile Met Asp Ala Gly Pro Val Val Val His Cys Ser Ala Gly Ile Gly
450 455 460

Arg Thr Gly Thr Phe Ile Val Ile Asp Ile Leu Ile Asp Ile Ile Arg
465 470 475 480

Glu Lys Gly Val Asp Cys Asp Ile Asp Val Pro Lys Thr Ile Gln Met
485 490 495

Val Arg Ser Gln Arg Ser Gly Met Val Gln Thr Glu Ala Gln Tyr Arg
500 505 510

Phe Ile Tyr Met Ala Val Gln His Tyr Ile Glu Thr Leu Gln Arg Arg
515 520 525

Ile Glu Glu Glu Gln Lys Ser Lys Arg Lys Gly His Glu Tyr Thr Asn
530 535 540

Ile Lys Tyr Ser Leu Ala Asp Gln Thr Ser Gly Asp Gln Ser Pro Leu
545 550 555 560

Pro Pro Cys Thr Pro Thr Pro Pro Cys Ala Glu Met Arg Glu Asp Ser
565 570 575

Ala Arg Val Tyr Glu Asn Val Gly Leu Met Gln Gln Gln Lys Ser Phe
580 585 590

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
Arg

<210> 152
<211> 348
<212> PRT
<213> Homo sapiens
<400> 152
Met Ala Gly Ser Leu Pro Pro Cys Val Val Asp Cys Gly Thr Gly Tyr
1 5 10 15
Thr Lys Leu Gly Tyr Ala Gly Asn Thr Glu Pro Gln Phe Ile Ile Pro
20 25 30
Ser Cys Ile Ala Ile Arg Glu Ser Ala Lys Val Val Asp Gln Ala Gln
35 40 45
Arg Arg Val Leu Arg Gly Val Asp Asp Leu Asp Phe Phe Ile Gly Asp
50 55 60
Glu Ala Ile Asp Lys Pro Thr Tyr Ala Thr Lys Trp Pro Ile Arg His
65 70 75 80
Gly Ile Ile Glu Asp Trp Asp Leu Met Glu Arg Phe Met Glu Gln Val
85 90 95
Val Phe Lys Tyr Leu Arg Ala Glu Pro Glu Asp His Tyr Phe Leu Met
100 105 110
Thr Glu Pro Pro Leu Asn Thr Pro Glu Asn Arg Glu Tyr Leu Ala Glu
115 120 125
Ile Met Phe Glu Ser Phe Asn Val Pro Gly Leu Tyr Ile Ala Val Gln
130 135 140
Ala Val Leu Ala Leu Ala Ala Ser Trp Thr Ser Arg Gln Val Gly Glu
145 150 155 160
Arg Thr Leu Thr Gly Ile Val Ile Asp Ser Gly Asp Gly Val Thr His
165 170 175
Val Ile Pro Val Ala Glu Gly Tyr Val Ile Gly Ser Cys Ile Lys His
180 185 190
Ile Pro Ile Ala Gly Arg Asp Ile Thr Tyr Phe Ile Gln Gln Leu Leu
195 200 205
Arg Glu Arg Glu Val Gly Ile Pro Pro Glu Gln Ser Leu Glu Thr Ala
210 215 220
Lys Ala Ile Lys Glu Lys Tyr Cys Tyr Ile Cys Pro Asp Ile Val Lys
225 230 235 240
Glu Phe Ala Lys Tyr Asp Val Asp Pro Arg Lys Trp Ile Lys Gln Tyr
245 250 255
Thr Gly Ile Asn Ala Ile Asn Gln Lys Lys Phe Val Ile Asp Val Gly
260 265 270
Tyr Glu Arg Phe Leu Gly Pro Glu Ile Phe Phe His Pro Glu Phe Ala
275 280 285
Asn Pro Asp Phe Met Glu Ser Ile Ser Asp Val Val Asp Glu Val Ile
290 295 300

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Gln Asn Cys Pro Ile Asp Val Arg Arg Pro Leu Tyr Lys Pro Glu Phe
305 310 315 320

Phe Gln Val Cys His Thr Lys Lys Asp Tyr Glu Glu Tyr Gly Pro Ser
325 330 335

Ile Cys Arg His Asn Pro Val Phe Gly Val Met Ser
340 345

<210> 153
<211> 248
<212> PRT
<213> Homo sapiens

<400> 153

Met Phe Leu Ala Lys Ala Leu Leu Glu Gly Ala Asp Arg Gly Leu Gly
1 5 10 15

Glu Ala Leu Gly Gly Leu Phe Gly Gly Gly Gly Gln Arg Arg Glu Gly
20 25 30

Gly Gly Arg Asn Ile Gly Gly Ile Val Gly Gly Ile Val Asn Phe Ile
35 40 45

Ser Glu Ala Ala Ala Ala Gln Tyr Thr Pro Glu Pro Pro Pro Thr Gln
50 55 60

Gln His Phe Thr Ser Val Glu Ala Ser Glu Ser Glu Glu Val Arg Arg
65 70 75 80

Phe Arg Gln Gln Phe Thr Gln Leu Ala Gly Pro Asp Met Glu Val Gly
85 90 95

Ala Thr Asp Leu Met Asn Ile Leu Asn Lys Val Leu Ser Lys His Lys
100 105 110

Asp Leu Lys Thr Asp Gly Phe Ser Leu Asp Thr Cys Arg Ser Ile Val
115 120 125

Ser Val Met Asp Ser Asp Thr Thr Gly Lys Leu Gly Phe Glu Glu Phe
130 135 140

Lys Tyr Leu Trp Asn Asn Ile Lys Lys Trp Gln Cys Val Tyr Lys Gln
145 150 155 160

Tyr Asp Arg Asp His Ser Gly Ser Leu Gly Ser Ser Gln Leu Arg Gly
165 170 175

Ala Leu Gln Ala Ala Gly Phe Gln Leu Asn Glu Gln Leu Tyr Gln Met
180 185 190

Ile Val Arg Arg Tyr Ala Asn Glu Asp Gly Asp Met Asp Phe Asn Asn
195 200 205

Phe Ile Ser Cys Leu Val Arg Leu Asp Ala Met Phe Arg Ala Phe Lys
210 215 220

Ser Leu Asp Arg Asp Arg Asp Gly Leu Ile Gln Val Ser Ile Lys Glu
225 230 235 240

Trp Leu Gln Leu Thr Met Tyr Ser
245

<210> 154
<211> 698

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

<212> PRT

<213> Homo sapiens

<400> 154

Met Ala Leu Gln Leu Glu Val Val His Gly Pro Asp Ile Ile Thr Glu
1 5 10 15Thr Asp Val Val Thr Glu Gly Val Ile Val Pro Glu Ala Val Leu Glu
20 25 30Ala Asp Val Ala Ile Glu Glu Asp Leu Glu Glu Asp Asp Gly Asp His
35 40 45Ile Leu Thr Ser Glu Leu Ile Thr Glu Thr Val Arg Val Pro Glu Gln
50 55 60Val Phe Val Ala Asp Leu Val Thr Gly Pro Asn Gly His Leu Glu His
65 70 75 80Val Val Gln Asp Cys Val Ser Gly Val Asp Ser Pro Thr Met Val Ser
85 90 95Glu Glu Val Leu Val Thr Asn Ser Asp Thr Glu Thr Val Ile Gln Ala
100 105 110Ala Gly Gly Val Pro Gly Ser Thr Val Thr Ile Lys Thr Glu Asp Asp
115 120 125Asp Asp Asp Asp Val Lys Ser Thr Ser Glu Asp Tyr Leu Met Ile Ser
130 135 140Leu Asp Asp Val Gly Glu Lys Leu Glu His Met Gly Asn Thr Pro Leu
145 150 155 160Lys Ile Gly Ser Asp Gly Ser Gln Glu Asp Ala Lys Glu Asp Gly Phe
165 170 175Gly Ser Glu Val Ile Lys Val Tyr Ile Phe Lys Ala Glu Ala Glu Asp
180 185 190Asp Val Glu Ile Gly Gly Thr Glu Met Ser Pro Glu Ser Glu Tyr Thr
195 200 205Ser Gly His Ser Val Ala Gly Val Leu Asp Gln Ser Arg Met Gln Arg
210 215 220Glu Lys Met Val Tyr Met Ala Val Lys Asp Ser Ser Gln Glu Glu Asp
225 230 235 240Asp Ile Arg Asp Glu Arg Arg Val Ser Arg Arg Tyr Glu Asp Cys Gln
245 250 255Ala Ser Gly Asn Thr Leu Asp Ser Ala Leu Glu Ser Arg Ser Ser Thr
260 265 270Ala Ala Gln Tyr Leu Gln Ile Cys Asp Gly Ile Asn Thr Asn Lys Val
275 280 285Leu Lys Gln Lys Ala Lys Lys Arg Arg Arg Gly Glu Thr Arg Gln Trp
290 295 300Gln Thr Ala Val Ile Ile Gly Pro Asp Gly Gln Pro Leu Thr Val Tyr
305 310 315 320

Pro Cys His Ile Cys Thr Lys Lys Phe Lys Ser Lys Gly Phe Leu Lys

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 325 330 335

Arg His Met Lys Asn His Pro Asp His Leu Met Arg Lys Lys Tyr Gln
 340 345 350

Cys Thr Asp Cys Asp Phe Thr Thr Asn Lys Lys Val Ser Phe His Asn
 355 360 365

His Leu Glu Ser His Lys Leu Ile Asn Lys Val Asp Lys Thr His Glu
 370 375 380

Phe Thr Glu Tyr Thr Arg Arg Tyr Arg Glu Ala Ser Pro Leu Ser Ser
 385 390 395 400

Asn Lys Leu Ile Leu Arg Asp Lys Glu Pro Lys Thr Asp Lys Cys Lys
 405 410 415

Tyr Cys Asp Tyr Glu Thr Ala Glu Gln Gly Leu Leu Asn Arg His Leu
 420 425 430

Leu Ala Val His Ser Lys Asn Phe Pro His Val Cys Val Glu Cys Gly
 435 440 445

Lys Gly Phe Arg His Pro Ser Glu Leu Lys Lys His Met Arg Thr His
 450 455 460

Thr Gly Glu Lys Pro Tyr Gln Cys Gln Tyr Cys Ile Phe Arg Cys Ala
 465 470 475 480

Asp Gln Ser Asn Leu Lys Thr His Ile Lys Ser Lys His Gly Asn Asn
 485 490 495

Leu Pro Tyr Lys Cys Glu His Cys Pro Gln Ala Phe Gly Asp Glu Arg
 500 505 510

Glu Leu Gln Arg His Leu Asp Leu Phe Gln Gly His Lys Thr His Gln
 515 520 525

Cys Pro His Cys Asp His Lys Ser Thr Asn Ser Ser Asp Leu Lys Arg
 530 535 540

His Ile Ile Ser Val His Thr Lys Asp Phe Pro His Lys Cys Glu Val
 545 550 555 560

Cys Asp Lys Gly Phe His Arg Pro Ser Glu Leu Lys Lys His Ser Asp
 565 570 575

Ile His Lys Gly Arg Lys Ile His Thr Cys Arg His Cys Asp Phe Lys
 580 585 590

Thr Ser Asp Pro Phe Ile Leu Ser Gly His Leu Leu Ser Val His Thr
 595 600 605

Lys Asp Gln Pro Leu Lys Cys Lys Gly Cys Thr Arg Gly Phe Arg Gln
 610 615 620

Gln Asn Glu Leu Lys Lys His Met Lys Thr His Thr Gly Arg Lys Ser
 625 630 635 640

Tyr Gln Cys Glu Tyr Cys Glu Tyr Ser Thr Thr Asp Ala Ser Gly Phe
 645 650 655

Lys Arg His Val Ile Ser Ile His Thr Lys Asp Tyr Pro His Arg Cys
 660 665 670

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Glu Phe Cys Asn Lys Gly Phe Arg Arg Pro Ser Glu Lys Asn Gln His
675 680 685

Ile Met Lys His His Lys Glu Ala Leu Met
690 695

<210> 155
<211> 771
<212> PRT
<213> Homo sapiens

<400> 155

Met Ile Met Gln Asp Phe Val Ala Gly Met Ala Gly Thr Ala His Ile
1 5 10 15

Asp Gly Asp His Ile Val Val Ser Val Pro Glu Ala Val Leu Val Ser
20 25 30

Asp Val Val Thr Asp Asp Gly Ile Thr Leu Asp His Gly Leu Ala Ala
35 40 45

Glu Val Val His Gly Pro Asp Ile Ile Thr Glu Thr Asp Val Val Thr
50 55 60

Glu Gly Val Ile Val Pro Glu Ala Val Leu Glu Ala Asp Val Ala Ile
65 70 75 80

Glu Glu Asp Leu Glu Glu Asp Asp Gly Asp His Ile Leu Thr Ser Glu
85 90 95

Leu Ile Thr Glu Thr Val Arg Val Pro Glu Gln Val Phe Val Ala Asp
100 105 110

Leu Val Thr Gly Pro Asn Gly His Leu Glu His Val Val Gln Asp Cys
115 120 125

Val Ser Gly Val Asp Ser Pro Thr Met Val Ser Glu Glu Val Leu Val
130 135 140

Thr Asn Ser Asp Thr Glu Thr Val Ile Gln Ala Ala Gly Gly Val Pro
145 150 155 160

Gly Ser Thr Val Thr Ile Lys Thr Glu Asp Asp Asp Asp Asp Val
165 170 175

Lys Ser Thr Ser Glu Asp Tyr Leu Met Ile Ser Leu Asp Asp Val Gly
180 185 190

Glu Lys Leu Glu His Met Gly Asn Thr Pro Leu Lys Ile Gly Ser Asp
195 200 205

Gly Ser Gln Glu Asp Ala Lys Glu Asp Gly Phe Gly Ser Glu Val Ile
210 215 220

Lys Val Tyr Ile Phe Lys Ala Glu Ala Glu Asp Asp Val Glu Ile Gly
225 230 235 240

Gly Thr Glu Ile Val Thr Glu Ser Glu Tyr Thr Ser Gly His Ser Val
245 250 255

Ala Gly Val Leu Asp Gln Ser Arg Met Gln Arg Glu Lys Met Val Tyr
260 265 270

Met Ala Val Lys Asp Ser Ser Gln Glu Glu Asp Asp Ile Ser Cys Ala
275 280 285

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Glu Ile Ala Asp Glu Val Tyr Met Glu Val Ile Val Gly Glu Glu Glu
290 295 300

Gly Thr Ser Leu Pro Glu Ile Gln Leu Glu Asp Ser Asp Val Asn Lys
305 310 315 320

Thr Val Val Pro Val Val Trp Ala Ala Ala Tyr Gly Asn Thr Leu Asp
325 330 335

Ser Ala Leu Glu Ser Arg Ser Ser Thr Ala Ala Gln Tyr Leu Gln Ile
340 345 350

Cys Asp Gly Ile Asn Thr Asn Lys Val Leu Lys Gln Lys Ala Lys Lys
355 360 365

Arg Arg Arg Gly Glu Thr Arg Gln Trp Gln Thr Ala Val Ile Ile Gly
370 375 380

Pro Asp Gly Gln Pro Leu Thr Val Tyr Pro Cys His Ile Cys Thr Lys
385 390 395 400

Lys Phe Lys Ser Arg Gly Phe Leu Lys Arg His Met Lys Asn His Pro
405 410 415

Asp His Leu Met Arg Lys Lys Tyr Gln Cys Thr Asp Cys Asp Phe Thr
420 425 430

Thr Asn Lys Lys Val Ser Phe His Asn His Leu Glu Ser His Lys Leu
435 440 445

Ile Asn Lys Val Asp Lys Thr His Glu Phe Thr Glu Tyr Thr Arg Arg
450 455 460

Tyr Arg Glu Ala Ser Pro Leu Ser Ser Asn Lys Leu Ile Leu Arg Asp
465 470 475 480

Lys Glu Pro Lys Met His Lys Cys Lys Tyr Cys Asp Tyr Glu Thr Ala
485 490 495

Glu Gln Gly Leu Leu Asn Arg His Leu Leu Ala Val His Ser Lys Asn
500 505 510

Phe Pro His Val Cys Val Glu Cys Gly Lys Gly Phe Arg His Pro Ser
515 520 525

Glu Leu Lys Lys His Met Arg Thr His Thr Gly Glu Lys Pro Tyr Gln
530 535 540

Cys Gln Tyr Cys Ile Phe Arg Cys Ala Asp Gln Ser Asn Leu Lys Thr
545 550 555 560

His Ile Lys Ser Lys His Gly Asn Asn Leu Pro Tyr Lys Cys Glu His
565 570 575

Cys Pro Gln Ala Phe Gly Asp Glu Arg Glu Leu Gln Arg His Leu Asp
580 585 590

Leu Phe Gln Gly His Lys Thr His Gln Cys Pro His Cys Asp His Lys
595 600 605

Ser Thr Asn Ser Ser Asp Leu Lys Arg His Ile Ile Ser Val His Thr
610 615 620

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Lys Asp Phe Pro His Lys Cys Glu Val Cys Asp Lys Gly Phe His Arg
625 630 635 640

Pro Ser Glu Leu Lys Lys His Ser Asp Ile His Lys Gly Arg Lys Ile
645 650 655

His Gln Cys Arg His Cys Asp Phe Lys Thr Ser Asp Pro Phe Ile Leu
660 665 670

Ser Gly His Ile Leu Ser Val His Thr Lys Asp Gln Pro Leu Lys Cys
675 680 685

Lys Arg Cys Lys Arg Gly Phe Arg Gln Gln Asn Glu Leu Lys Lys His
690 695 700

Met Lys Thr His Thr Gly Arg Lys Ile Tyr Gln Cys Glu Tyr Cys Glu
705 710 715 720

Tyr Ser Thr Thr Asp Ala Ser Gly Phe Lys Arg His Val Ile Ser Ile
725 730 735

His Thr Lys Asp Tyr Pro His Arg Cys Glu Phe Cys Lys Lys Gly Phe
740 745 750

Arg Arg Pro Ser Glu Lys Asn Gln His Ile Met Arg His His Lys Glu
755 760 765

Ala Leu Met
770

<210> 156
<211> 1390
<212> PRT
<213> Homo sapiens

<400> 156

Met Lys Ala Pro Ala Val Leu Ala Pro Gly Ile Leu Val Leu Leu Phe
1 5 10 15

Thr Leu Val Gln Arg Ser Asn Gly Glu Cys Lys Glu Ala Leu Ala Lys
20 25 30

Ser Glu Met Asn Val Asn Met Lys Tyr Gln Leu Pro Asn Phe Thr Ala
35 40 45

Glu Thr Pro Ile Gln Asn Val Ile Leu His Glu His His Ile Phe Leu
50 55 60

Gly Ala Thr Asn Tyr Ile Tyr Val Leu Asn Glu Glu Asp Leu Gln Lys
65 70 75 80

Val Ala Glu Tyr Lys Thr Gly Pro Val Leu Glu His Pro Asp Cys Phe
85 90 95

Pro Cys Gln Asp Cys Ser Ser Lys Ala Asn Leu Ser Gly Gly Val Trp
100 105 110

Lys Asp Asn Ile Asn Met Ala Leu Val Val Asp Thr Tyr Tyr Asp Asp
115 120 125

Gln Leu Ile Ser Cys Gly Ser Val Asn Arg Gly Thr Cys Gln Arg His
130 135 140

Val Phe Pro His Asn His Thr Ala Asp Ile Gln Ser Glu Val His Cys
145 150 155 160

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ile Phe Ser Pro Gln Ile Glu Glu Pro Ser Gln Cys Pro Asp Cys Val
165 170 175

Val Ser Ala Leu Gly Ala Lys Val Leu Ser Ser Val Lys Asp Arg Phe
180 185 190

Ile Asn Phe Phe Val Gly Asn Thr Ile Asn Ser Ser Tyr Phe Pro Asp
195 200 205

His Pro Leu His Ser Ile Ser Val Arg Arg Leu Lys Glu Thr Lys Asp
210 215 220

Gly Phe Met Phe Leu Thr Asp Gln Ser Tyr Ile Asp Val Leu Pro Glu
225 230 235 240

Phe Arg Asp Ser Tyr Pro Ile Lys Tyr Val His Ala Phe Glu Ser Asn
245 250 255

Asn Phe Ile Tyr Phe Leu Thr Val Gln Arg Glu Thr Leu Asp Ala Gln
260 265 270

Thr Phe His Thr Arg Ile Ile Arg Phe Cys Ser Ile Asn Ser Gly Leu
275 280 285

His Ser Tyr Met Glu Met Pro Leu Glu Cys Ile Leu Thr Glu Lys Arg
290 295 300

Lys Lys Arg Ser Thr Lys Lys Glu Val Phe Asn Ile Leu Gln Ala Ala
305 310 315 320

Tyr Val Ser Lys Pro Gly Ala Gln Leu Ala Arg Gln Ile Gly Ala Ser
325 330 335

Leu Asn Asp Asp Ile Leu Phe Gly Val Phe Ala Gln Ser Lys Pro Asp
340 345 350

Ser Ala Glu Pro Met Asp Arg Ser Ala Met Cys Ala Phe Pro Ile Lys
355 360 365

Tyr Val Asn Asp Phe Phe Asn Lys Ile Val Asn Lys Asn Asn Val Arg
370 375 380

Cys Leu Gln His Phe Tyr Gly Pro Asn His Glu His Cys Phe Asn Arg
385 390 395 400

Thr Leu Leu Arg Asn Ser Ser Gly Cys Glu Ala Arg Arg Asp Glu Tyr
405 410 415

Arg Thr Glu Phe Thr Thr Ala Leu Gln Arg Val Asp Leu Phe Met Gly
420 425 430

Gln Phe Ser Glu Val Leu Leu Thr Ser Ile Ser Thr Phe Ile Lys Gly
435 440 445

Asp Leu Thr Ile Ala Asn Leu Gly Thr Ser Glu Gly Arg Phe Met Gln
450 455 460

Val Val Val Ser Arg Ser Gly Pro Ser Thr Pro His Val Asn Phe Leu
465 470 475 480

Leu Asp Ser His Pro Val Ser Pro Glu Val Ile Val Glu His Thr Leu
485 490 495

Asn Gln Asn Gly Tyr Thr Leu Val Ile Thr Gly Lys Lys Ile Thr Lys

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 500 505 510

Ile Pro Leu Asn Gly Leu Gly Cys Arg His Phe Gln Ser Cys Ser Gln
 515 520 525

Cys Leu Ser Ala Pro Pro Phe Val Gln Cys Gly Trp Cys His Asp Lys
 530 535 540

Cys Val Arg Ser Glu Glu Cys Leu Ser Gly Thr Trp Thr Gln Gln Ile
 545 550 555 560

Cys Leu Pro Ala Ile Tyr Lys Val Phe Pro Asn Ser Ala Pro Leu Glu
 565 570 575

Gly Gly Thr Arg Leu Thr Ile Cys Gly Trp Asp Phe Gly Phe Arg Arg
 580 585 590

Asn Asn Lys Phe Asp Leu Lys Lys Thr Arg Val Leu Leu Gly Asn Glu
 595 600 605

Ser Cys Thr Leu Thr Leu Ser Glu Ser Thr Met Asn Thr Leu Lys Cys
 610 615 620

Thr Val Gly Pro Ala Met Asn Lys His Phe Asn Met Ser Ile Ile Ile
 625 630 635 640

Ser Asn Gly His Gly Thr Thr Gln Tyr Ser Thr Phe Ser Tyr Val Asp
 645 650 655

Pro Val Ile Thr Ser Ile Ser Pro Lys Tyr Gly Pro Met Ala Gly Gly
 660 665 670

Thr Leu Leu Thr Leu Thr Gly Asn Tyr Leu Asn Ser Gly Asn Ser Arg
 675 680 685

His Ile Ser Ile Gly Gly Lys Thr Cys Thr Leu Lys Ser Val Ser Asn
 690 695 700

Ser Ile Leu Glu Cys Tyr Thr Pro Ala Gln Thr Ile Ser Thr Glu Phe
 705 710 715 720

Ala Val Lys Leu Lys Ile Asp Leu Ala Asn Arg Glu Thr Ser Ile Phe
 725 730 735

Ser Tyr Arg Glu Asp Pro Ile Val Tyr Glu Ile His Pro Thr Lys Ser
 740 745 750

Phe Ile Ser Gly Gly Ser Thr Ile Thr Gly Val Gly Lys Asn Leu Asn
 755 760 765

Ser Val Ser Val Pro Arg Met Val Ile Asn Val His Glu Ala Gly Arg
 770 775 780

Asn Phe Thr Val Ala Cys Gln His Arg Ser Asn Ser Glu Ile Ile Cys
 785 790 795 800

Cys Thr Thr Pro Ser Leu Gln Gln Leu Asn Leu Gln Leu Pro Leu Lys
 805 810 815

Thr Lys Ala Phe Phe Met Leu Asp Gly Ile Leu Ser Lys Tyr Phe Asp
 820 825 830

Leu Ile Tyr Val His Asn Pro Val Phe Lys Pro Phe Glu Lys Pro Val
 835 840 845

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Met Ile Ser Met Gly Asn Glu Asn Val Leu Glu Ile Lys Gly Asn Asp
850 855 860

Ile Asp Pro Glu Ala Val Lys Gly Glu Val Leu Lys Val Gly Asn Lys
865 870 875 880

Ser Cys Glu Asn Ile His Leu His Ser Glu Ala Val Leu Cys Thr Val
885 890 895

Pro Asn Asp Leu Leu Lys Leu Asn Ser Glu Leu Asn Ile Glu Trp Lys
900 905 910

Gln Ala Ile Ser Ser Thr Val Leu Gly Lys Val Ile Val Gln Pro Asp
915 920 925

Gln Asn Phe Thr Gly Leu Ile Ala Gly Val Val Ser Ile Ser Thr Ala
930 935 940

Leu Leu Leu Leu Leu Gly Phe Phe Leu Trp Leu Lys Lys Arg Lys Gln
945 950 955 960

Ile Lys Asp Leu Gly Ser Glu Leu Val Arg Tyr Asp Ala Arg Val His
965 970 975

Thr Pro His Leu Asp Arg Leu Val Ser Ala Arg Ser Val Ser Pro Thr
980 985 990

Thr Glu Met Val Ser Asn Glu Ser Val Asp Tyr Arg Ala Thr Phe Pro
995 1000 1005

Glu Asp Gln Phe Pro Asn Ser Ser Gln Asn Gly Ser Cys Arg Gln
1010 1015 1020

Val Gln Tyr Pro Leu Thr Asp Met Ser Pro Ile Leu Thr Ser Gly
1025 1030 1035

Asp Ser Asp Ile Ser Ser Pro Leu Leu Gln Asn Thr Val His Ile
1040 1045 1050

Asp Leu Ser Ala Leu Asn Pro Glu Leu Val Gln Ala Val Gln His
1055 1060 1065

Val Val Ile Gly Pro Ser Ser Leu Ile Val His Phe Asn Glu Val
1070 1075 1080

Ile Gly Arg Gly His Phe Gly Cys Val Tyr His Gly Thr Leu Leu
1085 1090 1095

Asp Asn Asp Gly Lys Lys Ile His Cys Ala Val Lys Ser Leu Asn
1100 1105 1110

Arg Ile Thr Asp Ile Gly Glu Val Ser Gln Phe Leu Thr Glu Gly
1115 1120 1125

Ile Ile Met Lys Asp Phe Ser His Pro Asn Val Leu Ser Leu Leu
1130 1135 1140

Gly Ile Cys Leu Arg Ser Glu Gly Ser Pro Leu Val Val Leu Pro
1145 1150 1155

Tyr Met Lys His Gly Asp Leu Arg Asn Phe Ile Arg Asn Glu Thr
1160 1165 1170

His Asn Pro Thr Val Lys Asp Leu Ile Gly Phe Gly Leu Gln Val

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 1175 1180 1185

Ala Lys Gly Met Lys Tyr Leu Ala Ser Lys Lys Phe Val His Arg
 1190 1195 1200

Asp Leu Ala Ala Arg Asn Cys Met Leu Asp Glu Lys Phe Thr Val
 1205 1210 1215

Lys Val Ala Asp Phe Gly Leu Ala Arg Asp Met Tyr Asp Lys Glu
 1220 1225 1230

Tyr Tyr Ser Val His Asn Lys Thr Gly Ala Lys Leu Pro Val Lys
 1235 1240 1245

Trp Met Ala Leu Glu Ser Leu Gln Thr Gln Lys Phe Thr Thr Lys
 1250 1255 1260

Ser Asp Val Trp Ser Phe Gly Val Val Leu Trp Glu Leu Met Thr
 1265 1270 1275

Arg Gly Ala Pro Pro Tyr Pro Asp Val Asn Thr Phe Asp Ile Thr
 1280 1285 1290

Val Tyr Leu Leu Gln Gly Arg Arg Leu Leu Gln Pro Glu Tyr Cys
 1295 1300 1305

Pro Asp Pro Leu Tyr Glu Val Met Leu Lys Cys Trp His Pro Lys
 1310 1315 1320

Ala Glu Met Arg Pro Ser Phe Ser Glu Leu Val Ser Arg Ile Ser
 1325 1330 1335

Ala Ile Phe Ser Thr Phe Ile Gly Glu His Tyr Val His Val Asn
 1340 1345 1350

Ala Thr Tyr Val Asn Val Lys Cys Val Ala Pro Tyr Pro Ser Leu
 1355 1360 1365

Leu Ser Ser Glu Asp Asn Ala Asp Asp Glu Val Asp Thr Arg Pro
 1370 1375 1380

Ala Ser Phe Trp Glu Thr Ser
 1385 1390

<210> 157
 <211> 213
 <212> PRT
 <213> Homo sapiens

<400> 157

Met Thr Asp Ala Thr Val Ser Phe Ala Lys Asp Phe Leu Ala Gly Gly
 1 5 10 15

Val Ala Ala Ala Ile Ser Lys Met Ala Val Val Pro Ile Gln Arg Val
 20 25 30

Lys Leu Leu Leu Gln Val Gln His Ala Ser Lys Gln Val Thr Ala Asp
 35 40 45

Lys Gln Tyr Lys Gly Ile Ile Asp Cys Val Val Cys Ile Ser Lys Glu
 50 55 60

Gln Gly Val Leu Ser Phe Trp Arg Gly Asn Leu Ala Asn Val Ile Arg
 65 70 75 80

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Tyr Phe Pro Thr Gln Ala Phe Asn Phe Ala Phe Lys Asp Lys Tyr Lys
85 90 95

Gln Ile Phe Leu Gly Asp Val Asp Lys Arg Thr Gln Phe Trp Arg Tyr
100 105 110

Phe Glu Gly Asn Leu Thr Ser Gly Ser Ala Ala Gly Ala Thr Ser Leu
115 120 125

Cys Phe Val Tyr Pro Leu Asp Phe Ala Leu Thr Arg Leu Ala Ala Asn
130 135 140

Val Gly Lys Ala Gly Ala Glu Arg Glu Phe Arg Ser Leu Gly Asp Cys
145 150 155 160

Leu Val Lys Ile Tyr Lys Ser Asp Gly Ile Lys Gly Leu Tyr Gln Gly
165 170 175

Phe Asn Met Ser Val Gln Gly Ile Ile Ile Tyr Arg Ala Ala Tyr Phe
180 185 190

Ser Ile Tyr Asp Thr Ala Lys Gly Met Leu Pro Asp Pro Lys Asn Thr
195 200 205

His Ile Leu Ile Ser
210

<210> 158
<211> 608
<212> PRT
<213> Homo sapiens

<400> 158

Ser Gly Trp Glu Ser Tyr Tyr Lys Thr Glu Gly Asp Glu Glu Ala Glu
1 5 10 15

Glu Glu Gln Glu Glu Asn Leu Glu Ala Ser Gly Asp Tyr Lys Tyr Ser
20 25 30

Gly Arg Asp Ser Leu Ile Phe Leu Val Asp Ala Ser Lys Ala Met Phe
35 40 45

Glu Ser Gln Ser Glu Asp Glu Leu Thr Pro Phe Asp Met Ser Ile Gln
50 55 60

Cys Ile Gln Ser Val Tyr Ile Ser Lys Ile Ile Ser Ser Asp Arg Asp
65 70 75 80

Leu Leu Ala Val Val Phe Tyr Gly Thr Glu Lys Asp Lys Asn Ser Val
85 90 95

Asn Phe Lys Asn Ile Tyr Val Leu Gln Glu Leu Asp Asn Pro Gly Ala
100 105 110

Lys Arg Ile Leu Glu Leu Asp Gln Phe Lys Gly Gln Gln Gly Gln Lys
115 120 125

Arg Phe Gln Asp Met Met Gly His Gly Ser Asp Tyr Ser Leu Ser Glu
130 135 140

Val Leu Trp Val Cys Ala Asn Leu Phe Ser Asp Val Gln Phe Lys Met
145 150 155 160

Ser His Lys Arg Ile Met Leu Phe Thr Asn Glu Asp Asn Pro His Gly
165 170 175

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Asn Asp Ser Ala Lys Ala Ser Arg Ala Arg Thr Lys Ala Gly Asp Leu
180 185 190

Arg Asp Thr Gly Ile Phe Leu Asp Leu Met His Leu Lys Lys Pro Gly
195 200 205

Gly Phe Asp Ile Ser Leu Phe Tyr Arg Asp Ile Ile Ser Ile Ala Glu
210 215 220

Asp Glu Asp Leu Arg Val His Phe Glu Glu Ser Ser Lys Leu Glu Asp
225 230 235 240

Leu Leu Arg Lys Val Arg Ala Lys Glu Thr Arg Lys Arg Ala Leu Ser
245 250 255

Arg Leu Lys Leu Lys Leu Asn Lys Asp Ile Val Ile Ser Val Gly Ile
260 265 270

Tyr Asn Leu Val Gln Lys Ala Leu Lys Pro Pro Pro Ile Lys Leu Tyr
275 280 285

Arg Glu Thr Asn Glu Pro Val Lys Thr Lys Thr Arg Thr Phe Asn Thr
290 295 300

Ser Thr Gly Gly Leu Leu Leu Pro Ser Asp Thr Lys Arg Ser Gln Ile
305 310 315 320

Tyr Gly Ser Arg Gln Ile Ile Leu Glu Lys Glu Glu Thr Glu Glu Leu
325 330 335

Lys Arg Phe Asp Asp Pro Gly Leu Met Leu Met Gly Phe Lys Pro Leu
340 345 350

Val Leu Leu Lys Lys His His Tyr Leu Arg Pro Ser Leu Phe Val Tyr
355 360 365

Pro Glu Glu Ser Leu Val Ile Gly Ser Ser Thr Leu Phe Ser Ala Leu
370 375 380

Leu Ile Lys Cys Leu Glu Lys Glu Val Ala Ala Leu Cys Arg Tyr Thr
385 390 395 400

Pro Arg Arg Asn Ile Pro Pro Tyr Phe Val Ala Leu Val Pro Gln Glu
405 410 415

Glu Glu Leu Asp Asp Gln Lys Ile Gln Val Thr Pro Pro Gly Phe Gln
420 425 430

Leu Val Phe Leu Pro Phe Ala Asp Asp Lys Arg Lys Met Pro Phe Thr
435 440 445

Glu Lys Ile Met Ala Thr Pro Glu Gln Val Gly Lys Met Lys Ala Ile
450 455 460

Val Glu Lys Leu Arg Phe Thr Tyr Arg Ser Asp Ser Phe Glu Asn Pro
465 470 475 480

Val Leu Gln Gln His Phe Arg Asn Leu Glu Ala Leu Ala Leu Asp Leu
485 490 495

Met Glu Pro Glu Gln Ala Val Asp Leu Thr Leu Pro Lys Val Glu Ala
500 505 510

Met Asn Lys Arg Leu Gly Ser Leu Val Asp Glu Phe Lys Glu Leu Val

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 515 520 525

Tyr Pro Pro Asp Tyr Asn Pro Glu Gly Lys Val Thr Lys Arg Lys His
 530 535 540

Asp Asn Glu Gly Ser Gly Ser Lys Arg Pro Lys Val Glu Tyr Ser Glu
 545 550 555 560

Glu Glu Leu Lys Thr His Ile Ser Lys Gly Thr Leu Gly Lys Phe Thr
 565 570 575

Val Pro Met Leu Lys Glu Ala Cys Arg Ala Tyr Gly Leu Lys Ser Gly
 580 585 590

Leu Lys Lys Gln Glu Leu Leu Glu Ala Leu Thr Lys His Phe Gln Asp
 595 600 605

<210> 159
 <211> 168
 <212> PRT
 <213> Homo sapiens

<400> 159

Met Phe Gln Ile Pro Glu Phe Glu Pro Ser Glu Gln Glu Asp Ser Ser
 1 5 10 15

Ser Ala Glu Arg Gly Leu Gly Pro Ser Pro Ala Gly Asp Gly Pro Ser
 20 25 30

Gly Ser Gly Lys His His Arg Gln Ala Pro Gly Leu Leu Trp Asp Ala
 35 40 45

Ser His Gln Gln Glu Gln Pro Thr Ser Ser Ser His His Gly Gly Ala
 50 55 60

Gly Ala Val Glu Ile Arg Ser Arg His Ser Ser Tyr Pro Ala Gly Thr
 65 70 75 80

Glu Asp Asp Glu Gly Met Gly Glu Glu Pro Ser Pro Phe Arg Gly Arg
 85 90 95

Ser Arg Ser Ala Pro Pro Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg
 100 105 110

Glu Leu Arg Arg Met Ser Asp Glu Phe Val Asp Ser Phe Lys Lys Gly
 115 120 125

Leu Pro Arg Pro Lys Ser Ala Gly Thr Ala Thr Gln Met Arg Gln Ser
 130 135 140

Ser Ser Trp Thr Arg Val Phe Gln Ser Trp Trp Asp Arg Asn Leu Gly
 145 150 155 160

Arg Gly Ser Ser Ala Pro Ser Gln
 165

<210> 160
 <211> 192
 <212> PRT
 <213> Homo sapiens

<400> 160

Met Asp Gly Ser Gly Glu Gln Pro Arg Gly Gly Gly Pro Thr Ser Ser
 1 5 10 15

Glu Gln Ile Met Lys Thr Gly Ala Leu Leu Leu Gln Gly Phe Ile Gln

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 20 25 30

Asp Arg Ala Gly Arg Met Gly Gly Glu Ala Pro Glu Leu Ala Leu Asp
 35 40 45

Pro Val Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser Glu Cys Leu Lys
 50 55 60

Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Glu Leu Gln Arg Met Ile
 65 70 75 80

Ala Ala Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe Arg Val Ala
 85 90 95

Ala Asp Met Phe Ser Asp Gly Asn Phe Asn Trp Gly Arg Val Val Ala
 100 105 110

Leu Phe Tyr Phe Ala Ser Lys Leu Val Leu Lys Ala Leu Cys Thr Lys
 115 120 125

Val Pro Glu Leu Ile Arg Thr Ile Met Gly Trp Thr Leu Asp Phe Leu
 130 135 140

Arg Glu Arg Leu Leu Gly Trp Ile Gln Asp Gln Gly Gly Trp Asp Gly
 145 150 155 160

Leu Leu Ser Tyr Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe
 165 170 175

Val Ala Gly Val Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly
 180 185 190

<210> 161
 <211> 239
 <212> PRT
 <213> Homo sapiens

<400> 161

Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
 1 5 10 15

Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
 20 25 30

Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
 35 40 45

Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
 50 55 60

Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
 65 70 75 80

Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Thr
 85 90 95

Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Arg Asp Phe
 100 105 110

Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
 115 120 125

Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
 130 135 140

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
 145 150 155 160

Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
 165 170 175

Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
 180 185 190

Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro
 195 200 205

Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala
 210 215 220

Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr Leu Gly His Lys
 225 230 235

<210> 162
 <211> 160
 <212> PRT
 <213> Homo sapiens

<400> 162

Met Ser Glu Val Arg Pro Leu Ser Arg Asp Ile Leu Met Glu Thr Leu
 1 5 10 15

Leu Tyr Glu Gln Leu Leu Glu Pro Pro Thr Met Glu Val Leu Gly Met
 20 25 30

Thr Asp Ser Glu Glu Asp Leu Asp Pro Met Glu Asp Phe Asp Ser Leu
 35 40 45

Glu Cys Met Glu Gly Ser Asp Ala Leu Ala Leu Arg Leu Ala Cys Ile
 50 55 60

Gly Asp Glu Met Asp Val Ser Leu Arg Ala Pro Arg Leu Ala Gln Leu
 65 70 75 80

Ser Glu Val Ala Met His Ser Leu Gly Leu Ala Phe Ile Tyr Asp Gln
 85 90 95

Thr Glu Asp Ile Arg Asp Val Leu Arg Ser Phe Met Asp Gly Phe Thr
 100 105 110

Thr Leu Lys Glu Asn Ile Met Arg Phe Trp Arg Ser Pro Asn Pro Gly
 115 120 125

Ser Trp Val Ser Cys Glu Gln Val Leu Leu Ala Leu Leu Leu Leu Leu
 130 135 140

Ala Leu Leu Leu Pro Leu Leu Ser Gly Gly Leu His Leu Leu Leu Lys
 145 150 155 160

<210> 163
 <211> 198
 <212> PRT
 <213> Homo sapiens

<400> 163

Met Ala Lys Gln Pro Ser Asp Val Ser Ser Glu Cys Asp Arg Glu Gly
 1 5 10 15

Arg Gln Leu Gln Pro Ala Glu Arg Pro Pro Gln Leu Arg Pro Gly Ala
 20 25 30

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Pro Thr Ser Leu Gln Thr Glu Pro Gln Gly Asn Pro Glu Gly Asn His
 35 40 45

Gly Gly Glu Gly Asp Ser Cys Pro His Gly Ser Pro Gln Gly Pro Leu
 50 55 60

Ala Pro Pro Ala Ser Pro Gly Pro Phe Ala Thr Arg Ser Pro Leu Phe
 65 70 75 80

Ile Phe Met Arg Arg Ser Ser Leu Leu Ser Arg Ser Ser Ser Gly Tyr
 85 90 95

Phe Ser Phe Asp Thr Asp Arg Ser Pro Ala Pro Met Ser Cys Asp Lys
 100 105 110

Ser Thr Gln Thr Pro Ser Pro Pro Cys Gln Ala Phe Asn His Tyr Leu
 115 120 125

Ser Ala Met Ala Ser Met Arg Gln Ala Glu Pro Ala Asp Met Arg Pro
 130 135 140

Glu Ile Trp Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe Asn
 145 150 155 160

Ala Tyr Tyr Ala Arg Arg Val Phe Leu Asn Asn Tyr Gln Ala Ala Glu
 165 170 175

Asp His Pro Arg Met Val Ile Leu Arg Leu Leu Arg Tyr Ile Val Arg
 180 185 190

Leu Val Trp Arg Met His
 195

<210> 164
 <211> 404
 <212> PRT
 <213> Homo sapiens

<400> 164

Met Glu Ala Gly Glu Glu Pro Leu Leu Leu Ala Glu Leu Lys Pro Gly
 1 5 10 15

Arg Pro His Gln Phe Asp Trp Lys Ser Ser Cys Glu Thr Trp Ser Val
 20 25 30

Ala Phe Ser Pro Asp Gly Ser Trp Phe Ala Trp Ser Gln Gly His Cys
 35 40 45

Ile Val Lys Leu Ile Pro Trp Pro Leu Glu Glu Gln Phe Ile Pro Lys
 50 55 60

Gly Phe Glu Ala Lys Ser Arg Ser Ser Lys Asn Glu Thr Lys Gly Arg
 65 70 75 80

Gly Ser Pro Lys Glu Lys Thr Leu Asp Cys Gly Gln Ile Val Trp Gly
 85 90 95

Leu Ala Phe Ser Pro Trp Pro Ser Pro Pro Ser Arg Lys Leu Trp Ala
 100 105 110

Arg His His Pro Gln Val Pro Asp Val Ser Cys Leu Val Leu Ala Thr
 115 120 125

Gly Leu Asn Asp Gly Gln Ile Lys Ile Trp Glu Val Gln Thr Gly Leu
 130 135 140

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Leu Leu Leu Asn Leu Ser Gly His Gln Asp Val Val Arg Asp Leu Ser
145 150 155 160

Phe Thr Pro Ser Gly Ser Leu Ile Leu Val Ser Ala Ser Arg Asp Lys
165 170 175

Thr Leu Arg Ile Trp Asp Leu Asn Lys His Gly Lys Gln Ile Gln Val
180 185 190

Leu Ser Gly His Leu Gln Trp Val Tyr Cys Cys Ser Ile Ser Pro Asp
195 200 205

Cys Ser Met Leu Cys Ser Ala Ala Gly Glu Lys Ser Val Phe Leu Trp
210 215 220

Ser Met Arg Ser Tyr Thr Leu Ile Arg Lys Leu Glu Gly His Gln Ser
225 230 235 240

Ser Val Val Ser Cys Asp Phe Ser Pro Asp Ser Ala Leu Leu Val Thr
245 250 255

Ala Ser Tyr Asp Thr Asn Val Ile Met Trp Asp Pro Tyr Thr Gly Glu
260 265 270

Arg Leu Arg Ser Leu His His Thr Gln Val Asp Pro Ala Met Asp Asp
275 280 285

Ser Asp Val His Ile Ser Ser Leu Arg Ser Val Cys Phe Ser Pro Glu
290 295 300

Gly Leu Tyr Leu Ala Thr Val Ala Asp Asp Arg Leu Leu Arg Ile Trp
305 310 315 320

Ala Leu Glu Leu Lys Thr Pro Ile Ala Phe Ala Pro Met Thr Asn Gly
325 330 335

Leu Cys Cys Thr Phe Phe Pro His Gly Gly Val Ile Ala Thr Gly Thr
340 345 350

Arg Asp Gly His Val Gln Phe Trp Thr Ala Pro Arg Val Leu Ser Ser
355 360 365

Leu Lys His Leu Cys Arg Lys Ala Leu Arg Ser Phe Leu Thr Thr Tyr
370 375 380

Gln Val Leu Ala Leu Pro Ile Pro Lys Lys Met Lys Glu Phe Leu Thr
385 390 395 400

Tyr Arg Thr Phe

<210> 165
<211> 1453
<212> PRT
<213> Homo sapiens

<400> 165

Met Ile Lys Cys Leu Ser Val Glu Val Gln Ala Lys Leu Arg Ser Gly
1 5 10 15

Leu Ala Ile Ser Ser Leu Gly Gln Cys Val Glu Glu Leu Ala Leu Asn
20 25 30

Ser Ile Asp Ala Glu Ala Lys Cys Val Ala Val Arg Val Asn Met Glu
35 40 45

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Thr Phe Gln Val Gln Val Ile Asp Asn Gly Phe Gly Met Gly Ser Asp
 50 55 60
 Asp Val Glu Lys Val Gly Asn Arg Tyr Phe Thr Ser Lys Cys His Ser
 65 70 75 80
 Val Gln Asp Leu Glu Asn Pro Arg Phe Tyr Gly Phe Arg Gly Glu Ala
 85 90 95
 Leu Ala Asn Ile Ala Asp Met Ala Ser Ala Val Glu Ile Ser Ser Lys
 100 105 110
 Lys Asn Arg Thr Met Lys Thr Phe Val Lys Leu Phe Gln Ser Gly Lys
 115 120 125
 Ala Leu Lys Ala Cys Glu Ala Asp Val Thr Arg Ala Ser Ala Gly Thr
 130 135 140
 Thr Val Thr Val Tyr Asn Leu Phe Tyr Gln Leu Pro Val Arg Arg Lys
 145 150 155 160
 Cys Met Asp Pro Arg Leu Glu Phe Glu Lys Val Arg Gln Arg Ile Glu
 165 170 175
 Ala Leu Ser Leu Met His Pro Ser Ile Ser Phe Ser Leu Arg Asn Asp
 180 185 190
 Val Ser Gly Ser Met Val Leu Gln Leu Pro Lys Thr Lys Asp Val Cys
 195 200 205
 Ser Arg Phe Cys Gln Ile Tyr Gly Leu Gly Lys Ser Gln Lys Leu Arg
 210 215 220
 Glu Ile Ser Phe Lys Tyr Lys Glu Phe Glu Leu Ser Gly Tyr Ile Ser
 225 230 235 240
 Ser Glu Ala His Tyr Asn Lys Asn Met Gln Phe Leu Phe Val Asn Lys
 245 250 255
 Arg Leu Val Leu Arg Thr Lys Leu His Lys Leu Ile Asp Phe Leu Leu
 260 265 270
 Arg Lys Glu Ser Ile Ile Cys Lys Pro Lys Asn Gly Pro Thr Ser Arg
 275 280 285
 Gln Met Asn Ser Ser Leu Arg His Arg Ser Thr Pro Glu Leu Tyr Gly
 290 295 300
 Ile Tyr Val Ile Asn Val Gln Cys Gln Phe Cys Glu Tyr Asp Val Cys
 305 310 315 320
 Met Glu Pro Ala Lys Thr Leu Ile Glu Phe Gln Asn Trp Asp Thr Leu
 325 330 335
 Leu Phe Cys Ile Gln Glu Gly Val Lys Met Phe Leu Lys Gln Glu Lys
 340 345 350
 Leu Phe Val Glu Leu Ser Gly Glu Asp Ile Lys Glu Phe Ser Glu Asp
 355 360 365
 Asn Gly Phe Ser Leu Phe Asp Ala Thr Leu Gln Lys Arg Val Thr Ser
 370 375 380

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Asp Glu Arg Ser Asn Phe Gln Glu Ala Cys Asn Asn Ile Leu Asp Ser
385 390 395 400

Tyr Glu Met Phe Asn Leu Gln Ser Lys Ala Val Lys Arg Lys Thr Thr
405 410 415

Ala Glu Asn Val Asn Thr Gln Ser Ser Arg Asp Ser Glu Ala Thr Arg
420 425 430

Lys Asn Thr Asn Asp Ala Phe Leu Tyr Ile Tyr Glu Ser Gly Gly Pro
435 440 445

Gly His Ser Lys Met Thr Glu Pro Ser Leu Gln Asn Lys Asp Ser Ser
450 455 460

Cys Ser Glu Ser Lys Met Leu Glu Gln Glu Thr Ile Val Ala Ser Glu
465 470 475 480

Ala Gly Glu Asn Glu Lys His Lys Lys Ser Phe Leu Glu His Ser Ser
485 490 495

Leu Glu Asn Pro Cys Gly Thr Ser Leu Glu Met Phe Leu Ser Pro Phe
500 505 510

Gln Thr Pro Cys His Phe Glu Glu Ser Gly Gln Asp Leu Glu Ile Trp
515 520 525

Lys Glu Ser Thr Thr Val Asn Gly Met Ala Ala Asn Ile Leu Lys Asn
530 535 540

Asn Arg Ile Gln Asn Gln Pro Lys Arg Phe Lys Asp Ala Thr Glu Val
545 550 555 560

Gly Cys Gln Pro Leu Pro Phe Ala Thr Thr Leu Trp Gly Val His Ser
565 570 575

Ala Gln Thr Glu Lys Glu Lys Lys Lys Glu Ser Ser Asn Cys Gly Arg
580 585 590

Arg Asn Val Phe Ser Tyr Gly Arg Val Lys Leu Cys Ser Thr Gly Phe
595 600 605

Ile Thr His Val Val Gln Asn Glu Lys Thr Lys Ser Thr Glu Thr Glu
610 615 620

His Ser Phe Lys Asn Tyr Val Arg Pro Gly Pro Thr Arg Ala Gln Glu
625 630 635 640

Thr Phe Gly Asn Arg Thr Arg His Ser Val Glu Thr Pro Asp Ile Lys
645 650 655

Asp Leu Ala Ser Thr Leu Ser Lys Glu Ser Gly Gln Leu Pro Asn Lys
660 665 670

Lys Asn Cys Arg Thr Asn Ile Ser Tyr Gly Leu Glu Asn Glu Pro Thr
675 680 685

Ala Thr Tyr Thr Met Phe Ser Ala Phe Gln Glu Gly Ser Lys Lys Ser
690 695 700

Gln Thr Asp Cys Ile Leu Ser Asp Thr Ser Pro Ser Phe Pro Trp Tyr
705 710 715 720

Arg His Val Ser Asn Asp Ser Arg Lys Thr Asp Lys Leu Ile Gly Phe
725 730 735

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ser Lys Pro Ile Val Arg Lys Lys Leu Ser Leu Ser Ser Gln Leu Gly
740 745 750

Ser Leu Glu Lys Phe Lys Arg Gln Tyr Gly Lys Val Glu Asn Pro Leu
755 760 765

Asp Thr Glu Val Glu Glu Ser Asn Gly Val Thr Thr Asn Leu Ser Leu
770 775 780

Gln Val Glu Pro Asp Ile Leu Leu Lys Asp Lys Asn Arg Leu Glu Asn
785 790 795 800

Ser Asp Val Cys Lys Ile Thr Thr Met Glu His Ser Asp Ser Asp Ser
805 810 815

Ser Cys Gln Pro Ala Ser His Ile Leu Asp Ser Glu Lys Phe Pro Phe
820 825 830

Ser Lys Asp Glu Asp Cys Leu Glu Gln Gln Met Pro Ser Leu Arg Glu
835 840 845

Ser Pro Met Thr Leu Lys Glu Leu Ser Leu Phe Asn Arg Lys Pro Leu
850 855 860

Asp Leu Glu Lys Ser Ser Glu Ser Leu Ala Ser Lys Leu Ser Arg Leu
865 870 875 880

Lys Gly Ser Glu Arg Glu Thr Gln Thr Met Gly Met Met Ser Arg Phe
885 890 895

Asn Glu Leu Pro Asn Ser Asp Ser Ser Arg Lys Asp Ser Lys Leu Cys
900 905 910

Ser Val Leu Thr Gln Asp Phe Cys Met Leu Phe Asn Asn Lys His Glu
915 920 925

Lys Thr Glu Asn Gly Val Ile Pro Thr Ser Asp Ser Ala Thr Gln Asp
930 935 940

Asn Ser Phe Asn Lys Asn Ser Lys Thr His Ser Asn Ser Asn Thr Thr
945 950 955 960

Glu Asn Cys Val Ile Ser Glu Thr Pro Leu Val Leu Pro Tyr Asn Asn
965 970 975

Ser Lys Val Thr Gly Lys Asp Ser Asp Val Leu Ile Arg Ala Ser Glu
980 985 990

Gln Gln Ile Gly Ser Leu Asp Ser Pro Ser Gly Met Leu Met Asn Pro
995 1000 1005

Val Glu Asp Ala Thr Gly Asp Gln Asn Gly Ile Cys Phe Gln Ser
1010 1015 1020

Glu Glu Ser Lys Ala Arg Ala Cys Ser Glu Thr Glu Glu Ser Asn
1025 1030 1035

Thr Cys Cys Ser Asp Trp Gln Arg His Phe Asp Val Ala Leu Gly
1040 1045 1050

Arg Met Val Tyr Val Asn Lys Met Thr Gly Leu Ser Thr Phe Ile
1055 1060 1065

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ala Pro Thr Glu Asp Ile Gln Ala Ala Cys Thr Lys Asp Leu Thr
 1070 1075 1080

Thr Val Ala Val Asp Val Val Leu Glu Asn Gly Ser Gln Tyr Arg
 1085 1090 1095

Cys Gln Pro Phe Arg Ser Asp Leu Val Leu Pro Phe Leu Pro Arg
 1100 1105 1110

Ala Arg Ala Glu Arg Thr Val Met Arg Gln Asp Asn Arg Asp Thr
 1115 1120 1125

Val Asp Asp Thr Val Ser Ser Glu Ser Leu Gln Ser Leu Phe Ser
 1130 1135 1140

Glu Trp Asp Asn Pro Val Phe Ala Arg Tyr Pro Glu Val Ala Val
 1145 1150 1155

Asp Val Ser Ser Gly Gln Ala Glu Ser Leu Ala Val Lys Ile His
 1160 1165 1170

Asn Ile Leu Tyr Pro Tyr Arg Phe Thr Lys Gly Met Ile His Ser
 1175 1180 1185

Met Gln Val Leu Gln Gln Val Asp Asn Lys Phe Ile Ala Cys Leu
 1190 1195 1200

Met Ser Thr Lys Thr Glu Glu Asn Gly Glu Ala Gly Gly Asn Leu
 1205 1210 1215

Leu Val Leu Val Asp Gln His Ala Ala His Glu Arg Ile Arg Leu
 1220 1225 1230

Glu Gln Leu Ile Ile Asp Ser Tyr Glu Lys Gln Gln Ala Gln Gly
 1235 1240 1245

Ser Gly Arg Lys Lys Leu Leu Ser Ser Thr Leu Ile Pro Pro Leu
 1250 1255 1260

Glu Ile Thr Val Thr Glu Glu Gln Arg Arg Leu Leu Trp Cys Tyr
 1265 1270 1275

His Lys Asn Leu Glu Asp Leu Gly Leu Glu Phe Val Phe Pro Asp
 1280 1285 1290

Thr Ser Asp Ser Leu Val Leu Val Gly Lys Val Pro Leu Cys Phe
 1295 1300 1305

Val Glu Arg Glu Ala Asn Glu Leu Arg Arg Gly Arg Ser Thr Val
 1310 1315 1320

Thr Lys Ser Ile Val Glu Glu Phe Ile Arg Glu Gln Leu Glu Leu
 1325 1330 1335

Leu Gln Thr Thr Gly Gly Ile Gln Gly Thr Leu Pro Leu Thr Val
 1340 1345 1350

Gln Lys Val Leu Ala Ser Gln Ala Cys His Gly Ala Ile Lys Phe
 1355 1360 1365

Asn Asp Gly Leu Ser Leu Gln Glu Ser Cys Arg Leu Ile Glu Ala
 1370 1375 1380

Leu Ser Ser Cys Gln Leu Pro Phe Gln Cys Ala His Gly Arg Pro
 1385 1390 1395

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ser Met Leu Pro Leu Ala Asp Ile Asp His Leu Glu Gln Glu Lys
 1400 1405 1410

Gln Ile Lys Pro Asn Leu Thr Lys Leu Arg Lys Met Ala Gln Ala
 1415 1420 1425

Trp Arg Leu Phe Gly Lys Ala Glu Cys Asp Thr Arg Gln Ser Leu
 1430 1435 1440

Gln Gln Ser Met Pro Pro Cys Glu Pro Pro
 1445 1450

<210> 166
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 166

Ser Asn Val Pro His Lys Ser Ser Leu Pro Glu Gly Ile Arg Pro Gly
 1 5 10 15

Thr Val Leu Arg Ile Arg Gly Leu Val Pro Pro Asn Ala Ser Arg Phe
 20 25 30

His Val Asn Leu Leu Cys Gly Glu Glu Gln Gly Ser Asp Ala Ala Leu
 35 40 45

His Phe Asn Pro Arg Leu Asp Thr Ser Glu Val Val Phe Asn Ser Lys
 50 55 60

Glu Gln Gly Ser Trp Gly Arg Glu Glu Arg Gly Pro Gly Val Pro Phe
 65 70 75 80

Gln Arg Gly Gln Pro Phe Glu Val Leu Ile Ile Ala Ser Asp Asp Gly
 85 90 95

Phe Lys Ala Val Val Gly Asp Ala Gln Tyr His His Phe Arg His Arg
 100 105 110

Leu Pro Leu Ala Arg Val Arg Leu Val Glu Val Gly Gly Asp Val Gln
 115 120 125

Leu Asp Ser Val Arg Ile Phe
 130 135

<210> 167
 <211> 373
 <212> PRT
 <213> Homo sapiens

<400> 167

Met Thr Thr Ser Ala Ser Ser His Leu Asn Lys Gly Ile Lys Gln Val
 1 5 10 15

Tyr Met Ser Leu Pro Gln Gly Glu Lys Val Gln Ala Met Tyr Ile Trp
 20 25 30

Ile Asp Gly Thr Gly Glu Gly Leu Arg Cys Lys Thr Arg Thr Leu Asp
 35 40 45

Ser Glu Pro Lys Cys Val Glu Glu Leu Pro Glu Trp Asn Phe Asp Gly
 50 55 60

Ser Ser Thr Leu Gln Ser Glu Gly Ser Asn Ser Asp Met Tyr Leu Val
 65 70 75 80

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Pro Ala Ala Met Phe Arg Asp Pro Phe Arg Lys Asp Pro Asn Lys Leu
 85 90 95

Val Leu Cys Glu Val Phe Lys Tyr Asn Arg Arg Pro Ala Glu Thr Asn
 100 105 110

Leu Arg His Thr Cys Lys Arg Ile Met Asp Met Val Ser Asn Gln His
 115 120 125

Pro Trp Phe Gly Met Glu Gln Glu Tyr Thr Leu Met Gly Thr Asp Gly
 130 135 140

His Pro Phe Gly Trp Pro Ser Asn Gly Phe Pro Gly Pro Gln Gly Pro
 145 150 155 160

Tyr Tyr Cys Gly Val Gly Ala Asp Arg Ala Tyr Gly Arg Asp Ile Val
 165 170 175

Glu Ala His Tyr Arg Ala Cys Leu Tyr Ala Gly Val Lys Ile Ala Gly
 180 185 190

Thr Asn Ala Glu Val Met Pro Ala Gln Trp Glu Phe Gln Ile Gly Pro
 195 200 205

Cys Glu Gly Ile Ser Met Gly Asp His Leu Trp Val Ala Arg Phe Ile
 210 215 220

Leu His Arg Val Cys Glu Asp Phe Gly Val Ile Ala Thr Phe Asp Pro
 225 230 235 240

Lys Pro Ile Pro Gly Asn Trp Asn Gly Ala Gly Cys His Thr Asn Phe
 245 250 255

Ser Thr Lys Ala Met Arg Glu Glu Asn Gly Leu Lys Tyr Ile Glu Glu
 260 265 270

Ala Ile Glu Lys Leu Ser Lys Arg His Gln Tyr His Ile Arg Ala Tyr
 275 280 285

Asp Pro Lys Gly Gly Leu Asp Asn Ala Arg Arg Leu Thr Gly Phe His
 290 295 300

Glu Thr Ser Asn Ile Asn Asp Phe Ser Ala Gly Val Ala Asn Arg Ser
 305 310 315 320

Ala Ser Ile Arg Ile Pro Arg Thr Val Gly Gln Glu Lys Lys Gly Tyr
 325 330 335

Phe Glu Asp Arg Arg Pro Ser Ala Asn Cys Asp Pro Phe Ser Val Thr
 340 345 350

Glu Ala Leu Ile Arg Thr Cys Leu Leu Asn Glu Thr Gly Asp Glu Pro
 355 360 365

Phe Gln Tyr Lys Asn
 370

<210> 168
 <211> 387
 <212> PRT
 <213> Homo sapiens

<400> 168

Met Pro Gly His Leu Gln Glu Gly Phe Gly Cys Val Val Thr Asn Arg

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 1 5 10 15

Phe Asp Gln Leu Phe Asp Asp Glu Ser Asp Pro Phe Glu Val Leu Lys
 20 25 30

Ala Ala Glu Asn Lys Lys Lys Glu Ala Gly Gly Gly Gly Val Gly Gly
 35 40 45

Pro Gly Ala Lys Ser Ala Ala Gln Ala Ala Ala Gln Thr Asn Ser Asn
 50 55 60

Ala Ala Gly Lys Gln Leu Arg Lys Glu Ser Gln Lys Asp Arg Lys Asn
 65 70 75 80

Pro Leu Pro Pro Ser Val Gly Val Val Asp Lys Lys Glu Glu Thr Gln
 85 90 95

Pro Pro Val Ala Leu Lys Lys Glu Gly Ile Arg Arg Val Gly Arg Arg
 100 105 110

Pro Asp Gln Gln Leu Gln Gly Glu Gly Lys Ile Ile Asp Arg Arg Pro
 115 120 125

Glu Arg Arg Pro Pro Arg Glu Arg Arg Phe Glu Lys Pro Leu Glu Glu
 130 135 140

Lys Gly Glu Gly Gly Glu Phe Ser Val Asp Arg Pro Ile Ile Asp Arg
 145 150 155 160

Pro Ile Arg Gly Arg Gly Gly Leu Gly Arg Gly Arg Gly Gly Arg Gly
 165 170 175

Arg Gly Met Gly Arg Gly Asp Gly Phe Asp Ser Arg Gly Lys Arg Glu
 180 185 190

Phe Asp Arg His Ser Gly Ser Asp Arg Ser Gly Leu Lys His Glu Asp
 195 200 205

Lys Arg Gly Gly Ser Gly Ser His Asn Trp Gly Thr Val Lys Asp Glu
 210 215 220

Leu Thr Asp Leu Asp Gln Ser Asn Val Thr Glu Glu Thr Pro Glu Gly
 225 230 235 240

Glu Glu His His Pro Val Ala Asp Thr Glu Asn Lys Glu Asn Glu Val
 245 250 255

Glu Glu Val Lys Glu Glu Gly Pro Lys Glu Met Thr Leu Asp Glu Trp
 260 265 270

Lys Ala Ile Gln Asn Lys Asp Arg Ala Lys Val Glu Phe Asn Ile Arg
 275 280 285

Lys Pro Asn Glu Gly Ala Asp Gly Gln Trp Lys Lys Gly Phe Val Leu
 290 295 300

His Lys Ser Lys Ser Glu Glu Ala His Ala Glu Asp Ser Val Met Asp
 305 310 315 320

His His Phe Arg Lys Pro Ala Asn Asp Ile Thr Ser Gln Leu Glu Ile
 325 330 335

Asn Phe Gly Asp Leu Gly Arg Pro Gly Arg Gly Gly Arg Gly Gly Arg
 340 345 350

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Gly Gly Arg Gly Arg Gly Gly Arg Pro Asn Arg Gly Ser Arg Thr Asp
355 360 365

Lys Ser Ser Ala Ser Ala Pro Asp Val Asp Asp Pro Glu Ala Phe Pro
370 375 380

Ala Leu Ala
385

<210> 169
<211> 894
<212> PRT
<213> Homo sapiens

<400> 169

Met Arg Pro Met Arg Ile Phe Val Asn Asp Asp Arg His Val Met Ala
1 5 10 15

Lys His Ser Ser Val Tyr Pro Thr Gln Glu Glu Leu Glu Ala Val Gln
20 25 30

Asn Met Val Ser His Thr Glu Arg Ala Leu Lys Ala Val Ser Asp Trp
35 40 45

Ile Asp Glu Gln Glu Lys Gly Ser Ser Glu Gln Ala Glu Ser Asp Asn
50 55 60

Met Asp Val Pro Pro Glu Asp Asp Ser Lys Glu Gly Ala Gly Glu Gln
65 70 75 80

Lys Thr Glu His Met Thr Arg Thr Leu Arg Gly Val Met Arg Val Gly
85 90 95

Leu Val Ala Lys Cys Leu Leu Leu Lys Gly Asp Leu Asp Leu Glu Leu
100 105 110

Val Leu Leu Cys Lys Glu Lys Pro Thr Thr Ala Leu Leu Asp Lys Val
115 120 125

Ala Asp Asn Leu Ala Ile Gln Leu Ala Ala Val Thr Glu Asp Lys Tyr
130 135 140

Glu Ile Leu Gln Ser Val Asp Asp Ala Ala Ile Val Ile Lys Asn Thr
145 150 155 160

Lys Glu Pro Pro Leu Ser Leu Thr Ile His Leu Thr Ser Pro Val Val
165 170 175

Arg Glu Glu Met Glu Lys Val Leu Ala Gly Glu Thr Leu Ser Val Asn
180 185 190

Asp Pro Pro Asp Val Leu Asp Arg Gln Lys Cys Leu Ala Ala Leu Ala
195 200 205

Ser Leu Arg His Ala Lys Trp Phe Gln Ala Arg Ala Asn Gly Leu Lys
210 215 220

Ser Cys Val Ile Val Ile Arg Val Leu Arg Asp Leu Cys Thr Arg Val
225 230 235 240

Pro Thr Trp Gly Pro Leu Arg Gly Trp Pro Leu Glu Leu Leu Cys Glu
245 250 255

Lys Ser Ile Gly Thr Ala Asn Arg Pro Met Gly Ala Gly Glu Ala Leu
260 265 270

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Arg Arg Val Leu Glu Cys Leu Ala Ser Gly Ile Val Met Pro Asp Gly
275 280 285

Ser Gly Ile Tyr Asp Pro Cys Glu Lys Glu Ala Thr Asp Ala Ile Gly
290 295 300

His Leu Asp Arg Gln Gln Arg Glu Asp Ile Thr Gln Ser Ala Gln His
305 310 315 320

Ala Leu Arg Leu Ala Ala Phe Gly Gln Leu His Lys Val Leu Gly Met
325 330 335

Asp Pro Leu Pro Ser Lys Met Pro Lys Lys Pro Lys Asn Glu Asn Pro
340 345 350

Val Asp Tyr Thr Val Gln Ile Pro Pro Ser Thr Thr Tyr Ala Ile Thr
355 360 365

Pro Met Lys Arg Pro Met Glu Glu Asp Gly Glu Glu Lys Ser Pro Ser
370 375 380

Lys Lys Lys Lys Lys Ile Gln Lys Lys Glu Glu Lys Ala Glu Pro Pro
385 390 395 400

Gln Ala Met Asn Ala Leu Met Arg Leu Asn Gln Leu Lys Pro Gly Leu
405 410 415

Gln Tyr Lys Leu Val Ser Gln Thr Gly Pro Val His Ala Pro Ile Phe
420 425 430

Thr Met Ser Val Glu Val Asp Gly Asn Ser Phe Glu Ala Ser Gly Pro
435 440 445

Ser Lys Lys Thr Ala Lys Leu His Val Ala Val Lys Val Leu Gln Asp
450 455 460

Met Gly Leu Pro Thr Gly Ala Glu Gly Arg Asp Ser Ser Lys Gly Glu
465 470 475 480

Asp Ser Ala Glu Glu Thr Glu Ala Lys Pro Ala Val Val Ala Pro Ala
485 490 495

Pro Val Val Glu Ala Val Ser Thr Pro Ser Ala Ala Phe Pro Ser Asp
500 505 510

Ala Thr Ala Glu Gln Gly Pro Ile Leu Thr Lys His Gly Lys Asn Pro
515 520 525

Val Met Glu Leu Asn Glu Lys Arg Arg Gly Leu Lys Tyr Glu Leu Ile
530 535 540

Ser Glu Thr Gly Gly Ser His Asp Lys Arg Phe Val Met Glu Val Glu
545 550 555 560

Val Asp Gly Gln Lys Phe Gln Gly Ala Gly Ser Asn Lys Lys Val Ala
565 570 575

Lys Ala Tyr Ala Ala Leu Ala Ala Leu Glu Lys Leu Phe Pro Asp Thr
580 585 590

Pro Leu Ala Leu Asp Ala Asn Lys Lys Lys Arg Ala Pro Val Pro Val
595 600 605

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Arg Gly Gly Pro Lys Phe Ala Ala Lys Pro His Asn Pro Gly Phe Gly
610 615 620

Met Gly Gly Pro Met His Asn Glu Val Pro Pro Pro Pro Asn Leu Arg
625 630 635 640

Gly Arg Gly Arg Gly Gly Ser Ile Arg Gly Arg Gly Arg Gly Arg Gly
645 650 655

Phe Gly Gly Ala Asn His Gly Gly Tyr Met Asn Ala Gly Ala Gly Tyr
660 665 670

Gly Ser Tyr Gly Tyr Gly Gly Asn Ser Ala Thr Ala Gly Tyr Ser Gln
675 680 685

Phe Tyr Ser Asn Gly Gly His Ser Gly Asn Ala Ser Gly Gly Gly Gly
690 695 700

Gly Gly Gly Gly Gly Ser Ser Gly Tyr Gly Ser Tyr Tyr Gln Gly Asp
705 710 715 720

Asn Tyr Asn Ser Pro Val Pro Pro Lys His Ala Gly Lys Lys Gln Pro
725 730 735

His Gly Gly Gln Gln Lys Pro Ser Tyr Gly Ser Gly Tyr Gln Ser His
740 745 750

Gln Gly Gln Gln Gln Ser Tyr Asn Gln Ser Pro Tyr Ser Asn Tyr Gly
755 760 765

Pro Pro Gln Gly Lys Gln Lys Gly Tyr Asn His Gly Gln Gly Ser Tyr
770 775 780

Ser Tyr Ser Asn Ser Tyr Asn Ser Pro Gly Gly Gly Gly Gly Ser Asp
785 790 795 800

Tyr Asn Tyr Glu Ser Lys Phe Asn Tyr Ser Gly Ser Gly Gly Arg Ser
805 810 815

Gly Gly Asn Ser Tyr Gly Ser Gly Gly Ala Ser Tyr Asn Pro Gly Ser
820 825 830

His Gly Gly Tyr Gly Gly Gly Ser Gly Gly Gly Ser Ser Tyr Gln Gly
835 840 845

Lys Gln Gly Gly Tyr Ser Gln Ser Asn Tyr Asn Ser Pro Gly Ser Gly
850 855 860

Gln Asn Tyr Ser Gly Pro Pro Ser Ser Tyr Gln Ser Ser Gln Gly Gly
865 870 875 880

Tyr Gly Arg Asn Ala Asp His Ser Met Asn Tyr Gln Tyr Arg
885 890

<210> 170
<211> 533
<212> PRT
<213> Homo sapiens

<400> 170

Met Ile Ser Ser Ser Ser Val His Ser Arg Thr Phe Asn Thr Ser Asn
1 5 10 15

Ala Leu Gly Pro Val Cys Lys His Lys Lys Pro Leu Ser Ala Ala Lys
20 25 30

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ala Cys Ile Ser Glu Ile Leu Pro Ser Lys Phe Lys Pro Arg Leu Ser
35 40 45

Ala Pro Ser Ala Leu Leu Gln Glu Gln Lys Ser Ile Leu Leu Pro Ser
50 55 60

Glu Lys Ala Gln Ser Cys Glu Asn Leu Cys Val Ser Gly Ser Leu Asn
65 70 75 80

Asp Ser Lys Arg Gly Leu Pro Leu Gln Val Gly Gly Ser Ile Glu Asn
85 90 95

Leu Leu Met Arg Ser Arg Arg Asp Tyr Asp Ser Lys Ser Ser Ser Thr
100 105 110

Met Ser Leu Gln Glu Tyr Ser Thr Ser Gly Arg Arg Pro Cys Pro Leu
115 120 125

Ser Arg Lys Ala Gly Met Gln Phe Thr Met Leu Tyr Arg Asp Met His
130 135 140

Gln Ile Asn Arg Ser Gly Leu Phe Leu Gly Ser Ile Ser Ser Ser Ser
145 150 155 160

Ser Val Arg Asp Leu Ala Ser His Phe Glu Lys Ser Ser Leu Ala Leu
165 170 175

Ser Arg Gly Glu Leu Gly Pro Ser Gln Glu Gly Ser Glu His Ile Pro
180 185 190

Lys His Thr Val Ser Ser Arg Ile Thr Ala Phe Glu Gln Leu Ile Gln
195 200 205

Arg Ser Arg Ser Met Pro Ser Leu Asp Leu Ser Gly Arg Leu Ser Lys
210 215 220

Ser Pro Thr Pro Val Leu Ser Arg Gly Ser Leu Thr Ser Ala Arg Ser
225 230 235 240

Ala Glu Ser Leu Leu Glu Ser Thr Lys Leu His Pro Lys Glu Met Asp
245 250 255

Gly Met Asn Ser Ser Gly Val Tyr Ala Ser Pro Thr Cys Ser Asn Met
260 265 270

Ala His His Ala Leu Ser Phe Arg Gly Leu Val Pro Ser Glu Pro Leu
275 280 285

Ser Thr Cys Ser Asp Asp Val Asp Arg Cys Ser Asn Ile Ser Thr Asp
290 295 300

Ser Arg Glu Gly Ser Gly Gly Ser Val His Gly Asp Phe Pro Lys His
305 310 315 320

Arg Leu Asn Lys Cys Lys Gly Thr Cys Pro Ala Ser Tyr Thr Arg Phe
325 330 335

Thr Thr Ile Arg Lys His Glu Gln Gln Gln Thr Ser Arg Gln Pro Glu
340 345 350

Trp Arg Leu Asp Ala Arg Gly Asp Lys Ser Thr Leu Leu Arg Asn Ile
355 360 365

Tyr Leu Met Ser Pro Leu Pro Phe Arg Leu Lys Lys Pro Leu His His

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 370 375 380

His Pro Arg Gln Pro Ser Pro Gly Asp Ser Ser Gly Leu Leu Val Gly
 385 390 395 400

Gln Lys Pro Asp Leu Pro Ser Gln Pro His Gln Asp Gln Pro Pro Ser
 405 410 415

Gly Gly Lys Pro Val Val Pro Thr Arg Leu Ser Ser Arg His Thr Met
 420 425 430

Ala Arg Leu Ser Arg Ser Ser Glu Pro Ser Gln Glu Arg Pro Thr Ala
 435 440 445

Leu Glu Asp Tyr Pro Arg Ala Ile Asn Asn Gly Asn Ser Val Pro Tyr
 450 455 460

Ser Asp His Ser Leu Asp Arg Asn Asn Asn Pro Gln Ser Glu Leu Ala
 465 470 475 480

Pro Ser Arg Gly Gly Gly Ile Leu Cys Val Cys Leu Val Ser Pro Ala
 485 490 495

Arg Pro Ser Thr Leu Leu Ala Leu Ser Arg Pro Pro Leu Cys Pro Trp
 500 505 510

Cys Ser Phe Ser Gly Leu Ser Phe Val Phe Cys Leu Phe Cys Leu Ala
 515 520 525

Ile Asn His Gly Ser
 530

<210> 171
 <211> 379
 <212> PRT
 <213> Homo sapiens

<400> 171

Met Glu Gln Leu Ser Ser Ala Asn Thr Arg Phe Ala Leu Asp Leu Phe
 1 5 10 15

Leu Ala Leu Ser Glu Asn Asn Pro Ala Gly Asn Ile Phe Ile Ser Pro
 20 25 30

Phe Ser Ile Ser Ser Ala Met Ala Met Val Phe Leu Gly Thr Arg Gly
 35 40 45

Asn Thr Ala Ala Gln Leu Ser Lys Thr Phe His Phe Asn Thr Val Glu
 50 55 60

Glu Val His Ser Arg Phe Gln Ser Leu Asn Ala Asp Ile Asn Lys Arg
 65 70 75 80

Gly Ala Ser Tyr Ile Leu Lys Leu Ala Asn Arg Leu Tyr Gly Glu Lys
 85 90 95

Thr Tyr Asn Phe Leu Pro Glu Phe Leu Val Ser Thr Gln Lys Thr Tyr
 100 105 110

Gly Ala Asp Leu Ala Ser Val Asp Phe Gln His Ala Ser Glu Asp Ala
 115 120 125

Arg Lys Thr Ile Asn Gln Trp Val Lys Gly Gln Thr Glu Gly Lys Ile
 130 135 140

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Pro Glu Leu Leu Ala Ser Gly Met Val Asp Asn Met Thr Lys Leu Val
 145 150 155 160

Leu Val Asn Ala Ile Tyr Phe Lys Gly Asn Trp Lys Asp Lys Phe Met
 165 170 175

Lys Glu Ala Thr Thr Asn Ala Pro Phe Arg Leu Asn Lys Lys Asp Arg
 180 185 190

Lys Thr Val Lys Met Met Tyr Gln Lys Lys Lys Phe Ala Tyr Gly Tyr
 195 200 205

Ile Glu Asp Leu Lys Cys Arg Val Leu Glu Leu Pro Tyr Gln Gly Glu
 210 215 220

Glu Leu Ser Met Val Ile Leu Leu Pro Asp Asp Ile Glu Asp Glu Ser
 225 230 235 240

Thr Gly Leu Lys Lys Ile Glu Glu Gln Leu Thr Leu Glu Lys Leu His
 245 250 255

Glu Trp Thr Lys Pro Glu Asn Leu Asp Phe Ile Glu Val Asn Val Ser
 260 265 270

Leu Pro Arg Phe Lys Leu Glu Glu Ser Tyr Thr Leu Asn Ser Asp Leu
 275 280 285

Ala Arg Leu Gly Val Gln Asp Leu Phe Asn Ser Ser Lys Ala Asp Leu
 290 295 300

Ser Gly Met Ser Gly Ala Arg Asp Ile Phe Ile Ser Lys Ile Val His
 305 310 315 320

Lys Ser Phe Val Glu Val Asn Glu Glu Gly Thr Glu Ala Ala Ala Ala
 325 330 335

Thr Ala Gly Ile Ala Thr Phe Cys Met Leu Met Pro Glu Glu Asn Phe
 340 345 350

Thr Ala Asp His Pro Phe Leu Phe Phe Ile Arg His Asn Ser Ser Gly
 355 360 365

Ser Ile Leu Phe Leu Gly Arg Phe Ser Ser Pro
 370 375

<210> 172
 <211> 440
 <212> PRT
 <213> Homo sapiens

<400> 172

Met Ala Leu Leu Val Leu Gly Leu Val Ser Cys Thr Phe Phe Leu Ala
 1 5 10 15

Val Asn Gly Leu Tyr Ser Ser Ser Asp Asp Val Ile Glu Leu Thr Pro
 20 25 30

Ser Asn Phe Asn Arg Glu Val Ile Gln Ser Asp Ser Leu Trp Leu Val
 35 40 45

Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Gln Arg Leu Thr Pro Glu
 50 55 60

Trp Lys Lys Ala Ala Thr Ala Leu Lys Asp Val Val Lys Val Gly Ala
 65 70 75 80

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Val Asp Ala Asp Lys His His Ser Leu Gly Gly Gln Tyr Gly Val Gln
85 90 95

Gly Phe Pro Thr Ile Lys Ile Phe Gly Ser Asn Lys Asn Arg Pro Glu
100 105 110

Asp Tyr Gln Gly Gly Arg Thr Gly Glu Ala Ile Val Asp Ala Ala Leu
115 120 125

Ser Ala Leu Arg Gln Leu Val Lys Asp Arg Leu Gly Gly Arg Ser Gly
130 135 140

Gly Tyr Ser Ser Gly Lys Gln Gly Arg Ser Asp Ser Ser Ser Lys Lys
145 150 155 160

Asp Val Ile Glu Leu Thr Asp Asp Ser Phe Asp Lys Asn Val Leu Asp
165 170 175

Ser Glu Asp Val Trp Met Val Glu Phe Tyr Ala Pro Trp Cys Gly His
180 185 190

Cys Lys Asn Leu Glu Pro Glu Trp Ala Ala Ala Ala Ser Glu Val Lys
195 200 205

Glu Gln Thr Lys Gly Lys Val Lys Leu Ala Ala Val Asp Ala Thr Val
210 215 220

Asn Gln Val Leu Ala Ser Arg Tyr Gly Ile Arg Gly Phe Pro Thr Ile
225 230 235 240

Lys Ile Phe Gln Lys Gly Glu Ser Pro Val Asp Tyr Asp Gly Gly Arg
245 250 255

Thr Arg Ser Asp Ile Val Ser Arg Ala Leu Asp Leu Phe Ser Asp Asn
260 265 270

Ala Pro Pro Pro Glu Leu Leu Glu Ile Ile Asn Glu Asp Ile Ala Lys
275 280 285

Arg Thr Cys Glu Glu His Gln Leu Cys Val Val Ala Val Leu Pro His
290 295 300

Ile Leu Asp Thr Gly Ala Ala Gly Arg Asn Ser Tyr Leu Glu Val Leu
305 310 315 320

Leu Lys Leu Ala Asp Lys Tyr Lys Lys Lys Met Trp Gly Trp Leu Trp
325 330 335

Thr Glu Ala Gly Ala Gln Ser Glu Leu Glu Thr Ala Leu Gly Ile Gly
340 345 350

Gly Phe Gly Tyr Pro Ala Met Ala Ala Ile Asn Ala Arg Lys Met Lys
355 360 365

Phe Ala Leu Leu Lys Gly Ser Phe Ser Glu Gln Gly Ile Asn Glu Phe
370 375 380

Leu Arg Glu Leu Ser Phe Gly Arg Gly Ser Thr Ala Pro Val Gly Gly
385 390 395 400

Gly Ala Phe Pro Thr Ile Val Glu Arg Glu Pro Trp Asp Gly Arg Asp
405 410 415

Gly Glu Leu Pro Val Glu Asp Asp Ile Asp Leu Ser Asp Val Glu Leu

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 420 425 430

Asp Asp Leu Gly Lys Asp Glu Leu
 435 440

<210> 173
 <211> 193
 <212> PRT
 <213> Homo sapiens

<400> 173

Met Ala Arg Ala Arg Gln Glu Gly Ser Ser Pro Glu Pro Val Glu Gly
 1 5 10 15

Leu Ala Arg Asp Gly Pro Arg Pro Phe Pro Leu Gly Arg Leu Val Pro
 20 25 30

Ser Ala Val Ser Cys Gly Leu Cys Glu Pro Gly Leu Ala Ala Ala Pro
 35 40 45

Ala Ala Pro Thr Leu Leu Pro Ala Ala Tyr Leu Cys Ala Pro Thr Ala
 50 55 60

Pro Pro Ala Val Thr Ala Ala Leu Gly Gly Ser Arg Trp Pro Gly Gly
 65 70 75 80

Pro Arg Ser Arg Pro Arg Gly Pro Arg Pro Asp Gly Pro Gln Pro Ser
 85 90 95

Leu Ser Leu Ala Glu Gln His Leu Glu Ser Pro Val Pro Ser Ala Pro
 100 105 110

Gly Ala Leu Ala Gly Gly Pro Thr Gln Ala Ala Pro Gly Val Arg Gly
 115 120 125

Glu Glu Glu Gln Trp Ala Arg Glu Ile Gly Ala Gln Leu Arg Arg Met
 130 135 140

Ala Asp Asp Leu Asn Ala Gln Tyr Glu Arg Arg Arg Gln Glu Glu Gln
 145 150 155 160

Gln Arg His Arg Pro Ser Pro Trp Arg Val Leu Tyr Asn Leu Ile Met
 165 170 175

Gly Leu Leu Pro Leu Pro Arg Gly His Arg Ala Pro Glu Met Glu Pro
 180 185 190

Asn

<210> 174
 <211> 149
 <212> PRT
 <213> Homo sapiens

<400> 174

Met Pro Gly His Leu Gln Glu Gly Phe Gly Cys Val Val Thr Asn Arg
 1 5 10 15

Phe Asp Gln Leu Phe Asp Asp Glu Ser Asp Pro Phe Glu Val Leu Lys
 20 25 30

Ala Ala Glu Asn Lys Lys Lys Glu Ala Gly Arg Gly Gly Val Gly Gly
 35 40 45

Pro Gly Ala Lys Ser Ala Ala Gln Ala Ala Ala Gln Thr Asn Ser Asn

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 50 55 60

Ala Ala Gly Lys Gln Leu Arg Lys Glu Ser Gln Lys Asp Arg Lys Asn
 65 70 75 80

Pro Leu Pro Arg Ser Val Gly Val Val Asp Lys Lys Glu Glu Thr Gln
 85 90 95

Pro Pro Val Ala Leu Lys Lys Glu Gly Ile Arg Arg Val Gly Arg Arg
 100 105 110

Pro Asp Gln Gln Leu Gln Gly Glu Gly Lys Ile Ile Asp Arg Arg Pro
 115 120 125

Glu Arg Gln Pro Pro Cys Glu Arg Arg Phe Glu Lys Pro Leu Glu Glu
 130 135 140

Lys Gly Glu Gly Gly
 145

<210> 175
 <211> 390
 <212> PRT
 <213> Homo sapiens

<400> 175

Met Asn Ser Leu Ser Glu Ala Asn Thr Lys Phe Met Phe Asp Leu Phe
 1 5 10 15

Gln Gln Phe Arg Lys Ser Lys Glu Asn Asn Ile Phe Tyr Ser Pro Ile
 20 25 30

Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
 35 40 45

Thr Ala Gln Gln Ile Ser Lys Val Leu His Phe Asp Gln Val Thr Glu
 50 55 60

Asn Thr Thr Glu Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
 65 70 75 80

Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
 85 90 95

Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr
 100 105 110

Tyr Gln Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln
 115 120 125

Thr Ser Val Glu Ser Thr Asp Phe Ala Asn Ala Pro Glu Glu Ser Arg
 130 135 140

Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys
 145 150 155 160

Asn Leu Phe Pro Asp Gly Thr Ile Gly Asn Asp Thr Thr Leu Val Leu
 165 170 175

Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Asn Lys Phe Lys Lys
 180 185 190

Glu Asn Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys
 195 200 205

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ser Val Gln Met Met Arg Gln Tyr Asn Ser Phe Asn Phe Ala Leu Leu
 210 215 220

Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
 225 230 235 240

Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys
 245 250 255

Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu
 260 265 270

Gln Asn Met Arg Glu Thr Cys Val Asp Leu His Leu Pro Arg Phe Lys
 275 280 285

Met Glu Glu Ser Tyr Asp Leu Lys Asp Thr Leu Arg Thr Met Gly Met
 290 295 300

Val Asn Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly Met Thr Trp Ser
 305 310 315 320

His Gly Leu Ser Val Ser Lys Val Leu His Lys Ala Phe Val Glu Val
 325 330 335

Thr Glu Glu Gly Val Glu Ala Ala Ala Ala Thr Ala Val Val Val
 340 345 350

Glu Leu Ser Ser Pro Ser Thr Asn Glu Glu Phe Cys Cys Asn His Pro
 355 360 365

Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr
 370 375 380

Gly Arg Phe Ser Ser Pro
 385 390

<210> 176
 <211> 541
 <212> PRT
 <213> Homo sapiens

<400> 176

Met Val Ala Asp Pro Pro Arg Asp Ser Lys Gly Leu Ala Ala Ala Glu
 1 5 10 15

Pro Thr Ala Asn Gly Gly Leu Ala Leu Ala Ser Ile Glu Asp Gln Gly
 20 25 30

Ala Ala Ala Gly Gly Tyr Cys Gly Ser Arg Asp Gln Val Arg Arg Cys
 35 40 45

Leu Arg Ala Asn Leu Leu Val Leu Leu Thr Val Val Ala Val Val Ala
 50 55 60

Gly Val Ala Leu Gly Leu Gly Val Ser Gly Ala Gly Gly Ala Leu Ala
 65 70 75 80

Leu Gly pro Glu Arg Leu Ser Ala Phe Val Phe pro Gly Glu Leu Leu
 85 90 95

Leu Arg Leu Leu Arg Met Ile Ile Leu Pro Leu Val Val Cys Ser Leu
 100 105 110

Ile Gly Gly Ala Ala Ser Leu Asp Pro Gly Ala Leu Gly Arg Leu Gly
 115 120 125

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ala Trp Ala Leu Leu Phe Phe Leu Val Thr Thr Leu Leu Ala Ser Ala
130 135 140

Leu Gly Val Gly Leu Ala Leu Ala Leu Gln Pro Gly Ala Ala Ser Ala
145 150 155 160

Ala Ile Asn Ala Ser Val Gly Ala Ala Gly Ser Ala Glu Asn Ala Pro
165 170 175

Ser Lys Glu Val Leu Asp Ser Phe Leu Asp Leu Ala Arg Asn Ile Phe
180 185 190

Pro Ser Asn Leu Val Ser Ala Ala Phe Arg Ser Tyr Ser Thr Thr Tyr
195 200 205

Glu Glu Arg Asn Ile Thr Gly Thr Arg Val Lys Val Pro Val Gly Gln
210 215 220

Glu Val Glu Gly Met Asn Ile Leu Gly Leu Val Val Phe Ala Ile Val
225 230 235 240

Phe Gly Val Ala Leu Arg Lys Leu Gly Pro Glu Gly Glu Leu Leu Ile
245 250 255

Arg Phe Phe Asn Ser Phe Asn Glu Ala Thr Met Val Leu Val Ser Trp
260 265 270

Ile Met Trp Tyr Ala Pro Val Gly Ile Met Phe Leu Val Ala Gly Lys
275 280 285

Ile Val Glu Met Glu Asp Val Gly Leu Leu Phe Ala Arg Leu Gly Lys
290 295 300

Tyr Ile Leu Cys Cys Leu Leu Gly His Ala Ile His Gly Leu Leu Val
305 310 315 320

Leu Pro Leu Ile Tyr Phe Leu Phe Thr Arg Lys Asn Pro Tyr Arg Phe
325 330 335

Leu Trp Gly Ile Val Thr Pro Leu Ala Thr Ala Phe Gly Thr Ser Ser
340 345 350

Ser Ser Ala Thr Leu Pro Leu Met Met Lys Cys Val Glu Glu Asn Asn
355 360 365

Gly Val Ala Lys His Ile Ser Arg Phe Ile Leu Pro Ile Gly Ala Thr
370 375 380

Val Asn Met Asp Gly Ala Ala Leu Phe Gln Cys Val Ala Ala Val Phe
385 390 395 400

Ile Ala Gln Leu Ser Gln Gln Ser Leu Asp Phe Val Lys Ile Ile Thr
405 410 415

Ile Leu Val Thr Ala Thr Ala Ser Ser Val Gly Ala Ala Gly Ile Pro
420 425 430

Ala Gly Gly Val Leu Thr Leu Ala Ile Ile Leu Glu Ala Val Asn Leu
435 440 445

Pro Val Asp His Ile Ser Leu Ile Leu Ala Val Asp Trp Leu Val Asp
450 455 460

Arg Ser Cys Thr Val Leu Asn Val Glu Gly Asp Ala Leu Gly Ala Gly

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 465 470 475 480

Leu Leu Gln Asn Tyr Val Asp Arg Thr Glu Ser Arg Ser Thr Glu Pro
 485 490 495

Glu Leu Ile Gln Val Lys Ser Glu Leu Pro Leu Asp Pro Leu Pro Val
 500 505 510

Pro Thr Glu Glu Gly Asn Pro Leu Leu Lys His Tyr Arg Gly Pro Ala
 515 520 525

Gly Asp Ala Thr Val Ala Ser Glu Lys Glu Ser Val Met
 530 535 540

<210> 177
 <211> 482
 <212> PRT
 <213> Homo sapiens

<400> 177

Met Ala Ala Leu Met Thr Pro Gly Thr Gly Ala Pro Pro Ala Pro Gly
 1 5 10 15

Asp Phe Ser Gly Glu Gly Ser Gln Gly Leu Pro Asp Pro Ser Pro Glu
 20 25 30

Pro Lys Gln Leu Pro Glu Leu Ile Arg Met Lys Arg Asp Gly Gly Arg
 35 40 45

Leu Ser Glu Ala Asp Ile Arg Gly Phe Val Ala Ala Val Val Asn Gly
 50 55 60

Ser Ala Gln Gly Ala Gln Ile Gly Ala Met Leu Met Ala Ile Arg Leu
 65 70 75 80

Arg Gly Met Asp Leu Glu Glu Thr Ser Val Leu Thr Gln Ala Leu Ala
 85 90 95

Gln Ser Gly Gln Gln Leu Glu Trp Pro Glu Ala Trp Arg Gln Gln Leu
 100 105 110

Val Asp Lys His Ser Thr Gly Gly Val Gly Asp Lys Val Ser Leu Val
 115 120 125

Leu Ala Pro Ala Leu Ala Ala Cys Gly Cys Lys Val Pro Met Ile Ser
 130 135 140

Gly Arg Gly Leu Gly His Thr Gly Gly Thr Leu Asp Lys Leu Glu Ser
 145 150 155 160

Ile Pro Gly Phe Asn Val Ile Gln Ser Pro Glu Gln Met Gln Val Leu
 165 170 175

Leu Asp Gln Ala Gly Cys Cys Ile Val Gly Gln Ser Glu Gln Leu Val
 180 185 190

Pro Ala Asp Gly Ile Leu Tyr Ala Ala Arg Asp Val Thr Ala Thr Val
 195 200 205

Asp Ser Leu Pro Leu Ile Thr Ala Ser Ile Leu Ser Lys Lys Leu Val
 210 215 220

Glu Gly Leu Ser Ala Leu Val Val Asp Val Lys Phe Gly Gly Ala Ala
 225 230 235 240

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Val Phe Pro Asn Gln Glu Gln Ala Arg Glu Leu Ala Lys Thr Leu Val
245 250 255

Gly Val Gly Ala Ser Leu Gly Leu Arg Val Ala Ala Ala Leu Thr Ala
260 265 270

Met Asp Lys Pro Leu Gly Arg Cys Val Gly His Ala Leu Glu Val Glu
275 280 285

Glu Ala Leu Leu Cys Met Asp Gly Ala Gly Pro Pro Asp Leu Arg Asp
290 295 300

Leu Val Thr Thr Leu Gly Gly Ala Leu Leu Trp Leu Ser Gly His Ala
305 310 315 320

Gly Thr Gln Ala Gln Gly Ala Ala Arg Val Ala Ala Ala Leu Asp Asp
325 330 335

Gly Ser Ala Leu Gly Arg Phe Glu Arg Met Leu Ala Ala Gln Gly Val
340 345 350

Asp Pro Gly Leu Ala Arg Ala Leu Cys Ser Gly Ser Pro Ala Glu Arg
355 360 365

Arg Gln Leu Leu Pro Arg Ala Arg Glu Gln Glu Glu Leu Leu Ala Pro
370 375 380

Ala Asp Gly Thr Val Glu Leu Val Arg Ala Leu Pro Leu Ala Leu Val
385 390 395 400

Leu His Glu Leu Gly Ala Gly Arg Ser Arg Ala Gly Glu Pro Leu Arg
405 410 415

Leu Gly Val Gly Ala Glu Leu Leu Val Asp Val Gly Gln Arg Leu Arg
420 425 430

Arg Gly Thr Pro Trp Leu Arg Val His Arg Asp Gly Pro Ala Leu Ser
435 440 445

Gly Pro Gln Ser Arg Ala Leu Gln Glu Ala Leu Val Leu Ser Asp Arg
450 455 460

Ala Pro Phe Ala Ala Pro Leu Pro Phe Ala Glu Leu Val Leu Pro Pro
465 470 475 480

Gln Gln

<210> 178
<211> 399
<212> PRT
<213> Homo sapiens

<400> 178

Met Tyr Ser Pro Arg Gly ser Gln Gly Arg Gly Thr Ala Glu Ala Thr
1 5 10 15

Ala Asn Ser Pro Ser Pro Pro Ile Ala Pro Ser His Ser Arg Val Thr
20 25 30

Phe Ser Leu Ser Thr Leu His Thr Leu Ser Pro Pro Arg Pro Phe
35 40 45

Pro Ser Val Ser Arg Ala Ala Ala Gln Lys Pro His His Leu His Pro
50 55 60

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

His Ile Leu Leu Ala Gly Ser Ala Ala Val Pro Pro Arg Val Leu Lys
65 70 75 80

Ala Glu Met Asn Asn Thr Ala Ala Ser Pro Met Ser Thr Ala Thr Ser
85 90 95

Ser Ser Gly Arg Ser Thr Gly Lys Ser Ile Ser Phe Ala Thr Glu Leu
100 105 110

Gln Ser Met Met Tyr Ser Leu Gly Asp Ala Arg Arg Pro Leu His Glu
115 120 125

Thr Ala Val Leu Val Glu Asp Val Val His Thr Gln Leu Ile Asn Leu
130 135 140

Leu Gln Gln Ala Ala Glu Val Ser Gln Leu Arg Gly Ala Arg Val Ile
145 150 155 160

Thr Pro Glu Asp Leu Leu Phe Leu Met Arg Lys Asp Lys Lys Lys Leu
165 170 175

Arg Arg Leu Leu Lys Tyr Met Phe Ile Arg Asp Tyr Lys Ser Lys Ile
180 185 190

Val Lys Gly Ile Asp Glu Asp Asp Leu Leu Glu Asp Lys Leu Ser Gly
195 200 205

Ser Asn Asn Ala Asn Lys Arg Gln Lys Ile Ala Gln Asp Phe Leu Asn
210 215 220

Ser Ile Asp Gln Thr Gly Glu Leu Leu Ala Met Phe Glu Asp Asp Glu
225 230 235 240

Ile Asp Glu Val Lys Gln Glu Arg Met Glu Arg Ala Glu Arg Gln Thr
245 250 255

Arg Ile Met Asp Ser Ala Gln Tyr Ala Glu Phe Cys Glu Ser Arg Gln
260 265 270

Leu Ser Phe Ser Lys Lys Ala Ser Lys Phe Arg Asp Trp Leu Asp Cys
275 280 285

Ser Ser Met Glu Ile Lys Pro Asn Val Val Ala Met Glu Ile Leu Ala
290 295 300

Tyr Leu Ala Tyr Glu Thr Val Ala Gln Leu Val Asp Leu Ala Leu Leu
305 310 315 320

Val Arg Gln Asp Met Val Thr Lys Ala Gly Asp Pro Phe Ser His Ala
325 330 335

Ile Ser Ala Thr Phe Ile Gln Tyr His Asn Ser Ala Glu Ser Thr Ala
340 345 350

Ala Cys Gly Val Glu Ala His Ser Asp Ala Ile Gln Pro Cys His Ile
355 360 365

Arg Glu Ala Ile Arg Arg Tyr Ser His Arg Ile Gly Pro Leu Ser Pro
370 375 380

Phe Thr Asn Ala Tyr Arg Arg Asn Gly Met Ala Phe Leu Ala Cys
385 390 395

<210> 179

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

<211> 414
 <212> PRT
 <213> Homo sapiens

<400> 179

Met Ala Ala Leu Arg Tyr Ala Gly Leu Asp Asp Thr Asp Ser Glu Asp
 1 5 10 15

Glu Leu Pro Pro Gly Trp Glu Glu Arg Thr Thr Lys Asp Gly Trp Val
 20 25 30

Tyr Tyr Ala Asn His Thr Glu Glu Lys Thr Gln Trp Glu His Pro Lys
 35 40 45

Thr Gly Lys Arg Lys Arg Val Ala Gly Asp Leu Pro Tyr Gly Trp Glu
 50 55 60

Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val Asp His Ile Asn
 65 70 75 80

Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe Thr Val Asp Asp
 85 90 95

Asn Pro Thr Lys Pro Thr Thr Arg Gln Arg Tyr Asp Gly Ser Thr Thr
 100 105 110

Ala Met Glu Ile Leu Gln Gly Arg Asp Phe Thr Gly Lys Val Val Val
 115 120 125

Val Thr Gly Ala Asn Ser Gly Ile Gly Phe Glu Thr Ala Lys Ser Phe
 130 135 140

Ala Leu His Gly Ala His Val Ile Leu Ala Cys Arg Asn Met Ala Arg
 145 150 155 160

Ala Ser Glu Ala Val Ser Arg Ile Leu Glu Glu Trp His Lys Ala Lys
 165 170 175

Val Glu Ala Met Thr Leu Asp Leu Ala Leu Leu Arg Ser Val Gln His
 180 185 190

Phe Ala Glu Ala Phe Lys Ala Lys Asn Val Pro Leu His Val Leu Val
 195 200 205

Cys Asn Ala Ala Thr Phe Ala Leu Pro Trp Ser Leu Thr Lys Asp Gly
 210 215 220

Leu Glu Thr Thr Phe Gln Val Asn His Leu Gly His Phe Tyr Leu Val
 225 230 235 240

Gln Leu Leu Gln Asp Val Leu Cys Arg Ser Ala Pro Ala Arg Val Ile
 245 250 255

Val Val Ser Ser Glu Ser His Arg Phe Thr Asp Ile Asn Asp Ser Leu
 260 265 270

Gly Lys Leu Asp Phe Ser Arg Leu Ser Pro Thr Lys Asn Asp Tyr Trp
 275 280 285

Ala Met Leu Ala Tyr Asn Arg Ser Lys Leu Cys Asn Ile Leu Phe Ser
 290 295 300

Asn Glu Leu His Arg Arg Leu Ser Pro Arg Gly Val Thr Ser Asn Ala
 305 310 315 320

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Val His Pro Gly Asn Met Met Tyr Ser Asn Ile His Arg Ser Trp Trp
 325 330 335

Val Tyr Thr Leu Leu Phe Thr Leu Ala Arg Pro Phe Thr Lys Ser Met
 340 345 350

Gln Gln Gly Ala Ala Thr Thr Val Tyr Cys Ala Ala Val Pro Glu Leu
 355 360 365

Glu Gly Leu Gly Gly Met Tyr Phe Asn Asn Cys Cys Arg Cys Met Pro
 370 375 380

Ser Pro Glu Ala Gln Ser Glu Glu Thr Ala Arg Thr Leu Trp Ala Leu
 385 390 395 400

Ser Glu Arg Leu Ile Gln Glu Arg Leu Gly Ser Gln Ser Gly
 405 410

<210> 180
 <211> 295
 <212> PRT
 <213> Homo sapiens

<400> 180

Met Val Pro Val Leu Leu Ser Leu Leu Leu Leu Leu Gly Pro Ala Val
 1 5 10 15

Pro Gln Glu Asn Gln Asp Gly Arg Tyr Ser Leu Thr Tyr Ile Tyr Thr
 20 25 30

Gly Leu Ser Lys His Val Glu Asp Val Pro Ala Phe Gln Ala Leu Gly
 35 40 45

Ser Leu Asn Asp Leu Gln Phe Phe Arg Tyr Asn Ser Lys Asp Arg Lys
 50 55 60

Ser Gln Pro Met Gly Leu Trp Arg Gln Val Glu Gly Met Glu Asp Trp
 65 70 75 80

Lys Gln Asp Ser Gln Leu Gln Lys Ala Arg Glu Asp Ile Phe Met Glu
 85 90 95

Thr Leu Lys Asp Ile Val Glu Tyr Tyr Asn Asp Ser Asn Gly Ser His
 100 105 110

Val Leu Gln Gly Arg Phe Gly Cys Glu Ile Glu Asn Asn Arg Ser Ser
 115 120 125

Gly Ala Phe Trp Lys Tyr Tyr Tyr Asp Gly Lys Asp Tyr Ile Glu Phe
 130 135 140

Asn Lys Glu Ile Pro Ala Trp Val Pro Phe Asp Pro Ala Ala Gln Ile
 145 150 155 160

Thr Lys Gln Lys Trp Glu Ala Glu Pro Val Tyr Val Gln Arg Ala Lys
 165 170 175

Ala Tyr Leu Glu Glu Glu Cys Pro Ala Thr Leu Arg Lys Tyr Leu Lys
 180 185 190

Tyr Ser Lys Asn Ile Leu Asp Arg Gln Asp Pro Pro Ser Val Val Val
 195 200 205

Thr Ser His Gln Ala Pro Gly Glu Lys Lys Lys Leu Lys Cys Leu Ala
 210 215 220

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Tyr Asp Phe Tyr Pro Gly Lys Ile Asp Val His Trp Thr Arg Ala Gly
225 230 235 240

Glu Val Gln Glu Pro Glu Leu Arg Gly Asp Val Leu His Asn Gly Asn
245 250 255

Gly Thr Tyr Gln Ser Trp Val Val Val Ala Val Pro Pro Gln Asp Thr
260 265 270

Ala Pro Tyr Ser Cys His Val Gln His Ser Ser Leu Ala Gln Pro Leu
275 280 285

Val Val Pro Trp Glu Ala Ser
290 295

<210> 181
<211> 507
<212> PRT
<213> Homo sapiens

<400> 181

Met Ala Gly Ala Gly Pro Lys Arg Arg Ala Leu Ala Ala Pro Ala Ala
1 5 10 15

Glu Glu Lys Glu Glu Ala Arg Glu Lys Met Leu Ala Ala Lys Ser Ala
20 25 30

Asp Gly Ser Ala Pro Ala Gly Glu Gly Glu Gly Val Thr Leu Gln Arg
35 40 45

Asn Ile Thr Leu Leu Asn Gly Val Ala Ile Ile Val Gly Thr Ile Ile
50 55 60

Gly Ser Gly Ile Phe Val Thr Pro Thr Gly Val Leu Lys Glu Ala Gly
65 70 75 80

Ser Pro Gly Leu Ala Leu Val Val Trp Ala Ala Cys Gly Val Phe Ser
85 90 95

Ile Val Gly Ala Leu Cys Tyr Ala Glu Leu Gly Thr Thr Ile Ser Lys
100 105 110

Ser Gly Gly Asp Tyr Ala Tyr Met Leu Glu Val Tyr Gly Ser Leu Pro
115 120 125

Ala Phe Leu Lys Leu Trp Ile Glu Leu Leu Ile Ile Arg Pro Ser Ser
130 135 140

Gln Tyr Ile Val Ala Leu Val Phe Ala Thr Tyr Leu Leu Lys Pro Leu
145 150 155 160

Phe Pro Thr Cys Pro Val Pro Glu Glu Ala Ala Lys Leu Val Ala Cys
165 170 175

Leu Cys Val Leu Leu Leu Thr Ala Val Asn Cys Tyr Ser Val Lys Ala
180 185 190

Ala Thr Arg Val Gln Asp Ala Phe Ala Ala Ala Lys Leu Leu Ala Leu
195 200 205

Ala Leu Ile Ile Leu Leu Gly Phe Val Gln Ile Gly Lys Gly Asp Val
210 215 220

Ser Asn Leu Asp Pro Asn Phe Ser Phe Glu Gly Thr Lys Leu Asp Val
225 230 235 240

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Gly Asn Ile Val Leu Ala Leu Tyr Ser Gly Leu Phe Ala Tyr Gly Gly
 245 250 255

Trp Asn Tyr Leu Asn Phe Val Thr Glu Glu Met Ile Asn Pro Tyr Arg
 260 265 270

Asn Leu Pro Leu Ala Ile Ile Ile Ser Leu Pro Ile Val Thr Leu Val
 275 280 285

Tyr Val Leu Thr Asn Leu Ala Tyr Phe Thr Thr Leu Ser Thr Glu Gln
 290 295 300

Met Leu Ser Ser Glu Ala Val Ala Val Asp Phe Gly Asn Tyr His Leu
 305 310 315 320

Gly Val Met Ser Trp Ile Ile Pro Val Phe Val Gly Leu Ser Cys Phe
 325 330 335

Gly Ser Val Asn Gly Ser Leu Phe Thr Ser Ser Arg Leu Phe Phe Val
 340 345 350

Gly Ser Arg Glu Gly His Leu Pro Ser Ile Leu Ser Met Ile His Pro
 355 360 365

Gln Leu Leu Thr Pro Val Pro Ser Leu Val Phe Thr Cys Val Met Thr
 370 375 380

Leu Leu Tyr Ala Phe Ser Lys Asp Ile Phe Ser Val Ile Asn Phe Phe
 385 390 395 400

Ser Phe Phe Asn Trp Leu Cys Val Ala Leu Ala Ile Ile Gly Met Ile
 405 410 415

Trp Leu Arg His Arg Lys Pro Glu Leu Glu Arg Pro Ile Lys Val Asn
 420 425 430

Leu Ala Leu Pro Val Phe Phe Ile Leu Ala Cys Leu Phe Leu Ile Ala
 435 440 445

Val Ser Phe Trp Lys Thr Pro Val Glu Cys Gly Ile Gly Phe Thr Ile
 450 455 460

Ile Leu Ser Gly Leu Pro Val Tyr Phe Phe Gly Val Trp Trp Lys Asn
 465 470 475 480

Lys Pro Lys Trp Leu Leu Gln Gly Ile Phe Ser Thr Thr Val Leu Cys
 485 490 495

Gln Lys Leu Met Gln Val Val Pro Gln Glu Thr
 500 505

<210> 182
 <211> 1210
 <212> PRT
 <213> Homo sapiens

<400> 182

Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Ala
 1 5 10 15

Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
 20 25 30

Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
 35 40 45
 50 55 60
 Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
 65 70 75 80
 Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
 85 90 95
 Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
 100 105 110
 Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
 115 120 125
 Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
 130 135 140
 His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
 145 150 155 160
 Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
 165 170 175
 Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
 180 185 190
 Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
 195 200 205
 Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
 210 215 220
 Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
 225 230 235 240
 Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
 245 250 255
 Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
 260 265 270
 Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
 275 280 285
 Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
 290 295 300
 Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
 305 310 315 320
 Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
 325 330 335
 Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
 340 345 350
 Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
 355 360 365
 Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
 370 375 380

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
385 390 395 400

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
405 410 415

Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
420 425 430

His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
435 440 445

Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
450 455 460

Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465 470 475 480

Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
485 490 495

Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
500 505 510

Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
515 520 525

Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Lys Leu Leu Glu Gly
530 535 540

Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545 550 555 560

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
565 570 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
580 585 590

Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
595 600 605

Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
610 615 620

Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
625 630 635 640

Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu
645 650 655

Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His
660 665 670

Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg Glu Leu
675 680 685

Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala Leu Leu
690 695 700

Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser
705 710 715 720

Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 725 730 735

Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser
 740 745 750

Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser
 755 760 765

Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser
 770 775 780

Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp
 785 790 795 800

Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn
 805 810 815

Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg
 820 825 830

Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro
 835 840 845

Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala
 850 855 860

Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp
 865 870 875 880

Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp
 885 890 895

Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser
 900 905 910

Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu
 915 920 925

Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr
 930 935 940

Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys
 945 950 955 960

Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln
 965 970 975

Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro Ser Pro
 980 985 990

Thr Asp Ser Asn Phe Tyr Arg Ala Leu Met Asp Glu Glu Asp Met Asp
 995 1000 1005

Asp Val Val Asp Ala Asp Glu Tyr Leu Ile Pro Gln Gln Gly Phe
 1010 1015 1020

Phe Ser Ser Pro Ser Thr Ser Arg Thr Pro Leu Leu Ser Ser Leu
 1025 1030 1035

Ser Ala Thr Ser Asn Asn Ser Thr Val Ala Cys Ile Asp Arg Asn
 1040 1045 1050

Gly Leu Gln Ser Cys Pro Ile Lys Glu Asp Ser Phe Leu Gln Arg
 1055 1060 1065

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Tyr Ser Ser Asp Pro Thr Gly Ala Leu Thr Glu Asp Ser Ile Asp
1070 1075 1080

Asp Thr Phe Leu Pro Val Pro Glu Tyr Ile Asn Gln Ser Val Pro
1085 1090 1095

Lys Arg Pro Ala Gly Ser Val Gln Asn Pro Val Tyr His Asn Gln
1100 1105 1110

Pro Leu Asn Pro Ala Pro Ser Arg Asp Pro His Tyr Gln Asp Pro
1115 1120 1125

His Ser Thr Ala Val Gly Asn Pro Glu Tyr Leu Asn Thr Val Gln
1130 1135 1140

Pro Thr Cys Val Asn Ser Thr Phe Asp Ser Pro Ala His Trp Ala
1145 1150 1155

Gln Lys Gly Ser His Gln Ile Ser Leu Asp Asn Pro Asp Tyr Gln
1160 1165 1170

Gln Asp Phe Phe Pro Lys Glu Ala Lys Pro Asn Gly Ile Phe Lys
1175 1180 1185

Gly Ser Thr Ala Glu Asn Ala Glu Tyr Leu Arg Val Ala Pro Gln
1190 1195 1200

Ser Ser Glu Phe Ile Gly Ala
1205 1210

<210> 183
<211> 1371
<212> PRT
<213> Homo sapiens

<400> 183

Met Thr Thr Lys Arg Ser Leu Phe Val Arg Leu Val Pro Cys Arg Cys
1 5 10 15

Leu Arg Gly Glu Glu Thr Val Thr Thr Leu Asp Tyr Ser His Cys
20 25 30

Ser Leu Glu Gln Val Pro Lys Glu Ile Phe Thr Phe Glu Lys Thr Leu
35 40 45

Glu Glu Leu Tyr Leu Asp Ala Asn Gln Ile Glu Glu Leu Pro Lys Gln
50 55 60

Leu Phe Asn Cys Gln Ser Leu His Lys Leu Ser Leu Pro Asp Asn Asp
65 70 75 80

Leu Thr Thr Leu Pro Ala Ser Ile Ala Asn Leu Ile Asn Leu Arg Glu
85 90 95

Leu Asp Val Ser Lys Asn Gly Ile Gln Glu Phe Pro Glu Asn Ile Lys
100 105 110

Asn Cys Lys Val Leu Thr Ile Val Glu Ala Ser Val Asn Pro Ile Ser
115 120 125

Lys Leu Pro Asp Gly Phe Ser Gln Leu Leu Asn Leu Thr Gln Leu Tyr
130 135 140

Leu Asn Asp Ala Phe Leu Glu Phe Leu Pro Ala Asn Phe Gly Arg Leu
145 150 155 160

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Thr Lys Leu Gln Ile Leu Glu Leu Arg Glu Asn Gln Leu Lys Met Leu
165 170 175

Pro Lys Thr Met Asn Arg Leu Thr Gln Leu Glu Arg Leu Asp Leu Gly
180 185 190

Ser Asn Glu Phe Thr Glu Val Pro Glu Val Leu Glu Gln Leu Ser Gly
195 200 205

Leu Lys Glu Phe Trp Met Asp Ala Asn Arg Leu Thr Phe Ile Pro Gly
210 215 220

Phe Ile Gly Ser Leu Lys Gln Leu Thr Tyr Leu Asp Val Ser Lys Asn
225 230 235 240

Asn Ile Glu Met Val Glu Glu Gly Ile Ser Thr Cys Glu Asn Leu Gln
245 250 255

Asp Leu Leu Leu Ser Ser Asn Ser Leu Gln Gln Leu Pro Glu Thr Ile
260 265 270

Gly Ser Leu Lys Asn Ile Thr Thr Leu Lys Ile Asp Glu Asn Gln Leu
275 280 285

Met Tyr Leu Pro Asp Ser Ile Gly Gly Leu Ile Ser Val Glu Glu Leu
290 295 300

Asp Cys Ser Phe Asn Glu Val Glu Ala Leu Pro Ser Ser Ile Gly Gln
305 310 315 320

Leu Thr Asn Leu Arg Thr Phe Ala Ala Asp His Asn Tyr Leu Gln Gln
325 330 335

Leu Pro Pro Glu Ile Gly Ser Trp Lys Asn Ile Thr Val Leu Phe Leu
340 345 350

His Ser Asn Lys Leu Glu Thr Leu Pro Glu Glu Met Gly Asp Met Gln
355 360 365

Lys Leu Lys Val Ile Asn Leu Ser Asp Asn Arg Leu Lys Asn Leu Pro
370 375 380

Phe Ser Phe Thr Lys Leu Gln Gln Leu Thr Ala Met Trp Leu Ser Asp
385 390 395 400

Asn Gln Ser Lys Pro Leu Ile Pro Leu Gln Lys Glu Thr Asp Ser Glu
405 410 415

Thr Gln Lys Met Val Leu Thr Asn Tyr Met Phe Pro Gln Gln Pro Arg
420 425 430

Thr Glu Asp Val Met Phe Ile Ser Asp Asn Glu Ser Phe Asn Pro Ser
435 440 445

Leu Trp Glu Glu Gln Arg Lys Gln Arg Ala Gln Val Ala Phe Glu Cys
450 455 460

Asp Glu Asp Lys Asp Glu Arg Glu Ala Pro Pro Arg Glu Gly Asn Leu
465 470 475 480

Lys Arg Tyr Pro Thr Pro Tyr Pro Asp Glu Leu Lys Asn Met Val Lys
485 490 495

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Thr Val Gln Thr Ile Val His Arg Leu Lys Asp Glu Glu Thr Asn Glu
 500 505 510

Asp Ser Gly Arg Asp Leu Lys Pro His Glu Asp Gln Gln Asp Ile Asn
 515 520 525

Lys Asp Val Gly Val Lys Thr Ser Glu Ser Thr Thr Thr Val Lys Ser
 530 535 540

Lys Val Asp Glu Arg Glu Lys Tyr Met Ile Gly Asn Ser Val Gln Lys
 545 550 555 560

Ile Ser Glu Pro Glu Ala Glu Ile Ser Pro Gly Ser Leu Pro Val Thr
 565 570 575

Ala Asn Met Lys Ala Ser Glu Asn Leu Lys His Ile Val Asn His Asp
 580 585 590

Asp Val Phe Glu Glu Ser Glu Glu Leu Ser Ser Asp Glu Glu Met Lys
 595 600 605

Met Ala Glu Met Arg Pro Pro Leu Ile Glu Thr Ser Ile Asn Gln Pro
 610 615 620

Lys Val Val Ala Leu Ser Asn Asn Lys Lys Asp Asp Thr Lys Glu Thr
 625 630 635 640

Asp Ser Leu Ser Asp Glu Val Thr His Asn Ser Asn Gln Asn Asn Ser
 645 650 655

Asn Cys Ser Ser Pro Ser Arg Met Ser Asp Ser Val Ser Leu Asn Thr
 660 665 670

Asp Ser Ser Gln Asp Thr Ser Leu Cys Ser Pro Val Lys Gln Thr His
 675 680 685

Ile Asp Ile Asn Ser Lys Ile Arg Gln Glu Asp Glu Asn Phe Asn Ser
 690 695 700

Leu Leu Gln Asn Gly Asp Ile Leu Asn Ser Ser Thr Glu Glu Lys Phe
 705 710 715 720

Lys Ala His Asp Lys Lys Asp Phe Asn Leu Pro Glu Tyr Asp Leu Asn
 725 730 735

Val Glu Glu Arg Leu Val Leu Ile Glu Lys Ser Val Asp Ser Thr Ala
 740 745 750

Thr Ala Asp Asp Thr His Lys Leu Asp His Ile Asn Met Asn Leu Asn
 755 760 765

Lys Leu Ile Thr Asn Asp Thr Phe Gln Pro Glu Ile Met Glu Arg Ser
 770 775 780

Lys Thr Gln Asp Ile Val Leu Gly Thr Ser Phe Leu Ser Ile Asn Ser
 785 790 795 800

Lys Glu Glu Thr Glu His Leu Glu Asn Gly Asn Lys Tyr Pro Asn Leu
 805 810 815

Glu Ser Val Asn Lys Val Asn Gly His Ser Glu Glu Thr Ser Gln Ser
 820 825 830

Pro Asn Arg Thr Glu Pro His Asp Ser Asp Cys Ser Val Asp Leu Gly
 835 840 845

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ile Ser Lys Ser Thr Glu Asp Leu Ser Pro Gln Lys Ser Gly Pro Val
850 855 860

Gly Ser Val Val Lys Ser His Ser Ile Thr Asn Met Glu Ile Gly Gly
865 870 875 880

Leu Lys Ile Tyr Asp Ile Leu Ser Asp Asn Gly Pro Gln Gln Pro Ser
885 890 895

Thr Thr Val Lys Ile Thr Ser Ala Val Asp Gly Lys Asn Ile Val Arg
900 905 910

Ser Lys Ser Ala Thr Leu Leu Tyr Asp Gln Pro Leu Gln Val Phe Thr
915 920 925

Gly Ser Ser Ser Ser Ser Asp Leu Ile Ser Gly Thr Lys Ala Ile Phe
930 935 940

Lys Phe Asp Ser Asn His Asn Pro Glu Glu Pro Asn Ile Ile Arg Gly
945 950 955 960

Pro Thr Ser Gly Pro Gln Ser Ala Pro Gln Ile Tyr Gly Pro Pro Gln
965 970 975

Tyr Asn Ile Gln Tyr Ser Ser Ser Ala Ala Val Lys Asp Thr Leu Trp
980 985 990

His Ser Lys Gln Asn Pro Gln Ile Asp His Ala Ser Phe Pro Pro Gln
995 1000 1005

Leu Leu Pro Arg Ser Glu Ser Thr Glu Asn Gln Ser Tyr Ala Lys
1010 1015 1020

His Ser Ala Asn Met Asn Phe Ser Asn His Asn Asn Val Arg Ala
1025 1030 1035

Asn Thr Ala Tyr His Leu His Gln Arg Leu Gly Pro Ala Arg His
1040 1045 1050

Gly Glu Met Trp Ala Ile Ser Pro Asn Asp Arg Leu Ile Pro Ala
1055 1060 1065

Val Thr Arg Ser Thr Ile Gln Arg Gln Ser Ser Val Ser Ser Thr
1070 1075 1080

Ala Ser Val Asn Leu Gly Asp Pro Gly Ser Thr Arg Arg Ala Gln
1085 1090 1095

Ile Pro Glu Gly Asp Tyr Leu Ser Tyr Arg Glu Phe His Ser Ala
1100 1105 1110

Gly Arg Thr Pro Pro Met Met Pro Gly Ser Gln Arg Pro Leu Ser
1115 1120 1125

Ala Arg Thr Tyr Ser Ile Asp Gly Pro Asn Ala Ser Arg Pro Gln
1130 1135 1140

Ser Ala Arg Pro Ser Ile Asn Glu Ile Pro Glu Arg Thr Met Ser
1145 1150 1155

Val Ser Asp Phe Asn Tyr Ser Arg Thr Ser Pro Ser Lys Arg Pro
1160 1165 1170

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Asn Ala Arg Val Gly Ser Glu His Ser Leu Leu Asp Pro Pro Gly
 1175 1180 1185

Lys Ser Lys Val Pro Arg Asp Trp Arg Glu Gln Val Leu Arg His
 1190 1195 1200

Ile Glu Ala Lys Lys Leu Glu Lys Met Pro Leu Ser Asn Gly Gln
 1205 1210 1215

Met Gly Gln Pro Leu Arg Pro Gln Ala Asn Tyr Ser Gln Ile His
 1220 1225 1230

His Pro Pro Gln Ala Ser Val Ala Arg His Pro Ser Arg Glu Gln
 1235 1240 1245

Leu Ile Asp Tyr Leu Met Leu Lys Val Ala His Gln Pro Pro Tyr
 1250 1255 1260

Thr Gln Pro His Cys Ser Pro Arg Gln Gly His Glu Leu Ala Lys
 1265 1270 1275

Gln Glu Ile Arg Val Arg Val Glu Lys Asp Pro Glu Leu Gly Phe
 1280 1285 1290

Ser Ile Ser Gly Gly Val Gly Gly Arg Gly Asn Pro Phe Arg Pro
 1295 1300 1305

Asp Asp Asp Gly Ile Phe Val Thr Arg Val Gln Pro Glu Gly Pro
 1310 1315 1320

Ala Ser Lys Leu Leu Gln Pro Gly Asp Lys Ile Ile Gln Ala Asn
 1325 1330 1335

Gly Tyr Ser Phe Ile Asn Ile Glu His Gly Gln Ala Val Ser Leu
 1340 1345 1350

Leu Lys Thr Phe Gln Asn Thr Val Glu Leu Ile Ile Val Arg Glu
 1355 1360 1365

Val Ser Ser
 1370

<210> 184
 <211> 581
 <212> PRT
 <213> Homo sapiens

<400> 184

Met Ala Val Glu Asp Glu Gly Leu Arg Val Phe Gln Ser Val Lys Ile
 1 5 10 15

Lys Ile Gly Glu Ala Lys Asn Leu Pro Ser Tyr Pro Gly Pro Ser Lys
 20 25 30

Met Arg Asp Cys Tyr Cys Thr Val Asn Leu Asp Gln Glu Glu Val Phe
 35 40 45

Arg Thr Lys Ile Val Glu Lys Ser Leu Cys Pro Phe Tyr Gly Glu Asp
 50 55 60

Phe Tyr Cys Glu Ile Pro Arg Ser Phe Arg His Leu Ser Phe Tyr Ile
 65 70 75 80

Phe Asp Arg Asp Val Phe Arg Arg Asp Ser Ile Ile Gly Lys Val Ala
 85 90 95

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ile Gln Lys Glu Asp Leu Gln Lys Tyr His Asn Arg Asp Thr Trp Phe
100 105 110

Gln Leu Gln His Val Asp Ala Asp Ser Glu Val Gln Gly Lys Val His
115 120 125

Leu Glu Leu Arg Leu Ser Glu Val Ile Thr Asp Thr Gly Val Val Cys
130 135 140

His Lys Leu Ala Thr Arg Ile Val Glu Cys Gln Gly Leu Pro Ile Val
145 150 155 160

Asn Gly Gln Cys Asp Pro Tyr Ala Thr Val Thr Leu Ala Gly Pro Phe
165 170 175

Arg Ser Glu Ala Lys Lys Thr Lys Val Lys Arg Lys Thr Asn Asn Pro
180 185 190

Gln Phe Asp Glu Val Phe Tyr Phe Glu Val Thr Arg Pro Cys Ser Tyr
195 200 205

Ser Lys Lys Ser His Phe Asp Phe Glu Glu Glu Asp Val Asp Lys Leu
210 215 220

Glu Ile Arg Val Asp Leu Trp Asn Ala Ser Asn Leu Lys Phe Gly Asp
225 230 235 240

Glu Phe Leu Gly Glu Leu Arg Ile Pro Leu Lys Val Leu Arg Gln Ser
245 250 255

Ser Ser Tyr Glu Ala Trp Tyr Phe Leu Gln Pro Arg Asp Asn Gly Ser
260 265 270

Lys Ser Leu Lys Pro Asp Asp Leu Gly Ser Leu Arg Leu Asn Val Val
275 280 285

Tyr Thr Glu Asp His Val Phe Ser Ser Asp Tyr Tyr Ser Pro Leu Arg
290 295 300

Asp Leu Leu Leu Lys Ser Ala Asp Val Glu Pro Val Ser Ala Ser Ala
305 310 315 320

Ala His Ile Leu Gly Glu Val Cys Arg Glu Lys Gln Glu Ala Ala Val
325 330 335

Pro Leu Val Arg Leu Phe Leu His Tyr Gly Arg Val Val Pro Phe Ile
340 345 350

Ser Ala Ile Ala Ser Ala Glu Val Lys Arg Thr Gln Asp Pro Asn Thr
355 360 365

Ile Phe Arg Gly Asn Ser Leu Ala Ser Lys Cys Ile Asp Glu Thr Met
370 375 380

Lys Leu Ala Gly Met His Tyr Leu His Val Thr Leu Lys Pro Ala Ile
385 390 395 400

Glu Glu Ile Cys Gln Ser His Lys Pro Cys Glu Ile Asp Pro Val Lys
405 410 415

Leu Lys Asp Gly Glu Asn Leu Glu Asn Asn Met Glu Asn Leu Arg Gln
420 425 430

Tyr Val Asp Arg Val Phe His Ala Ile Thr Glu Ser Gly Val Ser Cys

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 435 440 445

Pro Thr Val Met Cys Asp Ile Phe Phe Ser Leu Arg Glu Ala Ala Ala
 450 455 460

Lys Arg Phe Gln Asp Asp Pro Asp Val Arg Tyr Thr Ala Val Ser Ser
 465 470 475 480

Phe Ile Phe Leu Arg Phe Phe Ala Pro Ala Ile Leu Ser Pro Asn Leu
 485 490 495

Phe Gln Leu Thr Pro His His Thr Asp Pro Gln Thr Ser Arg Thr Leu
 500 505 510

Thr Leu Ile Ser Lys Thr Val Gln Thr Leu Gly Ser Leu Ser Lys Ser
 515 520 525

Lys Ser Ala Ser Phe Lys Glu Ser Tyr Met Ala Thr Phe Tyr Glu Phe
 530 535 540

Phe Asn Glu Gln Lys Tyr Ala Asp Ala Val Lys Asn Phe Leu Asp Leu
 545 550 555 560

Ile Ser Ser Ser Gly Arg Arg Asp Pro Lys Ser Val Glu Gln Pro Ile
 565 570 575

Val Leu Lys Glu Gly
 580

<210> 185
 <211> 532
 <212> PRT
 <213> Homo sapiens

<400> 185

Met Glu Leu Asp Leu Ser Pro Pro His Leu Ser Ser Ser Pro Glu Asp
 1 5 10 15

Leu Cys Pro Ala Pro Gly Thr Pro Pro Gly Thr Pro Arg Pro Pro Asp
 20 25 30

Thr Pro Leu Pro Glu Glu Val Lys Arg Ser Gln Pro Leu Leu Ile Pro
 35 40 45

Thr Thr Gly Arg Lys Leu Arg Glu Glu Glu Arg Arg Ala Thr Ser Leu
 50 55 60

Pro Ser Ile Pro Asn Pro Phe Pro Glu Leu Cys Ser Pro Pro Ser Gln
 65 70 75 80

Ser Pro Ile Leu Gly Gly Pro Ser Ser Ala Arg Gly Leu Leu Pro Arg
 85 90 95

Asp Ala Ser Arg Pro His Val Val Lys Val Tyr Ser Glu Asp Gly Ala
 100 105 110

Cys Arg Ser Val Glu Val Ala Ala Gly Ala Thr Ala Arg His Val Cys
 115 120 125

Glu Met Leu Val Gln Arg Ala His Ala Leu Ser Asp Glu Thr Trp Gly
 130 135 140

Leu Val Glu Cys His Pro His Leu Ala Leu Glu Arg Gly Leu Glu Asp
 145 150 155 160

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

His Glu Ser Val Val Glu Val Gln Ala Ala Trp Pro Val Gly Gly Asp
 165 170 175

Ser Arg Phe Val Phe Arg Lys Asn Phe Ala Lys Tyr Glu Leu Phe Lys
 180 185 190

Ser Ser Pro His Ser Leu Phe Pro Glu Lys Met Val Ser Ser Cys Leu
 195 200 205

Asp Ala His Thr Gly Ile Ser His Glu Asp Leu Ile Gln Asn Phe Leu
 210 215 220

Asn Ala Gly Ser Phe Pro Glu Ile Gln Gly Phe Leu Gln Leu Arg Gly
 225 230 235 240

Ser Gly Arg Lys Leu Trp Lys Arg Phe Phe Cys Phe Leu Arg Arg Ser
 245 250 255

Gly Leu Tyr Tyr Ser Thr Lys Gly Thr Ser Lys Asp Pro Arg His Leu
 260 265 270

Gln Tyr Val Ala Asp Val Asn Glu Ser Asn Val Tyr Val Val Thr Gln
 275 280 285

Gly Arg Lys Leu Tyr Gly Met Pro Thr Asp Phe Gly Phe Cys Val Lys
 290 295 300

Pro Asn Lys Leu Arg Asn Gly His Lys Gly Leu Arg Ile Phe Cys Ser
 305 310 315 320

Glu Asp Glu Gln Ser Arg Thr Cys Trp Leu Ala Ala Phe Arg Leu Phe
 325 330 335

Lys Tyr Gly Val Gln Leu Tyr Lys Asn Tyr Gln Gln Ala Gln Ser Arg
 340 345 350

His Leu His Pro Ser Cys Leu Gly Ser Pro Pro Leu Arg Ser Ala Ser
 355 360 365

Asp Asn Thr Leu Val Ala Met Asp Phe Ser Gly His Ala Gly Arg Val
 370 375 380

Ile Glu Asn Pro Arg Glu Ala Leu Ser Val Ala Leu Glu Glu Ala Gln
 385 390 395 400

Ala Trp Arg Lys Lys Thr Asn His Arg Leu Ser Leu Pro Met Pro Ala
 405 410 415

Ser Gly Thr Ser Leu Ser Ala Ala Ile His Arg Thr Gln Leu Trp Phe
 420 425 430

His Gly Arg Ile Ser Arg Glu Glu Ser Gln Arg Leu Ile Gly Gln Gln
 435 440 445

Gly Leu Val Asp Gly Leu Phe Leu Val Arg Glu Ser Gln Arg Asn Pro
 450 455 460

Gln Gly Phe Val Leu Ser Leu Cys His Leu Gln Lys Val Lys His Tyr
 465 470 475 480

Leu Ile Leu Pro Ser Glu Glu Glu Gly Arg Leu Tyr Phe Ser Met Asp
 485 490 495

Asp Gly Gln Thr Arg Phe Thr Asp Leu Leu Gln Leu Val Glu Phe His
 500 505 510

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Gln Leu Asn Arg Gly Ile Leu Pro Cys Leu Leu Arg His Cys Cys Thr
 515 520 525

Arg Val Ala Leu
 530

<210> 186
 <211> 1342
 <212> PRT
 <213> Homo sapiens
 <400> 186

Met Arg Ala Asn Asp Ala Leu Gln Val Leu Gly Leu Leu Phe Ser Leu
 1 5 10 15

Ala Arg Gly Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr
 20 25 30

Leu Asn Gly Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr
 35 40 45

Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu
 50 55 60

Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile
 65 70 75 80

Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr
 85 90 95

Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp
 100 105 110

Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser
 115 120 125

His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser
 130 135 140

Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr
 145 150 155 160

Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val
 165 170 175

Lys Asp Asn Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly
 180 185 190

Arg Cys Trp Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr
 195 200 205

Ile Cys Ala Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn
 210 215 220

Gln Cys Cys His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp
 225 230 235 240

Thr Asp Cys Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val
 245 250 255

Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu
 260 265 270

Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 275 280 285

Ser Cys Pro His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala
 290 295 300

Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys
 305 310 315 320

Glu Pro Cys Gly Gly Leu Cys Pro Lys Ala Cys Glu Gly Thr Gly Ser
 325 330 335

Gly Ser Arg Phe Gln Thr Val Asp Ser Ser Asn Ile Asp Gly Phe Val
 340 345 350

Asn Cys Thr Lys Ile Leu Gly Asn Leu Asp Phe Leu Ile Thr Gly Leu
 355 360 365

Asn Gly Asp Pro Trp His Lys Ile Pro Ala Leu Asp Pro Glu Lys Leu
 370 375 380

Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly Tyr Leu Asn Ile Gln
 385 390 395 400

Ser Trp Pro Pro His Met His Asn Phe Ser Val Phe Ser Asn Leu Thr
 405 410 415

Thr Ile Gly Gly Arg Ser Leu Tyr Asn Arg Gly Phe Ser Leu Leu Ile
 420 425 430

Met Lys Asn Leu Asn Val Thr Ser Leu Gly Phe Arg Ser Leu Lys Glu
 435 440 445

Ile Ser Ala Gly Arg Ile Tyr Ile Ser Ala Asn Arg Gln Leu Cys Tyr
 450 455 460

His His Ser Leu Asn Trp Thr Lys Val Leu Arg Gly Pro Thr Glu Glu
 465 470 475 480

Arg Leu Asp Ile Lys His Asn Arg Pro Arg Arg Asp Cys Val Ala Glu
 485 490 495

Gly Lys Val Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp Gly Pro
 500 505 510

Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg Gly Gly Val
 515 520 525

Cys Val Thr His Cys Asn Phe Leu Asn Gly Glu Pro Arg Glu Phe Ala
 530 535 540

His Glu Ala Glu Cys Phe Ser Cys His Pro Glu Cys Gln Pro Met Glu
 545 550 555 560

Gly Thr Ala Thr Cys Asn Gly Ser Gly Ser Asp Thr Cys Ala Gln Cys
 565 570 575

Ala His Phe Arg Asp Gly Pro His Cys Val Ser Ser Cys Pro His Gly
 580 585 590

Val Leu Gly Ala Lys Gly Pro Ile Tyr Lys Tyr Pro Asp Val Gln Asn
 595 600 605

Glu Cys Arg Pro Cys His Glu Asn Cys Thr Gln Gly Cys Lys Gly Pro
 610 615 620

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Glu Leu Gln Asp Cys Leu Gly Gln Thr Leu Val Leu Ile Gly Lys Thr
625 630 635 640

His Leu Thr Met Ala Leu Thr Val Ile Ala Gly Leu Val Val Ile Phe
645 650 655

Met Met Leu Gly Gly Thr Phe Leu Tyr Trp Arg Gly Arg Arg Ile Gln
660 665 670

Asn Lys Arg Ala Met Arg Arg Tyr Leu Glu Arg Gly Glu Ser Ile Glu
675 680 685

Pro Leu Asp Pro Ser Glu Lys Ala Asn Lys Val Leu Ala Arg Ile Phe
690 695 700

Lys Glu Thr Glu Leu Arg Lys Leu Lys Val Leu Gly Ser Gly Val Phe
705 710 715 720

Gly Thr Val His Lys Gly Val Trp Ile Pro Glu Gly Glu Ser Ile Lys
725 730 735

Ile Pro Val Cys Ile Lys Val Ile Glu Asp Lys Ser Gly Arg Gln Ser
740 745 750

Phe Gln Ala Val Thr Asp His Met Leu Ala Ile Gly Ser Leu Asp His
755 760 765

Ala His Ile Val Arg Leu Leu Gly Leu Cys Pro Gly Ser Ser Leu Gln
770 775 780

Leu Val Thr Gln Tyr Leu Pro Leu Gly Ser Leu Leu Asp His Val Arg
785 790 795 800

Gln His Arg Gly Ala Leu Gly Pro Gln Leu Leu Leu Asn Trp Gly Val
805 810 815

Gln Ile Ala Lys Gly Met Tyr Tyr Leu Glu Glu His Gly Met Val His
820 825 830

Arg Asn Leu Ala Ala Arg Asn Val Leu Leu Lys Ser Pro Ser Gln Val
835 840 845

Gln Val Ala Asp Phe Gly Val Ala Asp Leu Leu Pro Pro Asp Asp Lys
850 855 860

Gln Leu Leu Tyr Ser Glu Ala Lys Thr Pro Ile Lys Trp Met Ala Leu
865 870 875 880

Glu Ser Ile His Phe Gly Lys Tyr Thr His Gln Ser Asp Val Trp Ser
885 890 895

Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ala Glu Pro Tyr
900 905 910

Ala Gly Leu Arg Leu Ala Glu Val Pro Asp Leu Leu Glu Lys Gly Glu
915 920 925

Arg Leu Ala Gln Pro Gln Ile Cys Thr Ile Asp Val Tyr Met Val Met
930 935 940

Val Lys Cys Trp Met Ile Asp Glu Asn Ile Arg Pro Thr Phe Lys Glu
945 950 955 960

Leu Ala Asn Glu Phe Thr Arg Met Ala Arg Asp Pro Pro Arg Tyr Leu

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 965 970 975

Val Ile Lys Arg Glu Ser Gly Pro Gly Ile Ala Pro Gly Pro Glu Pro
 980 985 990

His Gly Leu Thr Asn Lys Lys Leu Glu Glu Val Glu Leu Glu Pro Glu
 995 1000 1005

Leu Asp Leu Asp Leu Asp Leu Glu Ala Glu Glu Asp Asn Leu Ala
 1010 1015 1020

Thr Thr Thr Leu Gly Ser Ala Leu Ser Leu Pro Val Gly Thr Leu
 1025 1030 1035

Asn Arg Pro Arg Gly Ser Gln Ser Leu Leu Ser Pro Ser Ser Gly
 1040 1045 1050

Tyr Met Pro Met Asn Gln Gly Asn Leu Gly Glu Ser Cys Gln Glu
 1055 1060 1065

Ser Ala Val Ser Gly Ser Ser Glu Arg Cys Pro Arg Pro Val Ser
 1070 1075 1080

Leu His Pro Met Pro Arg Gly Cys Leu Ala Ser Glu Ser Ser Glu
 1085 1090 1095

Gly His Val Thr Gly Ser Glu Ala Glu Leu Gln Glu Lys Val Ser
 1100 1105 1110

Met Cys Arg Ser Arg Ser Arg Ser Arg Ser Pro Arg Pro Arg Gly
 1115 1120 1125

Asp Ser Ala Tyr His Ser Gln Arg His Ser Leu Leu Thr Pro Val
 1130 1135 1140

Thr Pro Leu Ser Pro Pro Gly Leu Glu Glu Glu Asp Val Asn Gly
 1145 1150 1155

Tyr Val Met Pro Asp Thr His Leu Lys Gly Thr Pro Ser Ser Arg
 1160 1165 1170

Glu Gly Thr Leu Ser Ser Val Gly Leu Ser Ser Val Leu Gly Thr
 1175 1180 1185

Glu Glu Glu Asp Glu Asp Glu Glu Tyr Glu Tyr Met Asn Arg Arg
 1190 1195 1200

Arg Arg His Ser Pro Pro His Pro Pro Arg Pro Ser Ser Leu Glu
 1205 1210 1215

Glu Leu Gly Tyr Glu Tyr Met Asp Val Gly Ser Asp Leu Ser Ala
 1220 1225 1230

Ser Leu Gly Ser Thr Gln Ser Cys Pro Leu His Pro Val Pro Ile
 1235 1240 1245

Met Pro Thr Ala Gly Thr Thr Pro Asp Glu Asp Tyr Glu Tyr Met
 1250 1255 1260

Asn Arg Gln Arg Asp Gly Gly Gly Pro Gly Gly Asp Tyr Ala Ala
 1265 1270 1275

Met Gly Ala Cys Pro Ala Ser Glu Gln Gly Tyr Glu Glu Met Arg
 1280 1285 1290

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ala Phe Gln Gly Pro Gly His Gln Ala Pro His Val His Tyr Ala
 1295 1300 1305

Arg Leu Lys Thr Leu Arg Ser Leu Glu Ala Thr Asp Ser Ala Phe
 1310 1315 1320

Asp Asn Pro Asp Tyr Trp His Ser Arg Leu Phe Pro Lys Ala Asn
 1325 1330 1335

Ala Gln Arg Thr
 1340

<210> 187
 <211> 1252
 <212> PRT
 <213> Homo sapiens

<400> 187

Met Ser Thr Thr Val Asn Val Asp Ser Leu Ala Glu Tyr Glu Lys Ser
 1 5 10 15

Gln Ile Lys Arg Ala Leu Glu Leu Gly Thr Val Met Thr Val Phe Ser
 20 25 30

Phe Arg Lys Ser Thr Pro Glu Arg Arg Thr Val Gln Val Ile Met Glu
 35 40 45

Thr Arg Gln Val Ala Trp Ser Lys Thr Ala Asp Lys Ile Glu Gly Phe
 50 55 60

Leu Asp Ile Met Glu Ile Lys Glu Ile Arg Pro Gly Lys Asn Ser Lys
 65 70 75 80

Asp Phe Glu Arg Ala Lys Ala Val Arg Gln Lys Glu Asp Cys Cys Phe
 85 90 95

Thr Ile Leu Tyr Gly Thr Gln Phe Val Leu Ser Thr Leu Ser Leu Ala
 100 105 110

Ala Asp Ser Lys Glu Asp Ala Val Asn Trp Leu Ser Gly Leu Lys Ile
 115 120 125

Leu His Gln Glu Ala Met Asn Ala Ser Thr Pro Thr Ile Ile Glu Ser
 130 135 140

Trp Leu Arg Lys Gln Ile Tyr Ser Val Asp Gln Thr Arg Arg Asn Ser
 145 150 155 160

Ile Ser Leu Arg Glu Leu Lys Thr Ile Leu Pro Leu Ile Asn Phe Lys
 165 170 175

Val Ser Ser Ala Lys Phe Leu Lys Asp Lys Phe Val Glu Ile Gly Ala
 180 185 190

His Lys Asp Glu Leu Ser Phe Glu Gln Phe His Leu Phe Tyr Lys Lys
 195 200 205

Leu Met Phe Glu Gln Gln Lys Ser Ile Leu Asp Glu Phe Lys Lys Asp
 210 215 220

Ser Ser Val Phe Ile Leu Gly Asn Thr Asp Arg Pro Asp Ala Ser Ala
 225 230 235 240

Val Tyr Leu His Asp Phe Gln Arg Phe Leu Ile His Glu Gln Gln Glu
 245 250 255

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

His Trp Ala Gln Asp Leu Asn Lys Val Arg Glu Arg Met Thr Lys Phe
 260 265 270

Ile Asp Asp Thr Met Arg Glu Thr Ala Glu Pro Phe Leu Phe Val Asp
 275 280 285

Glu Phe Leu Thr Tyr Leu Phe Ser Arg Glu Asn Ser Ile Trp Asp Glu
 290 295 300

Lys Tyr Asp Ala Val Asp Met Gln Asp Met Asn Asn Pro Leu Ser His
 305 310 315 320

Tyr Trp Ile Ser Ser Ser His Asn Thr Tyr Leu Thr Gly Asp Gln Leu
 325 330 335

Arg Ser Glu Ser Ser Pro Glu Ala Tyr Ile Arg Cys Leu Arg Met Gly
 340 345 350

Cys Arg Cys Ile Glu Leu Asp Cys Trp Asp Gly Pro Asp Gly Lys Pro
 355 360 365

Val Ile Tyr His Gly Trp Thr Arg Thr Thr Lys Ile Lys Phe Asp Asp
 370 375 380

Val Val Gln Ala Ile Lys Asp His Ala Phe Val Thr Ser Ser Phe Pro
 385 390 395 400

Val Ile Leu Ser Ile Glu Glu His Cys Ser Val Glu Gln Gln Arg His
 405 410 415

Met Ala Lys Ala Phe Lys Glu Val Phe Gly Asp Leu Leu Leu Thr Lys
 420 425 430

Pro Thr Glu Ala Ser Ala Asp Gln Leu Pro Ser Pro Ser Gln Leu Arg
 435 440 445

Glu Lys Ile Ile Ile Lys His Lys Lys Leu Gly Pro Arg Gly Asp Val
 450 455 460

Asp Val Asn Met Glu Asp Lys Lys Asp Glu His Lys Gln Gln Gly Glu
 465 470 475 480

Leu Tyr Met Trp Asp Ser Ile Asp Gln Lys Trp Thr Arg His Tyr Cys
 485 490 495

Ala Ile Ala Asp Ala Lys Leu Ser Phe Ser Asp Asp Ile Glu Gln Thr
 500 505 510

Met Glu Glu Glu Val Pro Gln Asp Ile Pro Pro Thr Glu Leu His Phe
 515 520 525

Gly Glu Lys Trp Phe His Lys Lys Val Glu Lys Arg Thr Ser Ala Glu
 530 535 540

Lys Leu Leu Gln Glu Tyr Cys Met Glu Thr Gly Gly Lys Asp Gly Thr
 545 550 555 560

Phe Leu Val Arg Glu Ser Glu Thr Phe Pro Asn Asp Tyr Thr Leu Ser
 565 570 575

Phe Trp Arg Ser Gly Arg Val Gln His Cys Arg Ile Arg Ser Thr Met
 580 585 590

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Glu Gly Gly Thr Leu Lys Tyr Tyr Leu Thr Asp Asn Leu Arg Phe Arg
 595 600 605

Arg Met Tyr Ala Leu Ile Gln His Tyr Arg Glu Thr His Leu Pro Cys
 610 615 620

Ala Glu Phe Glu Leu Arg Leu Thr Asp Pro Val Pro Asn Pro Asn Pro
 625 630 635 640

His Glu Ser Lys Pro Trp Tyr Tyr Asp Ser Leu Ser Arg Gly Glu Ala
 645 650 655

Glu Asp Met Leu Met Arg Ile Pro Arg Asp Gly Ala Phe Leu Ile Arg
 660 665 670

Lys Arg Glu Gly Ser Asp Ser Tyr Ala Ile Thr Phe Arg Ala Arg Gly
 675 680 685

Lys Val Lys His Cys Arg Ile Asn Arg Asp Gly Arg His Phe Val Leu
 690 695 700

Gly Thr Ser Ala Tyr Phe Glu Ser Leu Val Glu Leu Val Ser Tyr Tyr
 705 710 715 720

Glu Lys His Ser Leu Tyr Arg Lys Met Arg Leu Arg Tyr Pro Val Thr
 725 730 735

Pro Glu Leu Leu Glu Arg Tyr Asn Thr Glu Arg Asp Ile Asn Ser Leu
 740 745 750

Tyr Asp Val Ser Arg Met Tyr Val Asp Pro Ser Glu Ile Asn Pro Ser
 755 760 765

Met Pro Gln Arg Thr Val Lys Ala Leu Tyr Asp Tyr Lys Ala Lys Arg
 770 775 780

Ser Asp Glu Leu Ser Phe Cys Arg Gly Ala Leu Ile His Asn Val Ser
 785 790 795 800

Lys Glu Pro Gly Gly Trp Trp Lys Gly Asp Tyr Gly Thr Arg Ile Gln
 805 810 815

Gln Tyr Phe Pro Ser Asn Tyr Val Glu Asp Ile Ser Thr Ala Asp Phe
 820 825 830

Glu Glu Leu Glu Lys Gln Ile Ile Glu Asp Asn Pro Leu Gly Ser Leu
 835 840 845

Cys Arg Gly Ile Leu Asp Leu Asn Thr Tyr Asn Val Val Lys Ala Pro
 850 855 860

Gln Gly Lys Asn Gln Lys Ser Phe Val Phe Ile Leu Glu Pro Lys Glu
 865 870 875 880

Gln Gly Asp Pro Pro Val Glu Phe Ala Thr Asp Arg Val Glu Glu Leu
 885 890 895

Phe Glu Trp Phe Gln Ser Ile Arg Glu Ile Thr Trp Lys Ile Asp Ser
 900 905 910

Lys Glu Asn Asn Met Lys Tyr Trp Glu Lys Asn Gln Ser Ile Ala Ile
 915 920 925

Glu Leu Ser Asp Leu Val Val Tyr Cys Lys Pro Thr Ser Lys Thr Lys
 930 935 940

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Asp Asn Leu Glu Asn Pro Asp Phe Arg Glu Ile Arg Ser Phe Val Glu
 945 950 955 960
 Thr Lys Ala Asp Ser Ile Ile Arg Gln Lys Pro Val Asp Leu Leu Lys
 965 970 975
 Tyr Asn Gln Lys Gly Leu Thr Arg Val Tyr Pro Lys Gly Gln Arg Val
 980 985 990
 Asp Ser Ser Asn Tyr Asp Pro Phe Arg Leu Trp Leu Cys Gly Ser Gln
 995 1000 1005
 Met Val Ala Leu Asn Phe Gln Thr Ala Asp Lys Tyr Met Gln Met
 1010 1015 1020
 Asn His Ala Leu Phe Ser Leu Asn Gly Arg Thr Gly Tyr Val Leu
 1025 1030 1035
 Gln Pro Glu Ser Met Arg Thr Glu Lys Tyr Asp Pro Met Pro Pro
 1040 1045 1050
 Glu Ser Gln Arg Lys Ile Leu Met Thr Leu Thr Val Lys Val Leu
 1055 1060 1065
 Gly Ala Arg His Leu Pro Lys Leu Gly Arg Ser Ile Ala Cys Pro
 1070 1075 1080
 Phe Val Glu Val Glu Ile Cys Gly Ala Glu Tyr Gly Asn Asn Lys
 1085 1090 1095
 Phe Lys Thr Thr Val Val Asn Asp Asn Gly Leu Ser Pro Ile Trp
 1100 1105 1110
 Ala Pro Thr Gln Glu Lys Val Thr Phe Glu Ile Tyr Asp Pro Asn
 1115 1120 1125
 Leu Ala Phe Leu Arg Phe Val Val Tyr Glu Glu Asp Met Phe Ser
 1130 1135 1140
 Asp Pro Asn Phe Leu Ala His Ala Thr Tyr Pro Ile Lys Ala Val
 1145 1150 1155
 Lys Ser Gly Phe Arg Ser Val Pro Leu Lys Asn Gly Tyr Ser Glu
 1160 1165 1170
 Asp Ile Glu Leu Ala Ser Leu Leu Val Phe Cys Glu Met Arg Pro
 1175 1180 1185
 Val Leu Glu Ser Glu Glu Glu Leu Tyr Ser Ser Cys Arg Gln Leu
 1190 1195 1200
 Arg Arg Arg Gln Glu Glu Leu Asn Asn Gln Leu Phe Leu Tyr Asp
 1205 1210 1215
 Thr His Gln Asn Leu Arg Asn Ala Asn Arg Asp Ala Leu Val Lys
 1220 1225 1230
 Glu Phe Ser Val Asn Glu Asn His Ser Ser Cys Thr Arg Arg Asn
 1235 1240 1245
 Ala Thr Arg Gly
 1250

Protein: Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

<210> 188
 <211> 906
 <212> PRT
 <213> Homo sapiens

<400> 188

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly
 1 5 10 15

Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala
 20 25 30

Phe Gln Pro His His His His His His Leu Ser Pro His Pro Pro
 35 40 45

Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp
 50 55 60

Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser
 65 70 75 80

Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg
 85 90 95

Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn
 100 105 110

Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln
 115 120 125

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn
 130 135 140

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His
 145 150 155 160

Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly
 165 170 175

Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys
 180 185 190

Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala
 195 200 205

Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu
 210 215 220

Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu
 225 230 235 240

Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg
 245 250 255

Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu
 260 265 270

Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro
 275 280 285

Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala
 290 295 300

Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His
 305 310 315 320

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe
 325 330 335

Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu
 340 345 350

Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr
 355 360 365

Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys
 370 375 380

Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met
 385 390 395 400

Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys
 405 410 415

Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp
 420 425 430

Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu
 435 440 445

Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Asp Glu Arg Ala Asp
 450 455 460

Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg
 465 470 475 480

Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val
 485 490 495

Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser
 500 505 510

Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His
 515 520 525

Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro
 530 535 540

Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro
 545 550 555 560

Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp
 565 570 575

Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro
 580 585 590

Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro
 595 600 605

Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu
 610 615 620

Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr
 625 630 635 640

Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly
 645 650 655

Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 660 665 670

Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro
 675 680 685

Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Tyr Met Thr Pro Ser
 690 695 700

Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys
 705 710 715 720

Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn
 725 730 735

Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu
 740 745 750

Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu
 755 760 765

Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val
 770 775 780

Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe
 785 790 795 800

Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly
 805 810 815

Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn
 820 825 830

Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala
 835 840 845

Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu
 850 855 860

Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile
 865 870 875 880

Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val
 885 890 895

Ser Ile Ser Ser Pro Ala His Val Ala Thr
 900 905

<210> 189
 <211> 1242
 <212> PRT
 <213> Homo sapiens

<400> 189

Met Ala Ser Pro Pro Glu Ser Asp Gly Phe Ser Asp Val Arg Lys Val
 1 5 10 15

Gly Tyr Leu Arg Lys Pro Lys Ser Met His Lys Arg Phe Phe Val Leu
 20 25 30

Arg Ala Ala Ser Glu Ala Gly Gly Pro Ala Arg Leu Glu Tyr Tyr Glu
 35 40 45

Asn Glu Lys Lys Trp Arg His Lys Ser Ser Ala Pro Lys Arg Ser Ile
 50 55 60

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Pro Leu Glu Ser Cys Phe Asn Ile Asn Lys Arg Ala Asp Ser Lys Asn
 65 70 75 80

Lys His Leu Val Ala Leu Tyr Thr Arg Asp Glu His Phe Ala Ile Ala
 85 90 95

Ala Asp Ser Glu Ala Glu Gln Asp Ser Trp Tyr Gln Ala Leu Leu Gln
 100 105 110

Leu His Asn Arg Ala Lys Gly His His Asp Gly Ala Ala Ala Leu Gly
 115 120 125

Ala Gly Gly Gly Gly Gly Ser Cys Ser Gly Ser Ser Gly Leu Gly Glu
 130 135 140

Ala Gly Glu Asp Leu Ser Tyr Gly Asp Val Pro Pro Gly Pro Ala Phe
 145 150 155 160

Lys Glu Val Trp Gln Val Ile Leu Lys Pro Lys Gly Leu Gly Gln Thr
 165 170 175

Lys Asn Leu Ile Gly Ile Tyr Arg Leu Cys Leu Thr Ser Lys Thr Ile
 180 185 190

Ser Phe Val Lys Leu Asn Ser Glu Ala Ala Ala Val Val Leu Gln Leu
 195 200 205

Met Asn Ile Arg Arg Cys Gly His Ser Glu Asn Phe Phe Phe Ile Glu
 210 215 220

Val Gly Arg Ser Ala Val Thr Gly Pro Gly Glu Phe Trp Met Gln Val
 225 230 235 240

Asp Asp Ser Val Val Ala Gln Asn Met His Glu Thr Ile Leu Glu Ala
 245 250 255

Met Arg Ala Met Ser Asp Glu Phe Arg Pro Arg Ser Lys Ser Gln Ser
 260 265 270

Ser Ser Asn Cys Ser Asn Pro Ile Ser Val Pro Leu Arg Arg His His
 275 280 285

Leu Asn Asn Pro Pro Pro Ser Gln Val Gly Leu Thr Arg Arg Ser Arg
 290 295 300

Thr Glu Ser Ile Thr Ala Thr Ser Pro Ala Ser Met Val Gly Gly Lys
 305 310 315 320

Pro Gly Ser Phe Arg Val Arg Ala Ser Ser Asp Gly Glu Gly Thr Met
 325 330 335

Ser Arg Pro Ala Ser Val Asp Gly Ser Pro Val Ser Pro Ser Thr Asn
 340 345 350

Arg Thr His Ala His Arg His Arg Gly Ser Ala Arg Leu His Pro Pro
 355 360 365

Leu Asn His Ser Arg Ser Ile Pro Met Pro Ala Ser Arg Cys Ser Pro
 370 375 380

Ser Ala Thr Ser Pro Val Ser Leu Ser Ser Ser Ser Thr Ser Gly His
 385 390 395 400

Gly Ser Thr Ser Asp Cys Leu Phe Pro Arg Arg Ser Ser Ala Ser Val
 405 410 415

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ser Gly Ser Pro Ser Asp Gly Gly Phe Ile Ser Ser Asp Glu Tyr Gly
420 425 430

Ser Ser Pro Cys Asp Phe Arg Ser Ser Phe Arg Ser Val Thr Pro Asp
435 440 445

Ser Leu Gly His Thr Pro Pro Ala Arg Gly Glu Glu Glu Leu Ser Asn
450 455 460

Tyr Ile Cys Met Gly Gly Lys Gly Pro Ser Thr Leu Thr Ala Pro Asn
465 470 475 480

Gly His Tyr Ile Leu Ser Arg Gly Gly Asn Gly His Arg Cys Thr Pro
485 490 495

Gly Thr Gly Leu Gly Thr Ser Pro Ala Leu Ala Gly Asp Glu Ala Ala
500 505 510

Ser Ala Ala Asp Leu Asp Asn Arg Phe Arg Lys Arg Thr His Ser Ala
515 520 525

Gly Thr Ser Pro Thr Ile Thr His Gln Lys Thr Pro Ser Gln Ser Ser
530 535 540

Val Ala Ser Ile Glu Glu Tyr Thr Glu Met Met Pro Ala Tyr Pro Pro
545 550 555 560

Gly Gly Gly Ser Gly Gly Arg Leu Pro Gly His Arg His Ser Ala Phe
565 570 575

Val Pro Thr Arg Ser Tyr Pro Glu Glu Gly Leu Glu Met His Pro Leu
580 585 590

Glu Arg Arg Gly Gly His His Arg Pro Asp Ser Ser Thr Leu His Thr
595 600 605

Asp Asp Gly Tyr Met Pro Met Ser Pro Gly Val Ala Pro Val Pro Ser
610 615 620

Gly Arg Lys Gly Ser Gly Asp Tyr Met Pro Met Ser Pro Lys Ser Val
625 630 635 640

Ser Ala Pro Gln Gln Ile Ile Asn Pro Ile Arg Arg His Pro Gln Arg
645 650 655

Val Asp Pro Asn Gly Tyr Met Met Met Ser Pro Ser Gly Gly Cys Ser
660 665 670

Pro Asp Ile Gly Gly Gly Pro Ser Ser Ser Ser Ser Ser Ser Asn Ala
675 680 685

Val Pro Ser Gly Thr Ser Tyr Gly Lys Leu Trp Thr Asn Gly Val Gly
690 695 700

Gly His His Ser His Val Leu Pro His Pro Lys Pro Pro Val Glu Ser
705 710 715 720

Ser Gly Gly Lys Leu Leu Pro Cys Thr Gly Asp Tyr Met Asn Met Ser
725 730 735

Pro Val Gly Asp Ser Asn Thr Ser Ser Pro Ser Asp Cys Tyr Tyr Gly
740 745 750

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 Pro Glu Asp Pro Gln His Lys Pro Val Leu Ser Tyr Tyr Ser Leu Pro
 755 760 765

Arg Ser Phe Lys His Thr Gln Arg Pro Gly Glu Pro Glu Glu Gly Ala
 770 775 780

Arg His Gln His Leu Arg Leu Ser Thr Ser Ser Gly Arg Leu Leu Tyr
 785 790 795 800

Ala Ala Thr Ala Asp Asp Ser Ser Ser Ser Thr Ser Ser Asp Ser Leu
 805 810 815

Gly Gly Gly Tyr Cys Gly Ala Arg Leu Glu Pro Ser Leu Pro His Pro
 820 825 830

His His Gln Val Leu Gln Pro His Leu Pro Arg Lys Val Asp Thr Ala
 835 840 845

Ala Gln Thr Asn Ser Arg Leu Ala Arg Pro Thr Arg Leu Ser Leu Gly
 850 855 860

Asp Pro Lys Ala Ser Thr Leu Pro Arg Ala Arg Glu Gln Gln Gln Gln
 865 870 875 880

Gln Gln Pro Leu Leu His Pro Pro Glu Pro Lys Ser Pro Gly Glu Tyr
 885 890 895

Val Asn Ile Glu Phe Gly Ser Asp Gln Ser Gly Tyr Leu Ser Gly Pro
 900 905 910

Val Ala Phe His Ser Ser Pro Ser Val Arg Cys Pro Ser Gln Leu Gln
 915 920 925

Pro Ala Pro Arg Glu Glu Glu Thr Gly Thr Glu Glu Tyr Met Lys Met
 930 935 940

Asp Leu Gly Pro Gly Arg Arg Ala Ala Trp Gln Glu Ser Thr Gly Val
 945 950 955 960

Glu Met Gly Arg Leu Gly Pro Ala Pro Pro Gly Ala Ala Ser Ile Cys
 965 970 975

Arg Pro Thr Arg Ala Val Pro Ser Ser Arg Gly Asp Tyr Met Thr Met
 980 985 990

Gln Met Ser Cys Pro Arg Gln Ser Tyr Val Asp Thr Ser Pro Ala Ala
 995 1000 1005

Pro Val Ser Tyr Ala Asp Met Arg Thr Gly Ile Ala Ala Glu Glu
 1010 1015 1020

Val Ser Leu Pro Arg Ala Thr Met Ala Ala Ala Ser Ser Ser Ser
 1025 1030 1035

Ala Ala Ser Ala Ser Pro Thr Gly Pro Gln Gly Ala Ala Glu Leu
 1040 1045 1050

Ala Ala His Ser Ser Leu Leu Gly Gly Pro Gln Gly Pro Gly Gly
 1055 1060 1065

Met Ser Ala Phe Thr Arg Val Asn Leu Ser Pro Asn Arg Asn Gln
 1070 1075 1080

Ser Ala Lys Val Ile Arg Ala Asp Pro Gln Gly Cys Arg Arg Arg
 1085 1090 1095

protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

His Ser Ser Glu Thr Phe Ser Ser Thr Pro Ser Ala Thr Arg Val
1100 1105 1110

Gly Asn Thr Val Pro Phe Gly Ala Gly Ala Ala Val Gly Gly Gly
1115 1120 1125

Gly Gly Ser Ser Ser Ser Ser Glu Asp Val Lys Arg His Ser Ser
1130 1135 1140

Ala Ser Phe Glu Asn Val Trp Leu Arg Pro Gly Glu Leu Gly Gly
1145 1150 1155

Ala Pro Lys Glu Pro Ala Lys Leu Cys Gly Ala Ala Gly Gly Leu
1160 1165 1170

Glu Asn Gly Leu Asn Tyr Ile Asp Leu Asp Leu Val Lys Asp Phe
1175 1180 1185

Lys Gln Cys Pro Gln Glu Cys Thr Pro Glu Pro Gln Pro Pro Pro
1190 1195 1200

Pro Pro Pro Pro His Gln Pro Leu Gly Ser Gly Glu Ser Ser Ser
1205 1210 1215

Thr Arg Arg Ser Ser Glu Asp Leu Ser Ala Tyr Ala Ser Ile Ser
1220 1225 1230

Phe Gln Lys Gln Pro Glu Asp Arg Gln
1235 1240

<210> 190
<211> 1324
<212> PRT
<213> Homo sapiens

<400> 190

Met Ala Ser Pro Pro Arg His Gly Pro Pro Gly Pro Ala Ser Gly Asp
1 5 10 15

Gly Pro Asn Leu Asn Asn Asn Asn Asn Asn Asn His Ser Val Arg
20 25 30

Lys Cys Gly Tyr Leu Arg Lys Gln Lys His Gly His Lys Arg Phe Phe
35 40 45

Val Leu Arg Gly Pro Gly Ala Gly Gly Asp Lys Ala Thr Ala Gly Gly
50 55 60

Gly Ser Ala Pro Gln Pro Pro Arg Leu Glu Tyr Tyr Glu Ser Glu Lys
65 70 75 80

Asn Trp Arg Ser Lys Ala Gly Ala Pro Lys Arg Val Ile Ala Leu Asp
85 90 95

Cys Cys Leu Asn Ile Asn Lys Arg Ala Asp Pro Lys His Lys Tyr Leu
100 105 110

Ile Ala Leu Tyr Thr Lys Asp Glu Tyr Phe Ala Val Ala Ala Glu Asn
115 120 125

Glu Gln Glu Gln Glu Gly Trp Tyr Arg Ala Leu Thr Asp Leu Val Ser
130 135 140

Glu Gly Arg Ala Ala Ala Gly Asp Ala Pro Pro Ala Ala Ala Pro Ala

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 145 150 155 160

Ala Ser Cys Ser Ala Ser Leu Pro Gly Ala Val Gly Gly Ser Ala Gly
 165 170 175

Ala Ala Gly Ala Glu Asp Ser Tyr Gly Leu Val Ala Pro Ala Thr Ala
 180 185 190

Ala Tyr Arg Glu Val Trp Gln Val Asn Leu Lys Pro Lys Gly Leu Gly
 195 200 205

Gln Ser Lys Asn Leu Thr Gly Val Tyr Arg Leu Cys Leu Ser Ala Arg
 210 215 220

Thr Ile Gly Phe Val Lys Leu Asn Cys Glu Gln Pro Ser Val Thr Leu
 225 230 235 240

Gln Leu Met Asn Ile Arg Arg Cys Gly His Ser Asp Ser Phe Phe Phe
 245 250 255

Ile Glu Val Gly Arg Ser Ala Val Thr Gly Pro Gly Glu Leu Trp Met
 260 265 270

Gln Ala Asp Asp Ser Val Val Ala Gln Asn Ile His Glu Thr Ile Leu
 275 280 285

Glu Ala Met Lys Ala Leu Lys Glu Leu Phe Glu Phe Arg Pro Arg Ser
 290 295 300

Lys Ser Gln Ser Ser Gly Ser Ser Ala Thr His Pro Ile Ser Val Pro
 305 310 315 320

Gly Ala Arg Arg His His His Leu Val Asn Leu Pro Pro Ser Gln Thr
 325 330 335

Gly Leu Val Arg Arg Ser Arg Thr Asp Ser Leu Ala Ala Thr Pro Pro
 340 345 350

Ala Ala Lys Cys Ser Ser Cys Arg Val Arg Thr Ala Ser Glu Gly Asp
 355 360 365

Gly Gly Ala Ala Ala Gly Ala Ala Ala Ala Gly Ala Arg Pro Val Ser
 370 375 380

Val Ala Gly Ser Pro Leu Ser Pro Gly Pro Val Arg Ala Pro Leu Ser
 385 390 395 400

Arg Ser His Thr Leu Ile Gly Gly Cys Arg Ala Ala Gly Thr Lys Trp
 405 410 415

His Cys Phe Pro Ala Gly Gly Gly Leu Gln His Ser Arg Ser Met Ser
 420 425 430

Met Pro Val Glu His Leu Pro Pro Ala Ala Thr Ser Pro Gly Ser Leu
 435 440 445

Ser Ser Ser Ser Asp His Gly Trp Gly Ser Tyr Pro Pro Pro Gly
 450 455 460

Pro His Pro Leu Leu Pro His Pro Leu His His Gly Pro Gly Gln Arg
 465 470 475 480

Pro Ser Ser Gly Ser Ala Ser Ala Ser Gly Ser Pro Ser Asp Pro Gly
 485 490 495

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Phe Met Ser Leu Asp Glu Tyr Gly Ser Ser Pro Gly Asp Leu Arg Ala
500 505 510

Phe Cys Ser His Arg Ser Asn Thr Pro Glu Ser Ile Ala Glu Thr Pro
515 520 525

Pro Ala Arg Asp Gly Gly Gly Gly Glu Phe Tyr Gly Tyr Met Thr
530 535 540

Met Asp Arg Pro Leu Ser His Cys Gly Arg Ser Tyr Arg Arg Val Ser
545 550 555 560

Gly Asp Ala Ala Gln Asp Leu Asp Arg Gly Leu Arg Lys Arg Thr Tyr
565 570 575

Ser Leu Thr Thr Pro Ala Arg Gln Arg Pro Val Pro Gln Pro Ser Ser
580 585 590

Ala Ser Leu Asp Glu Tyr Thr Leu Met Arg Ala Thr Phe Ser Gly Ser
595 600 605

Ala Gly Arg Leu Cys Pro Ser Cys Pro Ala Ser Ser Pro Lys Val Ala
610 615 620

Tyr His Pro Tyr Pro Glu Asp Tyr Gly Asp Ile Glu Ile Gly Ser His
625 630 635 640

Arg Ser Ser Ser Ser Asn Leu Gly Ala Asp Asp Gly Tyr Met Pro Met
645 650 655

Thr Pro Gly Ala Ala Leu Ala Gly Ser Gly Ser Gly Ser Cys Arg Ser
660 665 670

Asp Asp Tyr Met Pro Met Ser Pro Ala Ser Val Ser Ala Pro Lys Gln
675 680 685

Ile Leu Gln Pro Arg Ala Ala Ala Ala Ala Ala Ala Val Pro Phe
690 695 700

Ala Gly Pro Ala Gly Pro Ala Pro Thr Phe Ala Ala Gly Arg Thr Phe
705 710 715 720

Pro Ala Ser Gly Gly Gly Tyr Lys Ala Ser Ser Pro Ala Glu Ser Ser
725 730 735

Pro Glu Asp Ser Gly Tyr Met Arg Met Trp Cys Gly Ser Lys Leu Ser
740 745 750

Met Glu His Ala Asp Gly Lys Leu Leu Pro Asn Gly Asp Tyr Leu Asn
755 760 765

Val Ser Pro Ser Asp Ala Val Thr Thr Gly Thr Pro Pro Asp Phe Phe
770 775 780

Ser Ala Ala Leu His Pro Gly Gly Glu Pro Leu Arg Gly Val Pro Gly
785 790 795 800

Cys Cys Tyr Ser Ser Leu Pro Arg Ser Tyr Lys Ala Pro Tyr Thr Cys
805 810 815

Gly Gly Asp Ser Asp Gln Tyr Val Leu Met Ser Ser Pro Val Gly Arg
820 825 830

Ile Leu Glu Glu Glu Arg Leu Glu Pro Gln Ala Thr Pro Gly Pro Thr

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 835 840 845

Gln Ala Ala Ser Ala Phe Gly Ala Gly Pro Thr Gln Pro Pro His Pro
 850 855 860

Val Val Pro Ser Pro Val Arg Pro Ser Gly Gly Arg Pro Glu Gly Phe
 865 870 875 880

Leu Gly Gln Arg Gly Arg Ala Val Arg Pro Thr Arg Leu Ser Leu Glu
 885 890 895

Gly Leu Pro Ser Leu Pro Ser Met His Glu Tyr Pro Leu Pro Pro Glu
 900 905 910

Pro Lys Ser Pro Gly Glu Tyr Ile Asn Ile Asp Phe Gly Glu Pro Gly
 915 920 925

Ala Arg Leu Ser Pro Pro Ala Pro Pro Leu Leu Ala Ser Ala Ala Ser
 930 935 940

Ser Ser Ser Leu Leu Ser Ala Ser Ser Pro Ala Leu Ser Leu Gly Ser
 945 950 955 960

Gly Thr Pro Gly Thr Ser Ser Asp Ser Arg Gln Arg Ser Pro Leu Ser
 965 970 975

Asp Tyr Met Asn Leu Asp Phe Ser Ser Pro Lys Ser Pro Lys Pro Gly
 980 985 990

Ala Pro Ser Gly His Pro Val Gly Ser Leu Asp Gly Leu Leu Ser Pro
 995 1000 1005

Glu Ala Ser Ser Pro Tyr Pro Pro Leu Pro Pro Arg Pro Ser Ala
 1010 1015 1020

Ser Pro Ser Ser Ser Leu Gln Pro Pro Pro Pro Pro Pro Ala Pro
 1025 1030 1035

Gly Glu Leu Tyr Arg Leu Pro Pro Ala Ser Ala Val Ala Thr Ala
 1040 1045 1050

Gln Gly Pro Gly Ala Ala Ser Ser Leu Ser Ser Asp Thr Gly Asp
 1055 1060 1065

Asn Gly Asp Tyr Thr Glu Met Ala Phe Gly Val Ala Ala Thr Pro
 1070 1075 1080

Pro Gln Pro Ile Ala Ala Pro Pro Lys Pro Glu Ala Ala Arg Val
 1085 1090 1095

Ala Ser Pro Thr Ser Gly Val Lys Arg Leu Ser Leu Met Glu Gln
 1100 1105 1110

Val Ser Gly Val Glu Ala Phe Leu Gln Ala Ser Gln Pro Pro Asp
 1115 1120 1125

Pro His Arg Gly Ala Lys Val Ile Arg Ala Asp Pro Gln Gly Gly
 1130 1135 1140

Arg Arg Arg His Ser Ser Glu Thr Phe Ser Ser Thr Thr Thr Val
 1145 1150 1155

Thr Pro Val Ser Pro Ser Phe Ala His Asn Pro Lys Arg His Asn
 1160 1165 1170

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ser Ala Ser Val Glu Asn Val Ser Leu Arg Lys Ser Ser Glu Gly
1175 1180 1185

Gly Val Gly Val Gly Pro Gly Gly Gly Asp Glu Pro Pro Thr Ser
1190 1195 1200

Pro Arg Gln Leu Gln Pro Ala Pro Pro Leu Ala Pro Gln Gly Arg
1205 1210 1215

Pro Trp Thr Pro Gly Gln Pro Gly Gly Leu Val Gly Cys Pro Gly
1220 1225 1230

Ser Gly Gly Ser Pro Met Arg Arg Glu Thr Ser Ala Gly Phe Gln
1235 1240 1245

Asn Gly Leu Lys Tyr Ile Ala Ile Asp Val Arg Glu Glu Pro Gly
1250 1255 1260

Leu Pro Pro Gln Pro Gln Pro Pro Pro Pro Pro Leu Pro Gln Pro
1265 1270 1275

Gly Asp Lys Ser Ser Trp Gly Arg Thr Arg Ser Leu Gly Gly Leu
1280 1285 1290

Ile Ser Ala Val Gly Val Gly Ser Thr Arg Gly Gly Cys Gly Gly
1295 1300 1305

Pro Gly Pro Gly Ala Pro Ala Pro Cys Pro Thr Thr Tyr Ala Gln
1310 1315 1320

His

<210> 191
<211> 168
<212> PRT
<213> Homo sapiens

<400> 191

Met Phe Gln Ile Pro Glu Phe Glu Pro Ser Glu Gln Glu Asp Ser Ser
1 5 10 15

Ser Ala Glu Arg Gly Leu Gly Pro Ser Pro Ala Gly Asp Gly Pro Ser
20 25 30

Gly Ser Gly Lys His His Arg Gln Ala Pro Gly Leu Leu Trp Asp Ala
35 40 45

Ser His Gln Gln Glu Gln Pro Thr Ser Ser Ser His His Gly Gly Ala
50 55 60

Gly Ala Val Glu Ile Arg Ser Arg His Ser Ser Tyr Pro Ala Gly Thr
65 70 75 80

Glu Asp Asp Glu Gly Met Gly Glu Glu Pro Ser Pro Phe Arg Gly Arg
85 90 95

Ser Arg Ser Ala Pro Pro Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg
100 105 110

Glu Leu Arg Arg Met Ser Asp Glu Phe Val Asp Ser Phe Lys Lys Gly
115 120 125

Leu Pro Arg Pro Lys Ser Ala Gly Thr Ala Thr Gln Met Arg Gln Ser
130 135 140

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ser Ser Trp Thr Arg Val Phe Gln Ser Trp Trp Asp Arg Asn Leu Gly
145 150 155 160

Arg Gly Ser Ser Ala Pro Ser Gln
165

<210> 192
<211> 373
<212> PRT
<213> Homo sapiens

<400> 192

Met Thr Thr Ser Ala Ser Ser His Leu Asn Lys Gly Ile Lys Gln Val
1 5 10 15

Tyr Met Ser Leu Pro Gln Gly Glu Lys Val Gln Ala Met Tyr Ile Trp
20 25 30

Ile Asp Gly Thr Gly Glu Gly Leu Arg Cys Lys Thr Arg Thr Leu Asp
35 40 45

Ser Glu Pro Lys Cys Val Glu Glu Leu Pro Glu Trp Asn Phe Asp Gly
50 55 60

Ser Ser Thr Leu Gln Ser Glu Gly Ser Asn Ser Asp Met Tyr Leu Val
65 70 75 80

Pro Ala Ala Met Phe Arg Asp Pro Phe Arg Lys Asp Pro Asn Lys Leu
85 90 95

Val Leu Cys Glu Val Phe Lys Tyr Asn Arg Arg Pro Ala Glu Thr Asn
100 105 110

Leu Arg His Thr Cys Lys Arg Ile Met Asp Met Val Ser Asn Gln His
115 120 125

Pro Trp Phe Gly Met Glu Gln Glu Tyr Thr Leu Met Gly Thr Asp Gly
130 135 140

His Pro Phe Gly Trp Pro Ser Asn Gly Phe Pro Gly Pro Gln Gly Pro
145 150 155 160

Tyr Tyr Cys Gly Val Gly Ala Asp Arg Ala Tyr Gly Arg Asp Ile Val
165 170 175

Glu Ala His Tyr Arg Ala Cys Leu Tyr Ala Gly Val Lys Ile Ala Gly
180 185 190

Thr Asn Ala Glu Val Met Pro Ala Gln Trp Glu Phe Gln Ile Gly Pro
195 200 205

Cys Glu Gly Ile Ser Met Gly Asp His Leu Trp Val Ala Arg Phe Ile
210 215 220

Leu His Arg Val Cys Glu Asp Phe Gly Val Ile Ala Thr Phe Asp Pro
225 230 235 240

Lys Pro Ile Pro Gly Asn Trp Asn Gly Ala Gly Cys His Thr Asn Phe
245 250 255

Ser Thr Lys Ala Met Arg Glu Glu Asn Gly Leu Lys Tyr Ile Glu Glu
260 265 270

Ala Ile Glu Lys Leu Ser Lys Arg His Gln Tyr His Ile Arg Ala Tyr

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 275 280 285

Asp Pro Lys Gly Gly Leu Asp Asn Ala Arg Arg Leu Thr Gly Phe His
 290 295 300

Glu Thr Ser Asn Ile Asn Asp Phe Ser Ala Gly Val Ala Asn Arg Ser
 305 310 315 320

Ala Ser Ile Arg Ile Pro Arg Thr Val Gly Gln Glu Lys Lys Gly Tyr
 325 330 335

Phe Glu Asp Arg Arg Pro Ser Ala Asn Cys Asp Pro Phe Ser Val Thr
 340 345 350

Glu Ala Leu Ile Arg Thr Cys Leu Leu Asn Glu Thr Gly Asp Glu Pro
 355 360 365

Phe Gln Tyr Lys Asn
 370

<210> 193
 <211> 379
 <212> PRT
 <213> Homo sapiens

<400> 193

Met Glu Gln Leu Ser Ser Ala Asn Thr Arg Phe Ala Leu Asp Leu Phe
 1 5 10 15

Leu Ala Leu Ser Glu Asn Asn Pro Ala Gly Asn Ile Phe Ile Ser Pro
 20 25 30

Phe Ser Ile Ser Ser Ala Met Ala Met Val Phe Leu Gly Thr Arg Gly
 35 40 45

Asn Thr Ala Ala Gln Leu Ser Lys Thr Phe His Phe Asn Thr Val Glu
 50 55 60

Glu Val His Ser Arg Phe Gln Ser Leu Asn Ala Asp Ile Asn Lys Arg
 65 70 75 80

Gly Ala Ser Tyr Ile Leu Lys Leu Ala Asn Arg Leu Tyr Gly Glu Lys
 85 90 95

Thr Tyr Asn Phe Leu Pro Glu Phe Leu Val Ser Thr Gln Lys Thr Tyr
 100 105 110

Gly Ala Asp Leu Ala Ser Val Asp Phe Gln His Ala Ser Glu Asp Ala
 115 120 125

Arg Lys Thr Ile Asn Gln Trp Val Lys Gly Gln Thr Glu Gly Lys Ile
 130 135 140

Pro Glu Leu Leu Ala Ser Gly Met Val Asp Asn Met Thr Lys Leu Val
 145 150 155 160

Leu Val Asn Ala Ile Tyr Phe Lys Gly Asn Trp Lys Asp Lys Phe Met
 165 170 175

Lys Glu Ala Thr Thr Asn Ala Pro Phe Arg Leu Asn Lys Lys Asp Arg
 180 185 190

Lys Thr Val Lys Met Met Tyr Gln Lys Lys Lys Phe Ala Tyr Gly Tyr
 195 200 205

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ile Glu Asp Leu Lys Cys Arg Val Leu Glu Leu Pro Tyr Gln Gly Glu
 210 215 220

Glu Leu Ser Met Val Ile Leu Leu Pro Asp Asp Ile Glu Asp Glu Ser
 225 230 235 240

Thr Gly Leu Lys Lys Ile Glu Glu Gln Leu Thr Leu Glu Lys Leu His
 245 250 255

Glu Trp Thr Lys Pro Glu Asn Leu Asp Phe Ile Glu Val Asn Val Ser
 260 265 270

Leu Pro Arg Phe Lys Leu Glu Glu Ser Tyr Thr Leu Asn Ser Asp Leu
 275 280 285

Ala Arg Leu Gly Val Gln Asp Leu Phe Asn Ser Ser Lys Ala Asp Leu
 290 295 300

Ser Gly Met Ser Gly Ala Arg Asp Ile Phe Ile Ser Lys Ile Val His
 305 310 315 320

Lys Ser Phe Val Glu Val Asn Glu Glu Gly Thr Glu Ala Ala Ala Ala
 325 330 335

Thr Ala Gly Ile Ala Thr Phe Cys Met Leu Met Pro Glu Glu Asn Phe
 340 345 350

Thr Ala Asp His Pro Phe Leu Phe Phe Ile Arg His Asn Ser Ser Gly
 355 360 365

Ser Ile Leu Phe Leu Gly Arg Phe Ser Ser Pro
 370 375

<210> 194
 <211> 271
 <212> PRT
 <213> Homo sapiens

<400> 194

Met Ala Ala Pro Gln Asp Val His Val Arg Ile Cys Asn Gln Glu Ile
 1 5 10 15

Val Lys Phe Asp Leu Glu Val Lys Ala Leu Ile Gln Asp Ile Arg Asp
 20 25 30

Cys Ser Gly Pro Leu Ser Ala Leu Thr Glu Leu Asn Thr Lys Val Lys
 35 40 45

Glu Lys Phe Gln Gln Leu Arg His Arg Ile Gln Pro Val Leu Tyr Gln
 50 55 60

Arg Ala Phe Ile Trp Thr Ala Ser Thr Phe Phe Phe Lys Leu Thr Tyr
 65 70 75 80

Ser Leu Thr Asp Phe Ser Ser Thr Gln His Asp Phe Asn Ser Pro Thr
 85 90 95

Thr Pro Val Thr Phe Ser Asp Leu Glu Gln Leu Ala Lys Glu Gln Asp
 100 105 110

Lys Glu Ser Glu Lys Gln Leu Leu Leu Gln Glu Val Glu Asn His Lys
 115 120 125

Lys Gln Met Leu Ser Asn Gln Ala Ser Trp Arg Lys Ala Asn Leu Thr
 130 135 140

Protein complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Cys Lys Ile Ala Ile Asp Asn Leu Glu Lys Ala Glu Leu Leu Gln Gly
145 150 155 160

Gly Asp Leu Leu Arg Gln Arg Lys Thr Thr Lys Glu Ser Leu Ala Gln
165 170 175

Thr Ser Ser Thr Ile Thr Glu Ser Leu Met Gly Ile Ser Arg Met Met
180 185 190

Ala Gln Gln Val Gln Gln Ser Glu Glu Ala Met Gln Ser Leu Val Thr
195 200 205

Ser Ser Arg Thr Ile Leu Asp Ala Asn Glu Glu Phe Lys Ser Met Ser
210 215 220

Gly Thr Ile Gln Leu Gly Arg Lys Leu Ile Thr Lys Tyr Asn Arg Arg
225 230 235 240

Glu Leu Thr Asp Lys Leu Leu Ile Phe Leu Ala Leu Arg Leu Phe Leu
245 250 255

Ala Thr Val Leu Tyr Ile Val Lys Lys Arg Leu Phe Pro Phe Leu
260 265 270

<210> 195
<211> 314
<212> PRT
<213> Homo sapiens

<400> 195

Met Glu Gly Val Glu Leu Lys Glu Glu Trp Gln Asp Glu Asp Phe Pro
1 5 10 15

Ile Pro Leu Pro Glu Asp Asp Ser Ile Glu Ala Asp Ile Leu Ala Ile
20 25 30

Thr Gly Pro Glu Asp Gln Pro Gly Ser Leu Glu Val Asn Gly Asn Lys
35 40 45

Val Arg Lys Lys Leu Met Ala Pro Asp Ile Ser Leu Thr Leu Asp Pro
50 55 60

Ser Asp Gly Ser Val Leu Ser Asp Asp Leu Asp Glu Ser Gly Glu Ile
65 70 75 80

Asp Leu Asp Gly Leu Asp Thr Pro Ser Glu Asn Ser Asn Glu Phe Glu
85 90 95

Trp Glu Asp Asp Leu Pro Lys Pro Lys Thr Thr Glu Val Ile Arg Lys
100 105 110

Gly Ser Ile Thr Glu Tyr Thr Ala Ala Glu Glu Lys Glu Asp Gly Arg
115 120 125

Arg Trp Arg Met Phe Arg Ile Gly Glu Gln Asp His Arg Val Asp Met
130 135 140

Lys Ala Ile Glu Pro Tyr Lys Lys Val Ile Ser His Gly Gly Tyr Tyr
145 150 155 160

Gly Asp Gly Leu Asn Ala Ile Val Val Phe Ala Val Cys Phe Met Pro
165 170 175

Glu Ser Ser Gln Pro Asn Tyr Arg Tyr Leu Met Asp Asn Leu Phe Lys
180 185 190

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Tyr Val Ile Gly Thr Leu Glu Leu Leu Val Ala Glu Asn Tyr Met Ile
195 200 205

Val Tyr Leu Asn Gly Ala Thr Thr Arg Arg Lys Met Pro Ser Leu Gly
210 215 220

Trp Leu Arg Lys Cys Tyr Gln Gln Ile Asp Arg Arg Leu Arg Lys Asn
225 230 235 240

Leu Lys Ser Leu Ile Ile Val His Pro Ser Trp Phe Ile Arg Thr Leu
245 250 255

Leu Ala Val Thr Arg Pro Phe Ile Ser Ser Lys Phe Ser Gln Lys Ile
260 265 270

Arg Tyr Val Phe Asn Leu Ala Glu Leu Ala Glu Leu Val Pro Met Glu
275 280 285

Tyr Val Gly Ile Pro Glu Cys Ile Lys Gln Val Asp Gln Glu Leu Asn
290 295 300

Gly Lys Gln Asp Glu Pro Lys Asn Glu Gln
305 310

<210> 196
<211> 193
<212> PRT
<213> Homo sapiens

<400> 196

Met Ala Arg Ala Arg Gln Glu Gly Ser Ser Pro Glu Pro Val Glu Gly
1 5 10 15

Leu Ala Arg Asp Gly Pro Arg Pro Phe Pro Leu Gly Arg Leu Val Pro
20 25 30

Ser Ala Val Ser Cys Gly Leu Cys Glu Pro Gly Leu Ala Ala Ala Pro
35 40 45

Ala Ala Pro Thr Leu Leu Pro Ala Ala Tyr Leu Cys Ala Pro Thr Ala
50 55 60

Pro Pro Ala Val Thr Ala Ala Leu Gly Gly Ser Arg Trp Pro Gly Gly
65 70 75 80

Pro Arg Ser Arg Pro Arg Gly Pro Arg Pro Asp Gly Pro Gln Pro Ser
85 90 95

Leu Ser Leu Ala Glu Gln His Leu Glu Ser Pro Val Pro Ser Ala Pro
100 105 110

Gly Ala Leu Ala Gly Gly Pro Thr Gln Ala Ala Pro Gly Val Arg Gly
115 120 125

Glu Glu Glu Gln Trp Ala Arg Glu Ile Gly Ala Gln Leu Arg Arg Met
130 135 140

Ala Asp Asp Leu Asn Ala Gln Tyr Glu Arg Arg Arg Gln Glu Glu Gln
145 150 155 160

Gln Arg His Arg Pro Ser Pro Trp Arg Val Leu Tyr Asn Leu Ile Met
165 170 175

Gly Leu Leu Pro Leu Pro Arg Gly His Arg Ala Pro Glu Met Glu Pro

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt
 180 185 190

Asn

<210> 197
 <211> 648
 <212> PRT
 <213> Homo sapiens

<400> 197

Met Glu His Ile Gln Gly Ala Trp Lys Thr Ile Ser Asn Gly Phe Gly
 1 5 10 15

Phe Lys Asp Ala Val Phe Asp Gly Ser Ser Cys Ile Ser Pro Thr Ile
 20 25 30

Val Gln Gln Phe Gly Tyr Gln Arg Arg Ala Ser Asp Asp Gly Lys Leu
 35 40 45

Thr Asp Pro Ser Lys Thr Ser Asn Thr Ile Arg Val Phe Leu Pro Asn
 50 55 60

Lys Gln Arg Thr Val Val Asn Val Arg Asn Gly Met Ser Leu His Asp
 65 70 75 80

Cys Leu Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu Cys Cys
 85 90 95

Ala Val Phe Arg Leu Leu His Glu His Lys Gly Lys Lys Ala Arg Leu
 100 105 110

Asp Trp Asn Thr Asp Ala Ala Ser Leu Ile Gly Glu Glu Leu Gln Val
 115 120 125

Asp Phe Leu Asp His Val Pro Leu Thr Thr His Asn Phe Ala Arg Lys
 130 135 140

Thr Phe Leu Lys Leu Ala Phe Cys Asp Ile Cys Gln Lys Phe Leu Leu
 145 150 155 160

Asn Gly Phe Arg Cys Gln Thr Cys Gly Tyr Lys Phe His Glu His Cys
 165 170 175

Ser Thr Lys Val Pro Thr Met Cys Val Asp Trp Ser Asn Ile Arg Gln
 180 185 190

Leu Leu Leu Phe Pro Asn Ser Thr Ile Gly Asp Ser Gly Val Pro Ala
 195 200 205

Leu Pro Ser Leu Thr Met Arg Arg Met Arg Glu Ser Val Ser Arg Met
 210 215 220

Pro Val Ser Ser Gln His Arg Tyr Ser Thr Pro His Ala Phe Thr Phe
 225 230 235 240

Asn Thr Ser Ser Pro Ser Ser Glu Gly Ser Leu Ser Gln Arg Gln Arg
 245 250 255

Ser Thr Ser Thr Pro Asn Val His Met Val Ser Thr Thr Leu Pro Val
 260 265 270

Asp Ser Arg Met Ile Glu Asp Ala Ile Arg Ser His Ser Glu Ser Ala
 275 280 285

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Ser Pro Ser Ala Leu Ser Ser Ser Pro Asn Asn Leu Ser Pro Thr Gly
290 295 300

Trp Ser Gln Pro Lys Thr Pro Val Pro Ala Gln Arg Glu Arg Ala Pro
305 310 315 320

Val Ser Gly Thr Gln Glu Lys Asn Lys Ile Arg Pro Arg Gly Gln Arg
325 330 335

Asp Ser Ser Tyr Tyr Trp Glu Ile Glu Ala Ser Glu Val Met Leu Ser
340 345 350

Thr Arg Ile Gly Ser Gly Ser Phe Gly Thr Val Tyr Lys Gly Lys Trp
355 360 365

His Gly Asp Val Ala Val Lys Ile Leu Lys Val Val Asp Pro Thr Pro
370 375 380

Glu Gln Phe Gln Ala Phe Arg Asn Glu Val Ala Val Leu Arg Lys Thr
385 390 395 400

Arg His Val Asn Ile Leu Leu Phe Met Gly Tyr Met Thr Lys Asp Asn
405 410 415

Leu Ala Ile Val Thr Gln Trp Cys Glu Gly Ser Ser Leu Tyr Lys His
420 425 430

Leu His Val Gln Glu Thr Lys Phe Gln Met Phe Gln Leu Ile Asp Ile
435 440 445

Ala Arg Gln Thr Ala Gln Gly Met Asp Tyr Leu His Ala Lys Asn Ile
450 455 460

Ile His Arg Asp Met Lys Ser Asn Asn Ile Phe Leu His Glu Gly Leu
465 470 475 480

Thr Val Lys Ile Gly Asp Phe Gly Leu Ala Thr Val Lys Ser Arg Trp
485 490 495

Ser Gly Ser Gln Gln Val Glu Gln Pro Thr Gly Ser Val Leu Trp Met
500 505 510

Ala Pro Glu Val Ile Arg Met Gln Asp Asn Asn Pro Phe Ser Phe Gln
515 520 525

Ser Asp Val Tyr Ser Tyr Gly Ile Val Leu Tyr Glu Leu Met Thr Gly
530 535 540

Glu Leu Pro Tyr Ser His Ile Asn Asn Arg Asp Gln Ile Ile Phe Met
545 550 555 560

Val Gly Arg Gly Tyr Ala Ser Pro Asp Leu Ser Lys Leu Tyr Lys Asn
565 570 575

Cys Pro Lys Ala Met Lys Arg Leu Val Ala Asp Cys Val Lys Lys Val
580 585 590

Lys Glu Glu Arg Pro Leu Phe Pro Gln Ile Leu Ser Ser Ile Glu Leu
595 600 605

Leu Gln His Ser Leu Pro Lys Ile Asn Arg Ser Ala Ser Glu Pro Ser
610 615 620

Leu His Arg Ala Ala His Thr Glu Asp Ile Asn Ala Cys Thr Leu Thr
625 630 635 640

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Thr Ser Pro Arg Leu Pro Val Phe
645

<210> 198
<211> 399
<212> PRT
<213> Homo sapiens

<400> 198

Met Tyr Ser Pro Arg Gly Ser Gln Gly Arg Gly Thr Ala Glu Ala Thr
1 5 10 15

Ala Asn Ser Pro Ser Pro Pro Ile Ala Pro Ser His Ser Arg Val Thr
20 25 30

Phe Ser Leu Ser Thr Leu His Thr Leu Ser Pro Pro Pro Arg Pro Phe
35 40 45

Pro Ser Val Ser Arg Ala Ala Ala Gln Lys Pro His His Leu His Pro
50 55 60

His Ile Leu Leu Ala Gly Ser Ala Ala Val Pro Pro Arg Val Leu Lys
65 70 75 80

Ala Glu Met Asn Asn Thr Ala Ala Ser Pro Met Ser Thr Ala Thr Ser
85 90 95

Ser Ser Gly Arg Ser Thr Gly Lys Ser Ile Ser Phe Ala Thr Glu Leu
100 105 110

Gln Ser Met Met Tyr Ser Leu Gly Asp Ala Arg Arg Pro Leu His Glu
115 120 125

Thr Ala Val Leu Val Glu Asp Val Val His Thr Gln Leu Ile Asn Leu
130 135 140

Leu Gln Gln Ala Ala Glu Val Ser Gln Leu Arg Gly Ala Arg Val Ile
145 150 155 160

Thr Pro Glu Asp Leu Leu Phe Leu Met Arg Lys Asp Lys Lys Lys Leu
165 170 175

Arg Arg Leu Leu Lys Tyr Met Phe Ile Arg Asp Tyr Lys Ser Lys Ile
180 185 190

Val Lys Gly Ile Asp Glu Asp Asp Leu Leu Glu Asp Lys Leu Ser Gly
195 200 205

Ser Asn Asn Ala Asn Lys Arg Gln Lys Ile Ala Gln Asp Phe Leu Asn
210 215 220

Ser Ile Asp Gln Thr Gly Glu Leu Leu Ala Met Phe Glu Asp Asp Glu
225 230 235 240

Ile Asp Glu Val Lys Gln Glu Arg Met Glu Arg Ala Glu Arg Gln Thr
245 250 255

Arg Ile Met Asp Ser Ala Gln Tyr Ala Glu Phe Cys Glu Ser Arg Gln
260 265 270

Leu Ser Phe Ser Lys Lys Ala Ser Lys Phe Arg Asp Trp Leu Asp Cys
275 280 285

Ser Ser Met Glu Ile Lys Pro Asn Val Val Ala Met Glu Ile Leu Ala

Protein Complexes of cellular networks underlying the development of cancer and other diseases.ST25.txt

Tyr Leu Ala Tyr Glu Thr Val Ala Gln Leu Val Asp Leu Ala Leu Leu
305 310 315 320

Val Arg Gln Asp Met Val Thr Lys Ala Gly Asp Pro Phe Ser His Ala
325 330 335

Ile Ser Ala Thr Phe Ile Gln Tyr His Asn Ser Ala Glu Ser Thr Ala
340 345 350

Ala Cys Gly Val Glu Ala His Ser Asp Ala Ile Gln Pro Cys His Ile
355 360 365

Arg Glu Ala Ile Arg Arg Tyr Ser His Arg Ile Gly Pro Leu Ser Pro
370 375 380

Phe Thr Asn Ala Tyr Arg Arg Asn Gly Met Ala Phe Leu Ala Cys
385 390 395